```
Qy      337 RGLGDHQLRVLDTNIQLKPFLLSVPQVTVLDVLQLELQEDDVVVMATDGLWDVLSNEQVA 396
             | |||:  : :|         :   :    |:|        :  |   :||:  :::| ||:|||:|||::
Db      200 PALGDYDYKCVDGKGPTEQLVSPEPEV----YEILRAEEDEFIILACDGIWDVMSNEELC 255

Qy      397 WLVRSPLPGNQEDPHRFSELAQMLIHSTQGKEDSLT 432
                |:| |   :  :   :   :  :     :|   :|   |:::
Db      256 EYVKSRLPVSDDLENVCNWVVDTCLH-KGSRDNMS 289


RESULT 15
P2CB_HUMAN
ID   P2CB_HUMAN     STANDARD;      PRT;   479 AA.
AC   O75688; Q9HAY8;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta).
GN   PPM1B OR PP2CB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM BETA 1).
RC   TISSUE=Liver;
RX   MEDLINE=98349020; PubMed=9684878;
RA   Marely A.E., Kline A., Crabtree G., Sullivan J.E., Beri R.K.;
RT   "The cloning expression and tissue distribution of human PP2Cbeta.";
RL   FEBS Lett. 431:121-124(1998).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM BETA-2).
RX   PubMed=10945995;
RA   Cheng A., Kaldis P., Solomon M.J.;
RT   "Dephosphorylation of human cyclin-dependent kinases by protein
RT   phosphatase type 2Calpha and beta2 isoforms.";
RL   J. Biol. Chem. 275:34744-34749(2000).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS BETA 1 AND BETA 2)
RA   Seroussi E., Shani N., Hayut A., Faier S., Ben-Meir D., Divinski I.,
RA   [illegible]
RT   "Protein phosphatase 1B. Cloning and characterization of two major
RT   transcripts generated by alternative use of 3' exons.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM BETA-2).
RC   TISSUE=Adrenal gland;
RA   Peng Y., Gu Y., Li Y., Fu S., Gu J., Zhang L., Jiang C., Yu Y.,
RA   Hao Z., Wang Y., Chen Z., Fu G.,
RT   "A novel gene expressed in human adrenal gland.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: ENZYME WITH A BROAD SPECIFICITY. DEPHOSPHORYLATES CDK2
CC       AND CDK6 IN VITRO.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC   -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: At least 2 isoforms, Beta-1/Beta-X/PPM1B2
CC       (shown here) and Beta-2/PPM1B1; are produced by alternative
CC       splicing.
CC    !- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART AND SKELETAL MUSCLE.
CC   -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC   --------------------------------------------------------------------------
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AJ005801; CAA06704.1; -.
DR   EMBL; AF294792; AAG02232.1; -.
DR   EMBL; AJ271832; CAC27992.1; -.
DR   EMBL; AJ271835; CAC27993.1; -.
DR   EMBL; AF136972; AAG49433.1; -.
DR   HSSP; P35813; 1A6Q.
DR   Genew; HGNC:9276; PPM1B.
DR   MIM; 603770; -.
DR   InterPro; IPR001932; PP2C-like.
DR   InterPro; IPR000222; PP2C.
DR   Pfam; PF00481; PP2C; 1.
DR   SMART; SM00331; PP2C_SIG; 1.
DR   SMART; SM00332; PP2Cc; 1.
DR   PROSITE; PS01032; PP2C; 1.
KW   Hydrolase, Magnesium, Manganese; Multigene family;
KW   Alternative splicing.
FT   METAL         37     37       MANGANESE 1 (BY SIMILARITY).
FT   METAL         38     38       MANGANESE 1 (BY SIMILARITY).
FT   METAL         60     60       MANGANESE 1 AND 2 (BY SIMILARITY).
FT   METAL        243    243       MANGANESE 2 (BY SIMILARITY).
FT   METAL        286    286       MANGANESE 2 (BY SIMILARITY).
FT   VARSPLIC     379    387       ASDEAEESG -> GAGDLEDPW (IN ISOFORM BETA-
FT                                 2).
FT   VARSPLIC     388    479       MISSING (IN ISOFORM BETA-2).
SQ   SEQUENCE   479 AA,  52642 MW;  A3A5797AD263DFBD CRC64;

  Query Match             7.7%;  Score 186.5;  DB 1;  Length 479;
  Best Local Similarity   20.6%;  Pred. No. 1.1e-06;
  Matches   69;  Conservative   57;  Mismatches  106;  Indels  103;  Gaps   10;

Qy      105 EEWLTLCPEEFLTGHYWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHL 164
             |:|                ::|::||| |    |            :  |      || :
Db       51 EDW------------SFFAVYDGHAGSRVA-------NYCSTHLLEHITTN---------- 82

Qy      165 NGRCICPSDPQFVEEKGIRAE---DLVIGALESAFQECDEVIGR--ELEASGQMGGCTAL 219
                        |  :    :  |    |     :  |     :  :  |  :  ||  :         :                | ||:
Db       83    ---EDFRAAGKSGSALELSVENVKNGIRTGFLKIDEYMRNFSDLRNGMDRSGSTAV 135

Qy      220 VAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEFTP--ETERQRIQQLAFVYPELLAGEF 277
                :       :|   | ||||||:| |    ::      :  :     |        |::|:|
Db      136 GVMISPKHIYFINCGDSRAVLYRNGQVCFSTQDHKPCNPREKERIQ-------------- 181

Qy      278 IRLEFPRRLKGEDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSR 337
                          :  :   |:  :                                  |:  |:|||||
Db      182       ------NAGGSVMIQ------------------------------RVNGSLAVSR 200

Qy      338 GLGDHQLRVLDTNIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAW 397
              |||:   : :|         :   :    |:|        :  |   :||:  :::| ||:|||:|||::
Db      201 ALGDYDYKCVDGKGPTEQLVSPEPEV---YEILRAEEDEFIILACDGIWDVMSNEELCE 256

Qy      398 LVRSPLPGNQEDPHRFSELAQMLIHSTQGKEDSLT 432
              |:| |   :  :   :   :  :     :|   :|   |:::
Db      257 YVKSRLPVSDDLENVCNWVVDTCLH-KGSRDNMS 289


Search completed. February 24, 2003, 14:35:00
Job time : 16 secs
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CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; D17411; BAA04233.1; -.
DR   EMBL; D17412; BAA04234.1; -.
DR   EMBL; D45859; BAA08293.1; -.
DR   EMBL; D45860; BAA08294.1; -.
DR   EMBL; D45861; BAA08295.1; -.
DR   EMBL; U09218; AAB60442.1; -.
DR   EMBL; AB007598; BAA84471.1; -.
DR   EMBL; AB007794; BAA84471.1; JOINED.
DR   EMBL; AB007795; BAA84471.1; JOINED.
DR   EMBL; AB007796; BAA84471.1; JOINED.
DR   EMBL; AB007797; BAA84471.1; JOINED.
DR   PIR; S34780; S34780.
DR   HSSP; P35813; 1A6Q.
DR   MGD; MGI:101841; Ppm1b.
DR   InterPro; IPR001932; PP2C-like.
DR   InterPro; IPR000222; PP2C.
DR   Pfam; PF00481; PP2C; 1.
DR   SMART; SM00331; PP2C_SIG; 1.
DR   SMART; SM00332; PP2Cc; 1.
DR   PROSITE; PS01032; PP2C; 1.
KW   Hydrolase; Magnesium; Manganese; Multigene family;
KW   Alternative splicing.
FT   METAL        37     37       MANGANESE 1 (BY SIMILARITY).
FT   METAL        38     38       MANGANESE 1 (BY SIMILARITY).
FT   METAL        60     60       MANGANESE 1 AND 2 (BY SIMILARITY).
FT   METAL       243    243       MANGANESE 2 (BY SIMILARITY).
FT   METAL       286    286       MANGANESE 2 (BY SIMILARITY).
FT   VARSPLIC    375    390       GAGDLEDSLVAL -> VQGHLTFKYLE (IN ISOFORM
FT                                BETA 2).
FT   VARSPLIC    375    390       GAGDLEDSLVAL -> FYQPSTAYSDNVFLL (IN
FT                                ISOFORM BETA 3).
FT   VARSPLIC    375    390       GAGDLEDSLVAL -> MAELSTSTCKPS (IN ISOFORM
FT                                BETA 4).
FT   VARSPLIC    388    390       VAL -> FYQPSTAYSDNVFLL (IN ISOFORM BETA
FT                                5).
SQ   SEQUENCE   390 AA;  42795 MW;  255C07B4276B9FD CRC64;

  Query Match             7.8%;  Score 190;  DB 1;  Length 390;
  Best Local Similarity   23.1%;  Pred. No. 4.6e-07;
  Matches   71;  Conservative   51;  Mismatches   99;  Indels   94;  Gaps   12;

Qy        120 YWALFDGHGGPAAAILAANTLHSCLRRQLEAVV--EGLVATQPPMHLNGRCICPSDPQFV 177
              :: ::| : :   |          : :    | | :    |    !        :|  : ||     |
Db         55 FFAVYDGHAGSRVA-------NYCSIHLLEHIITNEDFRAADK---SGSALEPS--V 99

Qy        178 E--EKGIRAEDLVIGALESAFQECDEVIGR--ELEASGQMGGCTALVAVSLQGKLYMANA 233
              |  : :  ||              : : : ||  :      :|          | ||:  :        :|   |
Db        100 ESVKIGIR-------TGFLKIDEYMRNFSDLRNGMDRSGSTAVGVMVSPKHMYFINC 149

Qy        234 GDSRAILVRRDEIRPLSFEFTP-EIERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDL 291
              |||||:| |   ::      :  :    |     |::|||                                  :
Db        150 GDSRAVLCRNGQVCFSTQDHKPCNPVEKERIQ-------------------------NA 183

Qy        292 GQKVLFRDHHMSGWSYKFVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNI 351
              |  |: :                                         |: |:|||| |||:   :  :|
Db        184 GGSVMIQ-----------------------------RVNGSLAVSRALGDYDYKCVDGKG 214

Qy        352 QLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPH 411
                 :    :    :|:        :  :  :|:: |::! ||:|:|:|:::    |:|  |   :  :   :
Db        215 PIEQLVSGEPEV-----TEIVRAEDDEFVVLACDGIWDVMSNEELCEFVKSRLEVSDDLEN 270

Qy        412 RFGKLAQMLIHSIQGKEDSLT 432
                 : :    :    :|  |:::
Db        271 VCNWVVDTCLH-KGSRDNMS 289
```

```
RESULT 14
P2CB_BOVIN
ID   P2CB_BOVIN     STANDARD;      PRT;   387 AA.
AC   O62830;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta).
GN   PPM1B.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Retina;
RX   MEDLINE=98146173; PubMed=9486768;
RA   Klumpp S., Selke D., Fischer D., Baumann A., Mueller F., Thanos S.;
RT   "Protein phosphatase type-2C isozymes present in vertebrate retinae:
RT   purification, characterization, and localization in photoreceptors.";
RL   J. Neurosci. Res. 51:328-338(1998).
CC   -!- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC   -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AJ005458; CAA06555.1; -.
DR   HSSP; P35813; 1A6Q.
DR   InterPro; IPR001932; PP2C-like.
DR   InterPro; IPR000222; PP2C.
DR   Pfam; PF00481; PP2C; 1.
DR   SMART; SM00331; PP2C_SIG; 1.
DR   SMART; SM00332; PP2Cc; 1.
DR   PROSITE; PS01032; PP2C; 1.
KW   Hydrolase; Magnesium; Manganese; Multigene family.
FT   METAL        37     37       MANGANESE 1 (BY SIMILARITY).
FT   METAL        38     38       MANGANESE 1 (BY SIMILARITY).
FT   METAL        60     60       MANGANESE 1 AND 2 (BY SIMILARITY).
FT   METAL       243    243       MANGANESE 2 (BY SIMILARITY).
FT   METAL       286    286       MANGANESE 2 (BY SIMILARITY).
SQ   SEQUENCE   387 AA;  42834 MW;  D70B95141250FFB1 CRC64;

  Query Match             7.8%;  Score 189.5;  DB 1;  Length 387;
  Best Local Similarity   22.3%;  Pred. No. 5e-07;
  Matches   75;  Conservative   56;  Mismatches  100;  Indels  105;  Gaps   13;

Qy        105 EEWLTLCPEEFLTGHYWALFDGHGGPAAAILAANTLHSCLRRQLEAVV--EGLVATQPPM 162
              |:|                 ::|::|||  |    |             :  |      ||  :     |     |
Db         51 EDW------------SFFAVYDGHAGSRVA------NYCSIHLLEHIITNNEDFRAAGK-- 90

Qy        163 HLNGRCICPSDPQFVE--EKGIRAEDLVIGALESAFQECDEVIGR--ELEASGQMGGCTA 218
                  :|   : ||      ||   : |||                  : | : || :      :|          | ||
Db         91 --SGSALEPS---VENVKNGIR----------TGFLKIDEYMRNFSDLRNGMDRSGSTA 134

Qy        219 LVAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEFTP-EIERQRIQQLAFVYPELLAGE 276
              :   :          :|    | |||||:| |    ::        :  :    |        |::|||
Db        135 VGVMISPKHIYFINCGDSRAVLYRSGQVCFSTQDHKPCNPREKERIQ-----------  181

Qy        277 FTRLEFPRRLKGDDLGQKVLFRDHHMSGWSYKFVEKSDLKYPLIHGQGRQARLLGTLAVS 336
                                 :  |    |:  :                                          |:  |:||||
Db        182 ---------NAGGSVMIQ---------------------------------RVNGSLAVS 199
```

```
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE Liver;
RX   MEDLINE 93203367; PubMed 1312947;
RA   Wenk J., Trompeter H.-I., Pettrich K. G., Cohen P.T.W., Campbell D.G.,
RA   Mieskes G.;
RT   "Molecular cloning and primary structure of a protein phosphatase 2C
RT   isoform.";
RL   FEBS Lett. 297:135-138(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE Brain;
RX   MEDLINE 95169115; PubMed-7532404;
RA   Schafer K., Braun T.;
RT   "Monoclonal anti-FLAG antibodies react with a new isoform of rat Mg2+
RT   dependent protein phosphatase beta.";
RL   Biochem. Biophys. Res. Commun. 207:708-714(1995).
CC    !  FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC   -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: At least 2 isoforms, 1/Beta 1 (shown here)
CC       and 2/Beta MPP; are produced by alternative splicing. Isoforms
CC       appear to differ in their C-terminus.
CC   -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; S90449; AAB21898.1; -.
DR   EMBL; S74572; AAB33430.1; -.
DR   PIR; S20392; S20392.
DR   HSSP; P35813; 1A6Q.
DR   InterPro; IPR001932; PP2C-like.
DR   InterPro; IPR000222; PP2C.
DR   Pfam; PF00481; PP2C; 1.
DR   SMART; SM00331; PP2C_SIG; 1.
DR   SMART; SM00332; PP2Cc; 1.
DR   PROSITE; PS01032; PP2C; 1.
KW   Hydrolase; Magnesium; Manganese; Multigene family;
KW   Alternative splicing.
FT   METAL        37     37       MANGANESE 1 (BY SIMILARITY).
FT   METAL        38     38       MANGANESE 1 (BY SIMILARITY).
FT   METAL        60     60       MANGANESE 1 AND 2 (BY SIMILARITY).
FT   METAL       243    243       MANGANESE 2 (BY SIMILARITY).
FT   METAL       286    286       MANGANESE 2 (BY SIMILARITY).
FT   VARSPLIC    379    390       GAGLLEDSLVAL -> FYQPSIPYSDNVSYYEWQT (IN
FT                                ISOFORM 2).
SQ   SEQUENCE   390 AA;  42899 MW;  D147615BC2FA140B CRC64;

  Query Match             7.9%;  Score 191.5;  DB 1;  Length 390;
  Best Local Similarity   21.2%;  Pred. No. 3.6e-07;
  Matches   71;  Conservative   55;  Mismatches  106;  Indels  103;  Gaps   10;

Qy        105 EEWLTLCPEEFLTGHYWALFDGHGGPAAAILAANTLHSCLRPQLEAVVEGLVATQPPMHL 164
              |:                    ::|::|||  |    |            :  |    || :
Db         51 EDW-----------SFFAVYDGHAGSRVA-------NYCSIHLLEHITTN---------- 82

Qy        165 [illegible] 219
                        | :   :: |    |      :  |      :  : |  : ||  :      :|         | ||:
Db         83 -------[illegible]GSTAV 135

Qy        220 VAVF[illegible]LAGEF 277
                :        :|   | ||||||:|  |    ::       :  :    |       |::|||
Db        136 [illegible] 181

Qy        278 [illegible]GTLAVSR 337
                             : |   |:  :                                   |:  |:|||||
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Db        182             NAGGSVMIQ                                  RVNGSLAVSR 200

Qy        338 [illegible]VAW 397
                  |||:   :  :|        :  :    |:|          :  |    :||:  ||:|  ||:|||:|||::
Db        201 ALGDYDYKCV[illegible]LEV      YETLKAEDDEFVVLA[illegible]GIWDVMSNEELCE 256

Qy        398 LVRSFLPCNQEDPHRFSKLAQMLIHSIQGKEDSLI 432
                  | | |    :  :    :   :  :        :|     :|    |:::
Db        257 FVNSRLEVSDDLENVCNWVVDTCLH  KGSRDNMS 289


RESULT 13
P2CB_MOUSE
ID   P2CB_MOUSE      STANDARD;      PRT;   390 AA.
AC   P36993;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta) (IA)
DE   (Protein phosphatase 1B).
GN   PPM1B OR PPPM1B OR PP2C2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID 10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE 94099613; PubMed-8274020;
RA   Terasawa T., Kobayashi T., Murakami T., Ohnishi M., Kato S.,
RA   Tanaka O., Kondo H., Yamamoto H., Takeuchi T., Tamura S.;
RT   "Molecular cloning of a novel isotype of Mg(2+)-dependent protein
RT   phosphatase beta (type 2C beta) enriched in brain and heart.";
RL   Arch. Biochem. Biophys. 307:342-349(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (BETA 3, BETA 4 AND BETA 5).
RC   TISSUE-Testis;
RX   MEDLINE-95251388; PubMed-7733667;
RA   Kato S., Terasawa T., Kobayashi T., Ohnishi M., Sasahara Y.,
RA   Kusuda K., Yanagawa Y., Hiraga A., Matsui Y., Tamura S.;
RT   "Molecular cloning and expression of mouse Mg(2+) dependent protein
RT   phosphatase beta-4 (type 2C beta-4).";
RL   Arch. Biochem. Biophys. 318:387-393(1995).
RN   [3]
RP   SEQUENCE FROM N.A. (BETA 3 AND BETA-4).
RC   TISSUE-Testis;
RX   MEDLINE-94313028; PubMed-8038726;
RA   Hou E.W., Kawai Y., Miyasaka H., Li S.S.;
RT   "Molecular cloning and expression of cDNAs encoding two isoforms of
RT   protein phosphatase 2C beta from mouse testis.";
RL   Biochem. Mol. Biol. Int. 32:773-780(1994).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN-129/Sv;
RX   MEDLINE 99398339, PubMed 10469137;
RA   Ohnishi M., Chida N., Kobayashi T., Wang H., Ikeda S., Hanada M.,
RA   Yanagawa Y., Katsura K., Hiraga A., Tamura S.;
RT   "Alternative promoters direct tissue specific expression of the mouse
RT   protein phosphatase 2Cbeta gene.";
RL   Eur. J. Biochem. 263:736-745(1999).
CC    !  FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC    !  SUBUNIT: MONOMER (BY SIMILARITY).
CC   -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; BETA-1 (SHOWN HERE), BETA-2,
CC       BETA-3, BETA 4 AND BETA 5, ARE PRODUCED BY ALTERNATIVE SPLICING.
CC       THEY ONLY DIFFER IN THEIR C-TERMINUS.
CC    !  TISSUE SPECIFICITY: BETA 1 IS EXPRESSED UBIQUITOUSLY, BETA 2 IS
CC       EXPRESSED EXCLUSIVELY IN BRAIN AND HEART; BETA 4 IS EXPRESSED
CC       EXCLUSIVELY IN BRAIN AND INTESTINE, BETA 3 AND BETA 5 ARE
CC       EXPRESSED EXCLUSIVELY IN TESTIS AND INTESTINE.
CC   -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC   --------------------------------------------------------------------------
```

```
FT   CONFLICT    124    124       E -> Q (IN REF. 2).
SQ   SEQUENCE   281 AA;  31549 MW;  FA384B2541B28D58 CRC64;

  Query Match             8.4%;  Score 202;  DB 1;  Length 281;
  Best Local Similarity   22.5%;  Pred. No. 3.7e-08;
  Matches   93;  Conservative   48;  Mismatches  114;  Indels  158;  Gaps   15;

Qy         55 SRPVRSPARGRILEWNAGYAEIINAEKSLLNEEQAAGKRCIERCEPGALEEWLIQTPEE 114
              |   :   |       : :   | ||   |::        ||       |     | ::|
Db          5 SEILERPEIPYDIIYEV-GVAENKNGKFRSIMEDVHTYVENFAGRLDWG             52

Qy        115 FLIGHYWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDP 174
                    |:|:||||  |    |:        ||: :
Db         53       YFAVFDGHAGIQASKWCGKHIPIII              -            - -  77

Qy        175 QFVEEKGIRAEDL   VIGALESAFQECDEVIGRELEASGQMGGCTALVAV         222
                    |: | |::     |     |    :|     || |    :|    :      |||| | |
Db         78       EQNILAEEIRDVRDVLNDSFLAIDEEINTKLVGN    SGCTAAVCVLRWELPDSVS 130

Qy        223           SLQGKLYMANAGDSRAILVRRDEIRPLSPEFTPETERQRIQQLAFVYPELLAG 275
                         | |||  |: ||||  :| |                                   |
Db        131 DDSMDLAQHQRKLYIANVGDSRIVLFRN                           ---------G 159

Qy        276 EFTRLEFPRRLKGDDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLA 334
                  |: :                        ||    |        :|||::              |      ::|: | ||
Db        160 NSIRLLY                    DHKASDTLEMQRVEQAG -    --GLIMKSRVNGMLA 196

Qy        335 VSRGLGDHQLRVLDINIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQ 394
              |:| |||    :   |: :     ||    || ::|                 ||    :::| ||||||: ::
Db        197 VTRSLGD    KFFDSLVVGSPFTTSV-EIT ----      SEDKFLILACDGLWDVIDDQD 243

Qy        395 VAWLVRSFLPGNQEDPHRFSKLAQMLIHSTQGKEDSLTEEGQVSYDDVSVFVI 447
                  |::          |:              |::|:                  | |    : |:|:| |:
Db        244 ACELIKDIIEPNE             AAKVLVRYA          LENG   TTDNVTVMVV 279


RESULT 11
PDP2_HUMAN
ID   PDP2_HUMAN     STANDARD;      PRT;   529 AA.
AC   Q9P2J9;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   [Pyruvate dehydrogenase [lipoamide]] phosphatase 2, mitochondrial
DE   precursor (EC 3.1.3.43) (PDP 2) (Pyruvate dehydrogenase phosphatase,
DE   catalytic subunit 2) (PDPC 2).
GN   PDP2 OR KIAA1348.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20181126; PubMed=10718198;
RA   Nagase T., Kikuno R., Ishikawa K.-I., Hirosawa M., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XVI.
RT   The complete sequences of 150 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 7:65-73(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CATALYZES THE DEPHOSPHORYLATION AND CONCOMITANT
CC       REACTIVATION OF THE ALPHA SUBUNIT OF THE E1 COMPONENT OF THE
CC       PYRUVATE DEHYDROGENASE COMPLEX (BY SIMILARITY).
CC   -!- CATALYTIC ACTIVITY: [Pyruvate dehydrogenase (lipoamide)] phosphate
CC       + H(2)O = [pyruvate dehydrogenase (lipoamide)] + phosphate.
CC   -!- COFACTOR: MAGNESIUM DEPENDENT (BY SIMILARITY).
CC   -!- SUBUNIT: HETERODIMER OF A CATALYTIC SUBUNIT AND A FAD PROTEIN OF
CC       UNKNOWN FUNCTION (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC   --------------------------------------------------------------------------
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CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AB037769; BAA92586.1; ALT_INIT.
DR   EMBL; BC028030; AAH28030.1; -.
DR   InterPro; IPR001932; PP2C-like.
DR   InterPro; IPR000222; PP2C.
DR   Pfam; PF00481; PP2C; 2.
DR   SMART; SM00331; PP2C_SIG; 1.
DR   SMART; SM00332; PP2Cc; 1.
DR   PROSITE; PS01032; PP2C; 1.
KW   Hydrolase; Mitochondrion; Transit peptide; Magnesium.
FT   TRANSIT       1     66       MITOCHONDRION (POTENTIAL).
FT   CHAIN        67    529       [PYRUVATE DEHYDROGENASE [LIPOAMIDE]]-
FT                                PHOSPHATASE 2.
SQ   SEQUENCE   529 AA;  59978 MW;  252CAEBCDAF61A5C CRC64;

  Query Match             8.1%;  Score 195;  DB 1;  Length 529;
  Best Local Similarity   25.7%;  Pred. No. 2.9e-07;
  Matches  102;  Conservative   43;  Mismatches  112;  Indels  140;  Gaps   19;

Qy        118 GHYWALFDGHGGPAAAILAANTL----------HSCLRRQLEAVVEGLVATQPPMHLNGR 167
              |  : :||||||| | |     :   |                |   |   :|  :|  :      | :|
Db        134 GLMFGIFDGHGGHACAQAVSERLFYYVAVSLMSHQTL-EHMEGAMESMKPLLPILHWLKH 192

Qy        168 CICPSDPQFVE---------------------EKGIRAEDLVIGALESAFQECDEVIGRE 206
                  | |   : :                      | |:  |:      ||   :||   |   |   |
Db        193 ---PGDSIYKDVTSVHLDHLRVYWQELLDLHMEMGLSIEE----ALMYSFQRLDSDISLE 245

Qy        207 LEASGQ------------MGGCTALVAVSLQGKLYMANAGDSRAIL-VRRDEIRPLSPEF 253
              ::|   :                     | ||  :|         |::||||| |||| |: |
Db        246 IQAPLEDEVTRNLSLQVAFSGATACMAHVDGIHLHVANAGDCRAILGVQEDN-------- 297

Qy        254 TPETERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKVLFRDHHMSGWSYKRVEKS 313
                                    | :: |                 | |||:     :: :  |  |
Db        298 ---------------------GMWSCLP--------------LTRDHN----AWNQAELS 318

Qy        314 DLKYPLIHGQGR----QARLLGTLAVSRGLGDHQLR--------VLDINIQLK------- 354
               ||           : |       : ||||  |     |   ||  ||:                :|:        :
Db        319 RLKREHPESEDRTTIMEDRLLGVLIPCRAFGDVQLKWSKELQRSILERGFNTEALNIYQF 378

Qy        355 --------PFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGN 406
                      |:| : |:||        :|    |  |    :|:|:|||||:||||  |     ||      |
Db        379 TPPHYYTPPYLTAEPEVT---YHRLRPQ-DKFLVLASDGLWDMLSNEDVVRLVVGHLA-- 432

Qy        407 QEDPHRFSKLAQM-----LIHS--TQGKEDSLTEEGQ 436
               : | |: : |||         |: |    | |    | |  |
Db        433 EAPWHK-TDLAQFPANLGLMQSLLLQPKASGLHEADQ 468


RESULT 12
P2CB_RAT
ID   P2CB_RAT       STANDARD;      PRT;   390 AA.
AC   P35815; Q64046;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta) (IA)
DE   (Protein phosphatase 1B).
GN   PPM1B OR PPPM1B OR PP2C2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
```

```
RT   phosphatases.";
RL   Genes Dev. 13:2946-2957(1999).
CC   -!- FUNCTION: Responsible, together with PTC2, for the
CC       dephosphorylation of the cyclin-dependent protein kinase CDC28.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate
CC   -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY)
CC   -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC   --------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; Z23261; CAA80791.1; -.
DR   EMBL; Z35817; CAA84876.1; -.
DR   EMBL; U72346; AAB17351.1; -.
DR   PIR; S39832; S39832.
DR   PIR; S37333; S37333.
DR   HSSP; P35813; 1A6Q.
DR   SGD; S0000152; PTC3.
DR   InterPro; IPR001932; PP2C-like.
DR   InterPro; IPR000222; PP2C.
DR   Pfam; PF00481; PP2C; 1.
DR   SMART; SM00331; PP2C_SIG; 1.
DR   SMART; SM00332; PP2Cc; 1.
DR   PROSITE; PS01032; PP2C; 1.
KW   Hydrolase; Magnesium; Manganese; Multigene family.
FT   METAL        37     37       MANGANESE 1 (BY SIMILARITY).
FT   METAL        38     38       MANGANESE 1 (BY SIMILARITY).
FT   METAL        42     42       MANGANESE 1 AND 2 (BY SIMILARITY).
FT   METAL       234    234       MANGANESE 2 (BY SIMILARITY).
FT   METAL       284    284       MANGANESE 2 (BY SIMILARITY).
FT   CONFLICT    369    369       D -> G (IN REF. 2).
SQ   SEQUENCE   468 AA;  51290 MW;  [illegible] CRC64;

  Query Match             8.4%;  Score 203.5;  DB 1;  Length 468;
  Best Local Similarity   22.0%;  Pred. No. 5.7e-08;
  Matches  7[illegible];  Conservative   54;  Mismatches  121;  Indels  105;  Gaps   11;

Qy    104 FEFWLTLCPEEFLTGHYWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMH 163
          |   |    || |   :: :||||||| : |      : : | |::| |:    |::
Db     43 FPNLIAPSLPPHLA  FYGIFDGHGGSSVAPFCQSKMISILKKQ-ESFKSGMLE ---- 93

Qy    164 INGPCICPSDPQFVEEKGIRAEDLVIGALESAFQECDEVIGRELEASGQMGGCTALVAVS 223
             :|                          |   |   |  : :: :      |||| | :
Db     94 ---QG-------------------------LIDTELAIDVELIKDEKLKDDHSGCTATVILV 127

Qy    224 LQGK--LYMANAGDSRAILVRRDEIRPLSFEFTPE--TERQRIQQLAFVYPELLAGEFTR 279
           | |  |  ||:|||| :|         : :||:  |   :|: ||          : |  |
Db    128 SQLKKLLICANSGDSRTVLSTGGNSKAMSFDHKPTLLSEKSRI  -       VAADGFVE 178

Qy    280 LEFPRRLK[illegible]HHMFTWSYKRVE[illegible]ARLLGTLAVSRGL 339
          ::                                                |: | ||:|| :
Db    179 MD--------------------    .           .   .   .  RVNGNLALSRAI 192

Qy    340 GDHQLRVLDTNIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLV 399
          || :  :     :| :| |     |   |  :       |    ||: |::| ||:|| |:::: ||
Db    193 GDFEFK---SNTKLGPHEQVVTCVPDIICHNLNYDEDEFVILACDGIWDCLTSQECVDLV 249

Qy    400 R-SFLPGNQEDPHRFSKLAQMLIHSTQGKEDSLTEDGQVSYDDVSVFVIPLHSQGQESS 457
                ||        |:: :     |          ||    :  |::|: :: |   : : |
Db    250 HYGISQGNMTLSDISSRIVDVCCSPT        TEGSGIGCDNMSICIVALLKENESES 301


RESULT 10
P2C1_YEAST
ID   P2C1_YEAST     STANDARD;      PRT;   281 AA.
AC   P35182;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Protein phosphatase 2C homolog 1 (EC 3.1.3.16) (PP2C 1).
GN   PTC1 OR TPD1 OR YDL006W OR D2925.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93360976; PubMed=8395005;
RA   Maeda T., Tsai A.Y.M., Saito H.;
RT   "Mutations in a protein tyrosine phosphatase gene (PTP2) and a
RT   protein serine/threonine phosphatase gene (PTC1) cause a synthetic
RT   growth defect in Saccharomyces cerevisiae.";
RL   Mol. Cell. Biol. 13:5408-5417(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94254822; PubMed=8196609;
RA   Robinson M.K., van Zyl W.H., Phizicky E.M., Broach J.R.;
RT   "TPD1 of Saccharomyces cerevisiae encodes a protein phosphatase
RT   2C-like activity implicated in tRNA splicing and cell separation.";
RL   Mol. Cell. Biol. 14:3634-3645(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c;
RA   Andre B., Vissers S., Urrestarazu L.;
RL   Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 167-281 FROM N.A.
RC   STRAIN=S288C / AB972;
RA   Murphy L., Richards C., Gentles S., Harris D., Barrell B.G.,
RA   Rajandream M.A.;
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: IT HAS A SERINE AND A WEAK TYROSINE PHOSPHATASE ACTIVITY
CC       WITH RATIOS OF SERINE TO TYROSINE PHOSPHATASE ACTIVITY AS HIGH AS
CC       200:1. IT IS ESSENTIAL FOR GROWTH OR GERMINATION AT 37 DEGREES
CC       CELSIUS. MAY HAVE A ROLE IN THE HEAT SHOCK RESPONSE. INVOLVED IN
CC       TRNA SPLICING AND CELL SEPARATION.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS. MANGANESE IS
CC       ABOUT 20 TIMES MORE EFFICIENT THAN MAGNESIUM.
CC   -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; L14593; AAA[illegible]920.1; -.
DR   EMBL; Z48432; CAA88353.1; -.
DR   EMBL; Z74[illegible]; CAA[illegible]2.1; -.
DR   EMBL; Z48008; CAA88055.1; -.
DR   PIR; S[illegible]854; S[illegible]854.
DR   HSSP; P35813; 1A6Q.
DR   SGD; S0002164; PTC1.
DR   InterPro; IPR001932; PP2C-like.
DR   InterPro; IPR000222; PP2C.
DR   Pfam; PF00481; PP2C; 1.
DR   SMART; SM00331; PP2C_SIG; 1.
DR   SMART; SM00332; PP2Cc; 1.
DR   PROSITE; PS01032; PP2C; 1.
KW   Hydrolase; Magnesium; Manganese; Multigene family; Heat shock.
FT   METAL        36     36       MANGANESE 1 (BY SIMILARITY).
FT   METAL        37     37       MANGANESE 1 (BY SIMILARITY).
FT   METAL        58     58       MANGANESE 1 AND 2 (BY SIMILARITY).
FT   METAL       233    233       MANGANESE 2 (BY SIMILARITY).
FT   METAL       272    272       MANGANESE 2 (BY SIMILARITY).
FT   CONFLICT     53     53       Y -> G (IN REF. 2).
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RESULT 8
P2C1_SCHPO
ID   P2C1_SCHPO     STANDARD;      PRT;   347 AA.
AC   P40371;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Protein phosphatase 2C homolog 1 (EC 3.1.3.16) (PP2C-1).
GN   PTC1 OR SPCC4F11.02.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID 4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN 972;
RX   MEDLINE [illegible]; PubMed [illegible];
RA   Shiozaki K., Akhavan Niaki H., McGowan C.H., Russell P.;
RT   "Protein phosphatase 2C, encoded by ptc1+, is important in the heat
RT   shock response of Schizosaccharomyces pombe.";
RL   Mol. Cell. Biol. 14:3742-[illegible](1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN 972;
RX   MEDLINE 21848401; PubMed 11859360;
RA   Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA   Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA   Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA   Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA   James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA   Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA   Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA   Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA   Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA   Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA   Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA   Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).
CC   -!- FUNCTION: IT HAS A SERINE AND THREONINE PHOSPHATASE ACTIVITY
CC       HAS A SPECIALIZED ROLE IN THE HEAT SHOCK RESPONSE. MAY BE
CC       RESPONSIBLE FOR THE DEPHOSPHORYLATION OF HSP90. ALSO HAS A ROLE
CC       IN MAINTAINING SMODEC STABILITY.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC   -!- SUBUNIT: MONOMER.
CC   -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC   --------------------------------------------------------------------------
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CC   --------------------------------------------------------------------------
DR   EMBL; L26970; AAA35327.1; -.
DR   EMBL; AL117384; CAB55784.1; -.
DR   HSSP; P35813; 1A6Q.
DR   InterPro; IPR001932; PP2C-like.
DR   InterPro; IPR000222; PP2C.
DR   Pfam; PF00481; PP2C; 1.
DR   SMART; SM00331; PP2C_SIG; 1.
DR   SMART; SM00332; PP2Cc; 1.
DR   PROSITE; PS01032; PP2C; 1.
KW   Hydrolase; Magnesium; Manganese; Multigene family; Heat shock.
SQ   SEQUENCE   347 AA;  38676 MW;  50675A5456C2403B CRC64;

  Query Match             8.5%;  Score 205;  DB 1;  Length 347;
  Best Local Similarity   22.4%;  Pred. No. 2.9e-08;
  Matches   86;  Conservative   46;  Mismatches  116;  Indels  136;  Gaps   13;

Qy         40 SSSSPCAADASPPPDSRPV---RSPARCRTLP-----------WNACYAEIINAEKSEFN 85
              |     |:  |   ::||:      ::| |:|           | |   |  |
Db         27 SCHRENACPHRAPGETRPIATEMKPSKCNIVPVCNSEPPKACNWLACLMEDKNQRWRESM 86

Qy         86 EDQAACGKLCIKRCEEGAEEEWLLLCPEEFLIGHYWALFDGHGGPAAAILAANTLHSCLR 145
              ||   |        :||  ::             : |::||| |  |:      ||  |
Db         87 EDIHIC------LYDFGGNQD-----------DGFVAVYDGHAGIQASDYCQKNLHKVLL 129

Qy        146 RQLEAVVEGLVAIQPPMHLNGRCDPCSDPQPVLLKGIRALDEVIGALESAPQECDEVIGR 205
               :        |  :|                        : ||   ::  | |  |  |  :
Db        130 EK--------VRNLP------------------------DRLVIDLMDEIFVEVNSKIAK 157

Qy        206 ELEASCQMGGCTALVAVSLQGK------LYMANAGDSRAILVRRDEIRPLSFEPTPEIER 259
                     : |||| ||     |      ||  ||||:|  :|  |  :   ||::
Db        158 --ATHNDICGGTAAVAFFRYEKNRTRRVLYTANAGDARIVLCRDGKAIRLSYDH------ 209

Qy        260 QRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKVLFRDHHMSGWSYKRVEKSDLKYPL 319
                                         || |  :              :|| :
Db        210 ---------------------------KGSDANES             RRVTQ        222

Qy        320 IHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQLKPFLLSVPQVTVLDVDQLELQEDDVV 379
              : |   | |: | |||:| |||  |: |   :   ||             ::    |:
Db        223 LGGLMVQNRINGVLAVTRALGDFYLKEL---VSAHPFITET---------RIWNGHDEFF 270

Qy        380 VMATDGLWDVLSNEQVAWLVRSFL 403
              ::| ||||||:|:::    ||:|:
Db        271 IIACDGLWDVVSDQEAVDFVRNFV 294


RESULT 9
P2C3_YEAST
ID   P2C3_YEAST     STANDARD;      PRT;   468 AA.
AC   P34221; Q92330;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Protein phosphatase 2C homolog 3 (EC 3.1.3.16) (PP2C-3).
GN   PTC3 OR YBL056W OR YBL0511 OR YBL0513.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID 4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN S288c;
RX   MEDLINE 94205266; PubMed 8154187;
RA   Scherens B., el Bakkoury M., Vierendeels F., Dubois E., Messenguy F.;
RT   "Sequencing and functional analysis of a 32,560 bp segment on the
RT   left arm of yeast chromosome II. Identification of 26 open reading
RT   frames, including the KIP1 and SEC17 genes.";
RL   Yeast 9:1355-1371(1993).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Maeda T., Wurlger-Murphy S.M., Saito H.;
RL   Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   FUNCTION.
RX   PubMed 10580002;
RA   Cheng A., Ross K.E., Kaldis P., Solomon M.J.;
RT   "Dephosphorylation of cyclin-dependent kinases by type 2C protein
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; L34881; AAA67420.1; -.
DR   EMBL; AL031579; CAA20880.1; -.
DR   HSSP; P35813; 1A6Q.
DR   InterPro; IPR001932; PP2C-like.
DR   InterPro; IPR000222; PP2C.
DR   Pfam; PF00481; PP2C; 1.
DR   SMART; SM00331; PP2C_SIG; 1.
DR   SMART; SM00332; PP2Cc; 1.
DR   PROSITE; PS01032; PP2C; 1.
KW   Hydrolase; Magnesium; Manganese; Multigene family.
FT   METAL         37     37       MANGANESE 1 (BY SIMILARITY).
FT   METAL         38     38       MANGANESE 1 (BY SIMILARITY).
FT   METAL         63     63       MANGANESE 1 AND 2 (BY SIMILARITY).
FT   METAL        233    233       MANGANESE 2 (BY SIMILARITY).
FT   METAL        282    282       MANGANESE 2 (BY SIMILARITY).
SQ   SEQUENCE   370 AA;  40878 MW;  DBDDB826F412AC59 CRC64;

  Query Match             9.4%;  Score 226.5;  DB 1;  Length 370;
  Best Local Similarity   23.8%;  Pred. No. 7.6e-10;
  Matches   81;  Conservative   51;  Mismatches  105;  Indels  103;  Gaps   12;

Qy        120 YWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEE 179
              :: : ||||     |           |: |  :::                    | | |
Db         58 FFGVFDGHGGDRVA--------KYCRQHLPDIIK---------- -------SQPSF--W 89

Qy        180 KGIRAFDLVIGALESAFQECDEVIGRELEASGQMGGCTALVAVSLQGK-LYMANAGDSRA 238
              ||    |        |||:| |    |    : :: :       ||||  |: :   : :| |||||||
Db         90 KGNYIE      ALKSGFLAALNALMQLRDMQDHPSCTAITALIVDHQVIYCANAGDSRT 144

Qy        239 IIVRRGEIRPLSEEFTP--ETERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKVL 296
              :| |:     ||||:  |   : |: ||                 |||             | |
Db        145 VLGRKGTAEPLSFDHKPNNEVEKARI -        TAAGGFI-             DFG - - 180

Qy        297 FRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQLKPF 356
                                                 |: |:|||:|| :||  :  :     :        |
Db        181 -------------------------------RVNGGLALSRAIGDFFYKKDGSLPPEKQI 209

Qy        357 LLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSKL 416
              : : | | : ::|        :|: :::| ||:||      ::||     ||   :     |            |
Db        210 VTAFPDVVIHNIDP-    PDDEFLILACDGIWDCKSSQQVVEFVRRGIVARQSLEVICENL 265

Qy        417 AQMLIHSTQGKEDSLTEEGQVSYDDVSVFVIPLHSQGQE 455
                   | |         :|    :   |:::: ::   || :| |
Db        266 MDRCLASN          SPSCGKGCDNMTICIVAPLKPGNLF 298


RESULT 7
FEM2_HUMAN
ID   FEM2_HUMAN      STANDARD;      PRT,   454 AA.
AC   P49593; Q96PM2;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Ca(2+)/calmodulin-dependent protein kinase phosphatase (EC 3.1.3.16)
DE   (CaMKPase) (hFEM-2).
GN   KIAA0015.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   PubMed 11559703;
RA   Tan K.M.L., Chan S.L., Tan K.O., Yu V.C.;
RT   "The Caenorhabditis elegans sex-determining protein fem-2 and its
RT   human homologue, hFEM-2, are Ca2+/calmodulin dependent protein kinase
RT   phosphatases that promote apoptosis.";
RL   J. Biol. Chem. 276:44193-44202(2001).
```

```
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RX   MEDLINE=96051387; PubMed 7584026;
RA   Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayasi Y.,
RA   Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
RT   "Prediction of the coding sequences of unidentified human genes. I.
RT   The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
RT   analysis of randomly sampled cDNA clones from human immature myeloid
RT   cell line KG-1.";
RL   DNA Res. 1:27-35(1994).
CC   -!- FUNCTION: Dephosphorylates and concomitantly deactivates CaM-
CC       kinase II activated upon autophosphorylation, and CaM kinases IV
CC       and I activated upon phosphorylation by CaM kinase kinase.
CC       Promotes apoptosis.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC   -!- SUBUNIT: Associates with FIAalpha.
CC   -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC   --------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; AF305840; AAL15579.1; -.
DR   EMBL; D13640; BAA02803.1; -.
DR   InterPro; IPR001932; PP2C-like.
DR   InterPro; IPR000222; PP2C.
DR   Pfam; PF00481; PP2C; 1.
DR   SMART; SM00331; PP2C_SIG; 1.
DR   SMART; SM00332; PP2Cc; 1.
DR   PROSITE; PS01032; PP2C; 1.
KW   Hydrolase; Magnesium; Manganese; Apoptosis; Multigene family.
FT   DOMAIN      101    107       POLY-GLU.
FT   METAL       360    360       MANGANESE 2 (BY SIMILARITY).
FT   METAL       404    404       MANGANESE 2 (BY SIMILARITY).
FT   CONFLICT    202    202       D -> G (IN REF. 2).
SQ   SEQUENCE   454 AA;  49888 MW;  2A5626233B1BC9CF CRC64;

  Query Match             9.0%;  Score 216.5;  DB 1;  Length 454;
  Best Local Similarity   24.5%;  Pred. No. 5.7e-09;
  Matches   81;  Conservative   48;  Mismatches   88;  Indels  113;  Gaps   11;

Qy        120 YWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEE 179
              |:|:|||||    ||   ||   :|:     || |                          |:||:
Db        193 YFAVFDGHGPVDAARYAAVHVHTNAARQPE                          LPTDPE      228

Qy        180 KGIRAFDLVIGALESAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAI 239
                           |||   ||:   |::    |: :           | |  :  |:          |:|  |||: |
Db        229                GALREAFRRTDQMFLRKAKRERLQSGTTGVCALIAGATLHVAWLGDSQVI 278

Qy        240 IVRRGEIRPLSEEFTPE-TERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKVLF 297
              ||:: ::  |      ||     |: ||: |                 ||
Db        279 LVQQGQVVKLMEPHRPERQDEKARIEAL---------GGFV--- ------------------ 310

Qy        298 RDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQLKPFL 357
                 ||   |                          |: ||||||| :||                  :   ||::
Db        311   SHMDCW                           EVNGTLAVSRAIGD - -        VPLKPYV 337

Qy        358 LSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSKLA 417
                        :         :| :::| || :||: :::|     |:|  |     |        |      :|
Db        338 SGEADA---ASRALTGSEDYLLLACDGFFDVVPHQEVVGLVQSHLTRQQGSGLR---VA 390

Qy        418 QMLIHSTQGKEDSLTEEGQVSYDDVSVFVI 447
               : |: :  :              |  |    |:|:::| |:
Db        391 EELVAAAR          ERG-SHDNITVMVV 411
```

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RESULT 5
P2C2_CAEEL
ID   P2C2_CAEEL     STANDARD;      PRT;   356 AA.
AC   P49596;
DT   01-FEB-1996 (Rel. 33, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Probable protein phosphatase 2C T23F11.1 (EC 3.1.3.16) (PP2C).
GN   T23F11.1.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Swinburne J.;
RL   Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   REVISIONS.
RA   Durbin R.;
RL   Submitted ([illegible]) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC   --------------------------------------------------------------------------
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; Z46343; CAA86456.2; -.
DR   HSSP; P35813; 1A6Q.
DR   WormPep; T23F11.1; CE24009.
DR   InterPro; IPR001932; PP2C-like.
DR   InterPro; IPR000222; PP2C.
DR   Pfam; PF00481; PP2C; 1.
DR   SMART; SM00331; PP2C_SIG; 1.
DR   SMART; SM00332; PP2Cc; 1.
DR   PROSITE; PS01032; PP2C; 1.
KW   Hypothetical protein; Hydrolase; Magnesium; Manganese.
FT   METAL        57     57       MANGANESE 1 (BY SIMILARITY).
FT   METAL        58     58       MANGANESE 1 (BY SIMILARITY).
FT   METAL        59     59       MANGANESE 1 AND 2 (BY SIMILARITY).
FT   METAL       228    228       MANGANESE 2 (BY SIMILARITY).
FT   METAL       277    277       MANGANESE 2 (BY SIMILARITY).
SQ   SEQUENCE   356 AA;  39064 MW;  ED0B0841FB0265B5 CRC64;

  Query Match             10.1%;  Score 244;  DB 1;  Length 356;
  Best Local Similarity   21.1%;  Pred. No. 3.1e-11;
  Matches   85;  Conservative   41;  Mismatches   96;  Indels  118;  Gaps   12;

Qy        120 YWALLDGHGGPAAALLAANTLHSTLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQPVEE 179
                ::|::|:|   :   :    |:  :  | |
Db         54 FFAVYDGHGGSKVSQYSGINLHKKVVAQKEF-----------------------------  84

Qy        180 KGIPAHDLVIGALESAPQPPPEVIGRELEASGQMPSPIALVAVGIGQKLYMANAGDSRAI 239
                  :  : |:: |  |: : :  |     : : |:: :   :| :|  ||||||:
Db         85 -----GEGNMKEAIEKGFLELDQQMRVDEEIKDEVSGTTAVVVLIKDDDVYCGNAGDSRAV 140

Qy        240 LVRRDEIRPLSFEFTP-ETERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKVLF 297
                    | :|:|:   |   |||  :|:              : ||
Db        141 SSVVGEARPLSFDHKPSHETEARRI---------------IAAG-------------- 169

Qy        298 RDHHMSGW-SYKPVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQLKPF 356
                    :|  : ||                      | ||:|| |||   :  ||      :
Db        170 ---------GWVEFNRVN--------------------GNLALSRALGDFALKKNDNKPAEEQI 204

Qy        357 LLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSKL 416
                : : | |      |:|   : : :|:| ||:|||::|::|      ||   |    : ||
Db        205 VTALPDVT-----TGKL-TPSDEFIVLACDGIWDVMTNQEVVDFVRLKL-ALKRDPQSIC-- 257

Qy        417 AQMLIHSIQGKEDSLT-------EEGQVSYDDVSVFVIPLHSQGQES 456
                         |: ||       : | :  |:::| ::  || |  ::
Db        258 -------EELLTRCLAPDCQMGGLGCDNMTVVLVGLLHGQSPDT 294


RESULT 6
P2C2_SCHPO
ID   P2C2_SCHPO     STANDARD;      PRT;   370 AA.
AC   Q09172;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Protein phosphatase 2C homolog 2 (EC 3.1.3.16) (PP2C-2).
GN   PTC2 OR SPCC1223.11.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID=4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RX   MEDLINE=95163582; PubMed=7859738;
RA   Shiozaki K., Russell P.;
RT   "Counteractive roles of protein phosphatase 2C (PP2C) and a MAP
RT   kinase kinase homolog in the osmoregulation of fission yeast.";
RL   EMBO J. 14:492-502(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RX   MEDLINE=21848401; PubMed=11859360;
RA   Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA   Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA   Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA   Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA   James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA   Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA   Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA   Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA   Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA   Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA   Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA   Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).
CC   -!- FUNCTION: HAS AN IMPORTANT ROLE IN OSMOTIC STABILITY AND CELL
CC       SHAPE CONTROL. IT MAY NEGATIVELY REGULATE THE OSMOSENSING SIGNAL
CC       TRANSMITTED THROUGH WIS1 MAP KINASE.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC   -!- SUBUNIT: MONOMER.
CC   -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC   --------------------------------------------------------------------------
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SQ   SEQUENCE   434 AA;  47505 MW;  4A4C54F04195F572 CRC64;

  Query Match             10.3%;  Score 248.5;  DB 1;  Length 434;
  Best Local Similarity   23.9%;  Pred. No. 2e-11;
  Matches   84;  Conservative   57;  Mismatches   90;  Indels  121;  Gaps   14;

Qy        119 HYWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVE 178
              |:: ::||:||                  :|  |  :           :| : ||         :|  |      :
Db        171 HFFGVYDGHGGSQVANYCRERMHLALAEE---------IAKEKPM------LCDGDTWLEK 216

Qy        179 EKGIRAEDLVIGALESAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSR 237
               |              || ::|    |       |:|: : :   | |::|||       :::|| ||||
Db        217 WK          KALPNSFLRVDS     EIESVAPETVGSVVAVVFPSHIFVANCGDSR 263

Qy        238 AILVRRLEIEEPLSPEETPTTEQRILQLAFVYFELLAGEETKLEEPRRLKGDLLGQKVLP 297
              |:|  '        ||| :   |: |                               |   |:|                 | ||:
Db        264 AVLCRGKTALPLSVDHKPDRE-----------------DEAARIE---------AAGGKVI- 298

Qy        298 RDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQLKPFL 357
                                          |    ||: |  :|:|| :||                 ||| :
Db        299 --------------------------QWNGARVFGVLAMSRSIGDR----    YLKPSI 324

Qy        358 LSVPQVTVLDVDQLELQHDDVVVMATDGLWDVLSNEQ--       -VAWIVRSFLPGNQE 408
               :  |:|  :        ..||| :.:|.||.|||      |                :  |     :  |
Db        325 IPDPEVTAVK--    FVKEDDFLILASDGVWDVMTDEEACEMARKRILLWHKKNAVAGD-- 378

Qy        409 DPHRFSKLAQMLI--HSTQGKEDSLTEEGQV---------SYDDVSVFVIPL 449
                          | :|        :||: :         :                  | |::||  |: |
Db        379 --------ASLIADERRKEGKDPAAMSAAEYLSKLAIQRGSKDNISVVVVDL 422


RESULT 4
P2C3_SCHPO
ID   P2C3_SCHPO     STANDARD;      PRT;   414 AA.
AC   Q09173;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Protein phosphatase 2C homolog 3 (EC 3.1.3.16) (PP2C 3).
GN   PTC3 OR SPAC2G11.07C.
OS   Schizosaccharomyces pombe (Fission yeast).
OC   Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC   Schizosaccharomycetales; Schizosaccharomycetaceae;
OC   Schizosaccharomyces.
OX   NCBI_TaxID 4896;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RX   MEDLINE=95163582; PubMed=7859738;
RA   Shiozaki K., Russell P.;
RT   "Counteractive roles of protein phosphatase 2C (PP2C) and a MAP
RT   kinase kinase homolog in the osmoregulation of fission yeast.";
RL   EMBO J. 14:492-502(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=972;
RX   MEDLINE=21848401; PubMed=11859360;
RA   Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA   Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA   Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA   Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA   Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA   Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA   James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA   Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA   Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E.,
RA   Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA   Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA   Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA   Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
RA   Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA   Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA   Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA   Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA   Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA   Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA   Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA   Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA   Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA   Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RT   "The genome sequence of Schizosaccharomyces pombe.";
RL   Nature 415:871-880(2002).
CC   -!- FUNCTION: HAS AN IMPORTANT ROLE IN OSMOTIC STABILITY AND CELL
CC       SHAPE CONTROL. IT MAY NEGATIVELY REGULATE THE OSMOSENSING SIGNAL
CC       TRANSMITTED THROUGH WIS1 MAP KINASE.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC   -!- SUBUNIT: MONOMER.
CC   -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC   --------------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------------
DR   EMBL; L34882; AAA67321.1; -.
DR   EMBL; Z54354; CAA91172.1; -.
DR   HSSP; P35813; 1A6Q.
DR   InterPro; IPR001932; PP2C-like.
DR   InterPro; IPR000222; PP2C.
DR   Pfam; PF00481; PP2C; 1.
DR   SMART; SM00331; PP2C_SIG; 1.
DR   SMART; SM00332; PP2Cc; 1.
DR   PROSITE; PS01032; PP2C; 1.
KW   Hydrolase; Magnesium; Manganese; Multigene family.
FT   METAL        37     37       MANGANESE 1 (BY SIMILARITY).
FT   METAL        38     38       MANGANESE 1 (BY SIMILARITY).
FT   METAL        62     62       MANGANESE 1 AND 2 (BY SIMILARITY).
FT   METAL       230    230       MANGANESE 2 (BY SIMILARITY).
FT   METAL       279    279       MANGANESE 2 (BY SIMILARITY).
FT   CONFLICT    196    196       K -> T (IN REF. 1)
SQ   SEQUENCE   414 AA;  44856 MW;  EFF3A416625A2B11 CRC64;

  Query Match             10.2%;  Score 246;  DB 1;  Length 414;
  Best Local Similarity   24.3%;  Pred. No. 3e-11;
  Matches   83;  Conservative   55;  Mismatches   99;  Indels  104;  Gaps   12;

Qy        120 YWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMELNGRCICPSDPQFVEE 179
              ::|::||||||     |        :  |        | :                                                              :|  |     :
Db         57 FFAVYDGHGGDRVAKWCGSNLHQILEK-----------------------------NPDF--Q 88

Qy        180 KGIRAEDLVIGALESAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAI 239
              ||       |  |   ||:|:|     |: |    :  :              ||||  .  :  :   |||  |||||||  :
Db         89 KG----DFV NALKSCFLNAPKAILDPDQFHIDPSGCTATVVLRVGNKLYCANAGDSRTV 143

Qy        240 LVRRLEIEEPLSPEETPTTEQRILQLAFVYFELLAGEETKLEEPRRLKGDLLGQKVLPRD 299
              |   :      :|||  :     |     |   : :  :    |                   |||  |                             ||
Db        144 LGSKGIAKPLSADHKPSNEAEKARICA      -     AGGFV-----------DFG------- 178

Qy        300 HHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQLKP---F 356
                                                 |:  |  ||:||  :||  :   :           |     |:|
Db        179                                    KVNGNLALSRAIGDFEFK    -NSNLEPEKQI 206

Qy        357 LLSVPQVTVLDVDQLELQHDDVVVMATDGLWDVLSNEQVAWIVRSFLPGNQEDPHRFSKL 416
               :  ::|  |  |  ::            :|:  ||:|  ||:||     :::||          ||        :                        |:
Db        207 VTALPDVVVHEI      TEDDEFVVLACDGIWDCKTSQQVIEFVRRGIVAGTS     LEKI 258

Qy        417 AQMLIHSTQGKEDSLTEEGQVSYDDVSVFVIPLHSQGQESS 457
              |:  |:  :       :        ||       :      |:::|  ::  |      :     :|:
Db        259 AENLMDNCIASD     TETTGLGCDNMTVCIVALLQENDKSA 296
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Qy        296 LFFDHHMSGWSYKFVEKSDEKYFLIHVSPQARLILLAVSPGHSHQLRVLLYNIQLRKD 355
                  :          ::                         |:|  | ||:|| :||              |||
Db        [illegible]  PWN              [illegible]                  YIKF 312

Qy        356 FLLSVPQVIVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVR-- - --------- 400
                ::    |:||  :              ::|||  :::|:|||||:::||:|     | |
Db        313 SVIPDPEVISV -    RRVKEDDCLILASDGLWDVMINEEVCDLARKRILLWHKKNAMAGE 368

Qy        401 SFLP      GNQEDPHRESK --LAQMLIHSTQCKEDSLTEEGQVSYDDVSVPVIPL 449
                : ||       |  :||     |      |::| :                :::|   |  |::||  |: |
Db        369 ALLPAEKRGEGKDPAAMSAAEYLSKMAL - -- - -- - QKG -SKKNISVVVVDL 411


RESULT 3
P2C1_ARATH
ID   P2C1_ARATH     STANDARD;      PRT;   434 AA.
AC   P49597; Q43717; Q94787;
DT   01-FEB-1996 (Rel. 33, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Protein phosphatase 2C ABI1 (EC 3.1.3.16) (PP2C) (Abscisic acid
DE   insensitive 1).
GN   ABI1 OR AT4G26080 OR F20B18.190.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A., AND VARIANT ASP-180.
RC   STRAIN=cv. Landsberg erecta;
RX   MEDLINE=94255767; PubMed=8197457;
RA   Meyer K., Leube M.P., Grill E.;
RT   "A protein phosphatase 2C involved in ABA signal transduction in
RT   Arabidopsis thaliana.";
RL   Science 264:1452-1455(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia; TISSUE=Leaf;
RX   MEDLINE=95007758; PubMed=7923358;
RA   Mindrinos M., Katagiri F., Yu G.L., Ausubel F.M.;
RT   "The A. thaliana disease resistance gene RPS2 encodes a protein
RT   containing a nucleotide-binding site and leucine-rich repeats.";
RL   Cell 78:1089-1099(1994).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia; TISSUE=Leaf;
RX   MEDLINE=94255766; PubMed=7910981;
RA   Leung J., Bouvier-Durand M., Morris P.C., Guerrier D., Chefdor F.,
RA   Giraudat J.;
RT   "Arabidopsis ABA response gene ABI1: features of a calcium-modulated
RT   protein phosphatase.";
RL   Science 264:1448-1452(1994).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=20083488; PubMed=10617198.
RA   Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA   Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA   Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
RA   Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA   Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA   Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA   Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA   Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA   Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA   Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA   Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA   Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA   Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA   Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA   De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA   Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA   Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA   Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA   Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA   Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA   Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA   Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA   Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA   Chefdor F., Cooke R., Berger C., Montfort A., Casacuberta E.,
RA   Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
RA   Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA   Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA   Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA   Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA   Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA   Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA   Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA   Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA   Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA   Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA   Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA   Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C.,
RA   Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA   Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA   Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA   Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA   Chen E., Marra M., Martienssen R., McCombie W.R.;
RT   "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:769-777(1999).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RA   Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT   "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RT   SSP consortium (Salk/Stanford/PGEC).";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: INVOLVED IN ABSCISIC ACID (ABA) SIGNALING PATHWAY.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
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CC   --------------------------------------------------------------------------
DR   EMBL; X78886; CAA55484.1; -.
DR   EMBL; U12856; AAA50237.1; -.
DR   EMBL; X77116; CAA54383.1; -.
DR   EMBL; AL049483; CAB39673.1; -.
DR   EMBL; AL161564; CAB79463.1; -.
DR   EMBL; AY035073; AAK59578.1; -.
DR   HSSP; P35813; 1A6Q.
DR   InterPro; IPR002048; EF-hand.
DR   InterPro; IPR001932; PP2C-like.
DR   InterPro; IPR000222; PP2C.
DR   Pfam; PF00481; PP2C; 1.
DR   SMART; SM00331; PP2C_SIG; 1.
DR   SMART; SM00332; PP2Cc; 1.
DR   PROSITE; PS00018; EF_HAND; 1.
DR   PROSITE; PS01032; PP2C; 1.
KW   Hydrolase; Magnesium; Manganese; Multigene family; Calcium-binding.
FT   CA_BIND      93    104       EF-HAND (POTENTIAL).
FT   DOMAIN      417    420       POLY-VAL.
FT   VARIANT     180    180       G -> D (WILTY PHENOTYPE AND ABA-
FT                                INSENSITIVE SEED GERMINATION AND GROWTH).
FT   CONFLICT     24     24       G -> R (IN REF. 5).
FT   CONFLICT    105    105       I -> V (IN REF. 1).
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CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
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CC   --------------------------------------------------------------------------
DR   EMBL; D38109; BAA07287.1; -.
DR   EMBL; AC008153; AAC51448.1; -.
DR   HSSP; P35813; 1A6Q.
DR   InterPro; IPR001932; PP2C-like.
DR   InterPro; IPR000222; PP2C.
DR   Pfam; PF00481; PP2C; 1.
DR   SMART; SM00331; PP2C_SIG; 1.
DR   SMART; SM00332; PP2Cc; 1.
DR   PROSITE; PS01032; PP2C; 1.
KW   Hydrolase; Magnesium; Manganese; Multigene family.
SQ   SEQUENCE   399 AA;  43350 MW;  83B82E32FEC71D4D CRC64;

  Query Match             11.4%;  Score 275;  DB 1;  Length 399;
  Best Local Similarity   25.2%;  Pred. No. 1.8e-13;
  Matches  120;  Conservative   69;  Mismatches  159;  Indels  128;  Gaps   20;

Qy          7 RRR--FLPCFPLPAPPPPCPHASPVPYPRPRPLEGSSSSPC  AADASERPDSRPVESPA 62
              |||    ||     : |          |         |: |       |: ||     |:: | :::   ||
Db         27 RRRLDLLPSIKIVADSAVAPPLENCPKPQKPEIVVLSFLPSNLSSSNVEFENKEARSAV 96

Qy         63 RGRTLPWNAGYAEIINAEKSEFNEDQAACGKLCIRRCEFGAEEEWLTLCPEEFL-----T 117
                                :   ||       :    :        :|  ||  :        |:  ::: |    ||
Db         87 TNSN      --SVTFAFSFFSDVPKIGTTSVCGRRRDM---EDAVSIHP-SFLQRNSEN 134

Qy        118 CHYWALPDGHGCPAAAILAANTIHSCLRRQLEAV-----VPGLVATQPPMHLNGPCICPS 172
                |:: :|||||     |         ||   :::::|  :           | :|  :     |
Db        135 HHFYGVFDGHGCSHVAEKCRERLHDIVKKEVEVMASLEWTETMVFSLQFML--   -    185

Qy        173 DPQFVEEKGIRAEDLVI-GALESAFQECD-EVIGRELEASGQMGGCTALVAVSLQGKLYM 230
                      :|      |    :||:  ||    |        |    |:        :  :|  |         ||:|:|       |:  :
Db        186 -----KEVSQEECNLVVNGATRSMFNSCRCELQSPQCDAVGS----TAVVSVVTPEKIIV 236

Qy        231 ANACDSRAILVRRDEIEPLSPEHTPE  TERQRIQQIAFVYPELLACEFTELEFPRKLKC 288
              :|  |||||:|  |          |||  :      |:         |     ||||
Db        237 SNCGDSRAVLCRNGVAIPLSVDHKPDRPDELIRIQQ              ---  -  272

Qy        289 DPLGQKVLRRDHHMSCWSYKKVFKSDLKYPLIHGQCPQAPLLGTLAVSRGLCDHQLRVLD 348
                    |  :|:::  |                                                    ||:||  ||:||  :||:
Db        273 --AGGRVIYWD---------------------------GARVLGVLAMSRAIGDN------ 298

Qy        349 TNIQLKPFLLSVPQVTVLDVDQLELQPDDVVVMATDGLWDVLSNEQVAWLVRSFLPG--- 405
                       |||:::    |:|||  |                ||:  :::|:||||||:  ||          :  |    |  |
Db        299 ---YLKPYVIPDPEVTVTD      RTDEDECLILASDGLWDVVPNETACGVARMCLRGAGA 351

Qy        406 --NQEDPHRFSKLAQMLIHSTQCKEDSLTEEGQVSYDDVSVFVIPLHSQ--GQESS 457
                   : :     |           | :|:                    :|     :      ; |:|||  |:   |    :       |  ||
Db        352 GDDSDAAHNACSDAALLLTKL      -ALARQ    SSDNVSVVVVDLKKRRNNQASS 399


RESULT 2
P2C2_ARATH
ID   P2C2_ARATH     STANDARD;      PRT;   423 AA.
AC   O04719;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Protein phosphatase 2C ABI2 (EC 3.1.3.16) (PP2C) (Abscisic acid-
DE   insensitive 2).
GN   ABI2 OR [illegible] OR MUM17.19.
OS   Arabidopsis thaliana (Mouse-ear cress).
```

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OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Landsberg erecta, and cv. Columbia;
RX   MEDLINE=97308526; PubMed=9165752;
RA   Leung J., Merlot S., Giraudat J.;
RT   "The Arabidopsis ABSCISIC ACID-INSENSITIVE2 (ABI2) and ABI1 genes
RT   encode homologous protein phosphatases 2C involved in abscisic acid
RT   signal transduction.";
RL   Plant Cell 9:759-771(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Landsberg erecta;
RA   Rodriguez P.L., Grill E.;
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=20181125; PubMed=10718197;
RA   Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
RA   Tabata S.;
RT   "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT   features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT   clones.";
RL   DNA Res. 7:31-63(2000).
CC   -!- FUNCTION: INVOLVED IN ABSCISIC ACID (ABA) SIGNALING PATHWAY.
CC   -!- CATALYTIC ACTIVITY: A phosphoprotein + H(2)O = a protein +
CC       phosphate.
CC   -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
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CC   --------------------------------------------------------------------------
DR   EMBL; Y08966; CAA70163.1; -.
DR   EMBL; Y08965; CAA70162.1; -.
DR   EMBL; Y11840; CAA72538.1; -.
DR   EMBL; AB024035; BAA97035.1; -.
DR   HSSP; P35813; 1A6Q.
DR   InterPro; IPR001932; PP2C-like.
DR   InterPro; IPR000222; PP2C.
DR   Pfam; PF00481; PP2C; 1.
DR   SMART; SM00331; PP2C_SIG; 1.
DR   SMART; SM00332; PP2Cc; 1.
DR   PROSITE; PS01032; PP2C; 1.
KW   Hydrolase; Magnesium; Manganese; Multigene family; Calcium-binding.
FT   CA_BIND      70     81       EF-HAND (POTENTIAL).
SQ   SEQUENCE   423 AA;  46306 MW;  67CAAC76DA531A71 CRC64;

  Query Match             10.4%;  Score 251;  DB 1;  Length 423;
  Best Local Similarity   26.1%;  Pred. No. 1.3e-11;
  Matches   93;  Conservative   52;  Mismatches   99;  Indels  122;  Gaps   16;

Qy        116 LTCHYWALPDGHGCPAAAILAANTIHSCLRRQLEAVVPGLVATQPPMHLNGRCICPSDPQ 175
                |: |:: ::|||||     |              : |    |     |: |  |:  :|                   |  |
Db        156 LSAHFFCVYDGHGCSQVA   -  - NYCRERMHLALTEEIVKEKPE        PCDGDTW 201

Qy        176 FVEEKGIRAEDLVIGALESAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGD 235
                  :||   :              || ::|     |   |         |     :|   |::||           ::::||    |
Db        202 --QEKWKK        ALFNSFMRVDSEIETVAHAPETVGSTSVVAVVFPTHIFVANCGD 251

Qy        236 SRAILVRRDEIRPLSEEHTPETERQRIQQLAFVYPELLAGEFTRLEFPRKLKGDDLGQKV 295
                |||:| |           || :    |: :                                    :        :|                 |  ||
Db        252 SRAVLCRGKTPLALSVDHKPDRE                          DEAARIE          AAGGKV 287
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OM protein - protein search, using sw model

Run on:          February 24, 2003, 14:34:00 ; Search time 14 Seconds
                                                 (without alignments)
                                                 1359.831 Million cell updates/sec

Title:           US-09-866-987-8
Perfect score:   2415
Sequence:        1 MGAGWERPPEELPSEELPAPR..........DEVSVEVIPLHSQGQESSDH 459

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters:       112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       SwissProt_40.*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                 SUMMARIES
                   %
Result          Query
  No.   Score   Match Length DB   ID                        Description
                                                            -----------
    1     275    11.4    399  1  P2C4_ARATH                 P49598 arabidopsis
    2     251    10.4    423  1  P2C2_ARATH                 O04719 arabidopsis
    3   248.5    10.3    434  1  P2C1_ARATH                 P49597 arabidopsis
    4     246    10.2    414  1  P2C3_SCHPO                 Q09173 schizosacch
    5     244    10.1    356  1  P2C2_CAEEL                 P49596 caenorhabdi
    6   226.5     9.4    370  1  P2C2_SCHPO                 Q09172 schizosacch
    7   216.5     9.0    454  1  FEM2_HUMAN                 P49593 homo sapien
    8     205     8.5    347  1  P2C1_SCHPO                 P40371 schizosacch
    9   203.5     8.4    468  1  P2C3_YEAST                 P34221 saccharomyc
   10     202     8.4    281  1  P2C1_YEAST                 P35182 saccharomyc
   11     195     8.1    529  1  PDP2_HUMAN                 Q9p2j9 homo sapien
   12   191.5     7.9    390  1  P2CB_RAT                   P35815 rattus norv
   13     190     7.9    390  1  P2CB_MOUSE                 P36993 mus musculu
   14   189.5     7.8    387  1  P2CB_BOVIN                 O62830 bos taurus
   15   186.5     7.7    479  1  P2CB_HUMAN                 O75688 homo sapien
   16   184.5     7.6    382  1  P2CA_MOUSE                 P49443 mus musculu
   17   183.5     7.6    382  1  P2CA_RABIT                 P35814 oryctolagus
   18   183.5     7.6    382  1  P2CA_RAT                   P20650 rattus norv
   19     183     7.6    530  1  PDP2_RAT                   O88484 rattus norv
   20   182.5     7.6    456  1  FEM2_RAT                   Q9WVR7 rattus norv
   21   181.5     7.5    382  1  P2CA_BOVIN                 O62829 bos taurus
   22   180.5     7.5    538  1  PDP1_RAT                   O88483 rattus norv
   23   179.5     7.4    382  1  P2CA_HUMAN                 P35813 homo sapien
   24   177.5     7.3    300  1  P2C_PARTE                  P49444 paramecium
   25     177     7.3    464  1  P2C2_YEAST                 P39966 saccharomyc
   26   173.5     7.2    388  1  P2C3_ARATH                 P49599 arabidopsis
   27   171.5     7.1    393  1  P2C4_YEAST                 P38089 saccharomyc
   28   170.5     7.1    538  1  PDP1_BOVIN                 P35816 bos taurus
   29   169.5     7.0    491  1  P2C1_CAEEL                 P49595 caenorhabdi
   30   166.5     6.9    538  1  PDP1_HUMAN                 Q9p0j1 homo sapien
   31   160.5     6.6    605  1  P2CD_HUMAN                 O15297 homo sapien
   32     160     6.6    598  1  P2CD_MOUSE                 Q9QZ67 mus musculu
   33   155.5     6.4    543  1  P2CG_BOVIN                 P79126 bos taurus
   34     154     6.4    542  1  P2CG_MOUSE                 Q61074 mus musculu
   35   153.5     6.4    546  1  P2CG_HUMAN                 O15355 homo sapien
   36     134     5.5    406  1  P2C_LEICH                  P36982 leishmania
   37   127.5     5.3    449  1  FEM2_CAEEL                 P49594 caenorhabdi
   38   117.5     4.9    504  1  TAB1_HUMAN                 Q15750 homo sapien
   39   113.5     4.7    581  1  KAPP_ARATH                 P46014 arabidopsis
   40     110     4.6    383  1  P2C4_SCHPO                 O14156 schizosacch
   41     108     4.5   2300  1  CYAA_NEUCR                 Q01631 neurospora
   42     104     4.3   2564  1  SPCQ_HUMAN                 Q9H254 homo sapien
   43     103     4.3    862  1  BCR2_ACEXY                 O82860 acetobacter
   44   102.5     4.2   1839  1  CYAA_SACKL                 P23466 saccharomyc
   45   101.5     4.2   2026  1  CYAA_YEAST                 P08678 saccharomyc


                                 ALIGNMENTS


RESULT 1
P2C4_ARATH
ID   P2C4_ARATH     STANDARD;      PRT;   399 AA.
AC   P49598;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Protein phosphatase 2C (EC 3.1.3.16) (PP2C).
GN   AT3G11410 OR F24K9.8.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=95116318; PubMed=7816619;
RA   Kuromori T., Yamamoto M.;
RT   "Cloning of cDNAs from Arabidopsis thaliana that encode putative
RT   protein phosphatase 2C and a human Dr1-like protein by transformation
RT   of a fission yeast mutant.";
RL   Nucleic Acids Res. 22:5296-5301(1994).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Columbia;
RX   MEDLINE=21016720; PubMed=11130713;
RA   Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
RA   Fartmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
RA   Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA   De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
RA   Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA   Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA   Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA   Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA   Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA   Conrad A., Hornischer K., Kauer G., Loehnert T.-H., Nordsiek G.,
RA   Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
RA   Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA   Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA   de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA   Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA   Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA   Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA   Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA   Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA   Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA   Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA   Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA   Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
RA   Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA   Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA   Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT   "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 408:820-822(2000).
```

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;  GENERAL INFORMATION:
;   APPLICANT: Roch, Jean Marc
;   APPLICANT:  Bartel, Paul L.
;   APPLICANT:  Heichman, Karen
;   TITLE OF INVENTION: Protein Protein Interactions in Neurodegenerative
;   TITLE OF INVENTION:  Diseases
;   FILE REFERENCE: Protein Interactions in ND
;   CURRENT APPLICATION NUMBER: US/09/973,964
;   CURRENT FILING DATE:  2001-10-11
;   PRIOR APPLICATION NUMBER: US 60/240,790
;   PRIOR FILING DATE: 2000-10-17
;   PRIOR APPLICATION NUMBER: US 60/304,775
;   PRIOR FILING DATE: 2001-07-13
;   NUMBER OF SEQ ID NOS: 8
;   SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 4
;    LENGTH: 372
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-973-964-4

  Query Match              8.2%;  Score 197.5;  DB 10;  Length 372;
  Best Local Similarity   22.7%;  Pred. No. 3.8e-09;
  Matches  103;  Conservative   60;  Mismatches  133;  Indels  157;  Gaps   21;

Qy         22 PGPHASPVPYRRPRFLRGSSSSPGAADASRRPDSR---PVRSPAR---GRILP----WNA 71
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Db         36 PTCHSSTSEPRCSRFDPDGSGSPATWDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENV 95

Qy         72 GYAEIINAEKSEENEDQAACGKLCIRRCEEGAEEEWLLLCPEEFLIGHYWALFDGHGGPA 131
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Db         96 GCASQIGKRKE--NEDRFDFAQL----------------IDEVL---YFAVYDGHGGPA 133

Qy        132 AAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEEKGIRAEDLVIGA 191
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Db        134 AADFCHTHMEKCIMDLLP-----------------------------KEKNLET----- L 159

Qy        192 LESAFQECDEVIGRELEASGQ----MGGCTALVAVSLQG-KLYMANAGDSRAILVRRDEI 246
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Db        160 LTLAFLEIDKAFSSHARLSADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKP 219

Qy        247 RPLSFEEFTPE--TERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKVLFRDHHMSG 304
                 |: : |||    |::|||::            | |           :  : |||
Db        220 MKLTIDHTPERKDEKERIKK--------CGGF------VAWNSLGQP--------    252

Qy        305 WSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQLKPFLLSVPQVT 364
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Db        253 ------------------HVNGR-----LAMTRSIGDLDLKTSG---------VIAEPETK 281

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Qy        425 QGKEDSLTEEGQVSY---DDVSVFVIPLHSQGQ 454
                    ::||:   : |     |: :    |:|   : |:
Db        320 NEAAHAVTEQA-IQYGTEDNSTAVVVPFGAWGK 351


RESULT 15
US-09-975-072-4
; Sequence 4, Application US/09975072
; Patent No. US20020115667A1
;  GENERAL INFORMATION:
;   APPLICANT: Roch, Jean Marc
;   APPLICANT:  Bartel, Paul L.
;   APPLICANT:  Heichman, Karen
;   TITLE OF INVENTION: Protein Protein Interactions in Neurodegenerative
;   TITLE OF INVENTION:  Diseases
;   FILE REFERENCE: Protein Interactions in ND
;   CURRENT APPLICATION NUMBER: US/09/975,072
;   CURRENT FILING DATE:  2001-10-12
;   PRIOR APPLICATION NUMBER: US 60/240,790
;   PRIOR FILING DATE: 2000-10-17
;   NUMBER OF SEQ ID NOS: 4
;   SOFTWARE: PatentIn Ver. 2.0
;  SEQ ID NO 4
;    LENGTH: 372
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-975-072-4

  Query Match              8.2%;  Score 197.5;  DB 10;  Length 372;
  Best Local Similarity   22.7%;  Pred. No. 3.8e-09;
  Matches  103;  Conservative   60;  Mismatches  133;  Indels  157;  Gaps   21;

Qy         22 PGPHASPVPYRRPRFLRGSSSSPGAADASRRPDSR---PVRSPAR---GRILP----WNA 71
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Db         36 PTCHSSTSEPRCSRFDPDGSGSPATWDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENV 95

Qy         72 GYAEIINAEKSEENEDQAACGKLCIRRCEEGAEEEWLLLCPEEFLIGHYWALFDGHGGPA 131
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Db        134 AADFCHTHMEKCIMDLLP-----------------------------KEKNLET----- L 159

Qy        192 LESAFQECDEVIGRELEASGQ----MGGCTALVAVSLQG-KLYMANAGDSRAILVRRDEI 246
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Db        160 LTLAFLEIDKAFSSHARLSADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKP 219

Qy        247 RPLSFEEFTPE--TERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKVLFRDHHMSG 304
                 |: : |||    |::|||::            | |           :  : |||
Db        220 MKLTIDHTPERKDEKERIKK--------CGGF------VAWNSLGQP--------    252

Qy        305 WSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQLKPFLLSVPQVT 364
                                   |  ||         ||::| :||   |:              ::: |:
Db        253 ------------------HVNGR-----LAMTRSIGDLDLKTSG---------VIAEPETK 281

Qy        365 VLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSKLAQMLIHST 424
                :    :|    :|   :|: |||:  :::::::    |        ||              |
Db        282 RI----KLHHADDSFLVLTTDGINFMVNSQEICDFV---------NQ----------CHDP 319

Qy        425 QGKEDSLTEEGQVSY---DDVSVFVIPLHSQGQ 454
                    ::||:   : |     |: :    |:|   : |:
Db        320 NEAAHAVTEQA-IQYGTEDNSTAVVVPFGAWGK 351


Search completed: February 24, 2003, 14:41:24
Job time : 15 secs
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Db        160 LTLAFLEIDKAFSSHARLSADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKP 219

Qy        247 RPLSFEEIPE--TERQRIQQLAFVYPELLAGEFIRLEFPRRLKGDDLGQKVLFRDHHMSG 304
                |: :  ||   |::||::          | |        :  : |||
Db        220 MKLFIDHTPEKRPEKERIKK---------GGGF--------VAWNSLGQP---------- 252

Qy        305 WSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSPGLGDHQLRVLDTNIQLKPFLLSVPQVT 364
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Qy        365 VLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSKLAQMLIHST 424
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Qy        425 QGKEDSLTEEGQVSY---DDVSVFVIPLHSQGQ 454
                   ::||:  : |   |: :  |:|  : |:
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RESULT 12
US-09-973-077-4
; Sequence 4, Application US/09973077
; Patent No. US20020114799A1
; GENERAL INFORMATION:
;  APPLICANT: Roch, Jean-Marc
;  APPLICANT: Bartel, Paul L.
;  APPLICANT: Heichman, Karen
;  TITLE OF INVENTION: Protein Protein Interactions in Neurodegenerative
;  TITLE OF INVENTION: Diseases
;  FILE REFERENCE: Protein Interactions in ND
;  CURRENT APPLICATION NUMBER: US/09/973,077
;  CURRENT FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/240,790
;  PRIOR FILING DATE: 2000-10-17
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 372
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-973-077-4

  Query Match             8.2%;  Score 197.5;  DB 10;  Length 372;
  Best Local Similarity   22.7%;  Pred. No. 3.8e-09;
  Matches  103;  Conservative   60;  Mismatches  133;  Indels  157;  Gaps   21;

Qy         22 PGPHASPVPYRRPRFLRCSSSSPCAADASRRPDSR---PVRSPAR---CRTLP----WNA 71
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Db         36 PTCHSSTSEPRCSRFDPDGSGSPATWDNFGIWDNRIDEPILLPPSIKYGKPIPKISLENV 95

Qy         72 GYAFLINAEKSEFNEDQAACGKIRIRRCEFCAEEWLRLCPHEEFLTGHYWALFDGHGGPA 131
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Qy        132 AAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEEKGIRAEDLVIGA 191
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Db        134 AADFCHIHMEKCIMDLLP----------------------------KEKNLEI------L 159

Qy        192 LESAFQECDEVIGRELEASGQ----MGGCTALVAVSLQG-KLYMANAGDSRAILVRRDEI 246
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Db        160 LTLAFLEIDKAFSSHARLSADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKP 219

Qy        247 RPLSFEEIPE--TERQRIQQLAFVYPELLAGEFIRLEFPRRLKGDDLGQKVLFRDHHMSG 304
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Qy        305 WSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSPGLGDHQLRVLDTNIQLKPFLLSVPQVT 364
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Qy        365 VLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSKLAQMLIHST 424
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Db        282 RI---KLHHADDSPLVLTTDGINEMVNSQEICDFV------NQ-------------CHDP 319

Qy        425 QGKEDSLTEEGQVSY---DDVSVFVIPLHSQGQ 454
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US-09-973-063-4
; Sequence 4, Application US/09973063
; Patent No. US20020115119A1
; GENERAL INFORMATION:
;  APPLICANT: Roch, Jean-Marc
;  APPLICANT: Bartel, Paul L.
;  APPLICANT: Heichman, Karen
;  TITLE OF INVENTION: Protein Protein Interactions in Neurodegenerative
;  TITLE OF INVENTION: Diseases
;  FILE REFERENCE: Protein Interactions in ND
;  CURRENT APPLICATION NUMBER: US/09/973,063
;  CURRENT FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/240,790
;  PRIOR FILING DATE: 2000-10-17
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 372
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-973-063-4

  Query Match             8.2%;  Score 197.5;  DB 10;  Length 372;
  Best Local Similarity   22.7%;  Pred. No. 3.8e-09;
  Matches  103;  Conservative   60;  Mismatches  133;  Indels  157;  Gaps   21;

Qy         22 PGPHASPVPYRRPRFLRCSSSSPCAADASRRPDSR---PVRSPAR---CRTLP----WNA 71
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Qy         72 GYAFLINAEKSEFNEDQAACGKIRIRRCEFCAEEWLRLCPHEEFLTGHYWALFDGHGGPA 131
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Db        134 AADFCHIHMEKCIMDLLP----------------------------KEKNLEI------L 159

Qy        192 LESAFQECDEVIGRELEASGQ----MGGCTALVAVSLQG-KLYMANAGDSRAILVRRDEI 246
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Db        160 LTLAFLEIDKAFSSHARLSADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKP 219

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Db        220 MKLFIDHTPEKRPEKERIKK---------GGGF--------VAWNSLGQP---------- 252

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Db        253 ----------------HVNGR-------LAMTRSIGDLDLKTSG--------VIAEPEIK 281

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RESULT 14
US-09-973-964-4
; Sequence 4, Application US/09973964
; Patent No. US20020115606A1
;  PRIOR FILING DATE: 2001-07-30
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 372
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-908-902-2

  Query Match              8.2%;  Score 197.5;  DB 9;  Length 372;
  Best Local Similarity   22.7%;  Pred. No. 3.86e-09;
  Matches  103;  Conservative   60;  Mismatches  133;  Indels  157;  Gaps   21;

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Db        134 AADFCHIHMEKCIMDLLP                                  KEKNLEI-    --L 159

Qy        192 LESAFQECDEVIGRELEASGQ      MGGCTALVAVSLQG KLYMANAGDSRAILVRRDEI 246
              |    || |  |:           |             | ||  ||:     |  :|  :|:  |||||| |:  :
Db        160 LTLAFLEIDKAFSSHARLSADATILISGTTATVALLRDGIELVVASVGDSRAILCRKGKP 219

Qy        247 RPLSFEETPE  TERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKVLFRDHHMSG 304
                 |:  : |||    |::||::                 | |              :    :  |||
Db        220 MKLTIDHTPERKDEKERIKK            GGG  --       VAWNSLGQP            252

Qy        305 WSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQLKPFLLSVPQVT 364
                                  |   ||           ||::|  :||   |:                  ::: |:
Db        253                     HVNGR        LAMIRSIGDLDLKISG          VIAEPEIK 281

Qy        365 VLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSKLAQMLIHST 424
                :      :|     :|   :|: |||:   :::::::      |              ||                   |
Db        282 RI    KLHHADDSFLVLTTDGINFMVNSQEICDFV        NQ                  CHDP 319

Qy        425 QGKEDSLTEEGQVSY    DDVSVFVIPLHSQGQ 454
                        ::||:   :  |     |:  :    |:|    :  |:
Db        320 NEAAHAVTEQA-IQYGTEDNSTAVVVPFGAWGK 351


RESULT 10
US-09-973-063-4
; Sequence 4, Application US/09973063
; Patent No. US20020106676A1
; GENERAL INFORMATION:
;  APPLICANT: Roch, Jean-Marc
;  APPLICANT:  Bartel, Paul L.
;  APPLICANT:  Heichman, Karen
;  TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
;  TITLE OF INVENTION:  Diseases
;  FILE REFERENCE: Protein Interactions in ND
;  CURRENT APPLICATION NUMBER: US/09/973,063
;  CURRENT FILING DATE:  2001-10-11
;  PRIOR APPLICATION NUMBER: US 60/240,790
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: US 60/304,775
;  PRIOR FILING DATE: 2001-07-12
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 372
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-973-063-4

  Query Match              8.2%;  Score 197.5;  DB 10;  Length 372;
  Best Local Similarity   22.7%;  Pred. No. 3.86e-09;
  Matches  103;  Conservative   60;  Mismatches  133;  Indels  157;  Gaps   21;

Qy         22 PGPHASPVPYRRPRFLRGSSSSPGAADASRRPDSR    PVRSPAR-   GRILP   --WNA 71
              |   |:|      |  ||      | ||    |       |:|     |:   |      |: :|       |
Db         36 PICHSSISEPRCSRFDPDGSGSPATWDNPGIWDNRIDEPILLPPSIKYGKPIPKISLENV 95

Qy         72 GYAEIINAEKSEFNEDQAACGKLCIRRCEFGAEEEWLILCPEEFLIGHYWALFDGHGGPA 131
              | |   |    |     |||:     :|                          :| |     |:|::||||||
Db         96 GCASQIGKRKE--NEDRFDFAQL-   -  ---     ----  -  IDEVL-   YFAVYDGHGGPA 133

Qy        132 AAILAANILHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEEKGIRAEDLVIGA 191
              ||        :   |:    |                                      :||  :
Db        134 AADFCHIHMEKCIMDLLP--   --    --      -                -KEKNLEI     -  L 159

Qy        192 LESAFQECDEVIGRELEASGQ      MGGCTALVAVSLQG KLYMANAGDSRAILVRRDEI 246
              |    || |  |:           |             | ||  ||:     |  :|  :|:  |||||| |:  :
Db        160 LTLAFLEIDKAFSSHARLSADATILISGTTATVALLRDGIELVVASVGDSRAILCRKGKP 219

Qy        247 RPLSFEETPE -TERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKVLFRDHHMSG 304
                 |:  : |||    |::||::                 | |              :    :  |||
Db        220 MKLTIDHTPERKDEKERIKK----------GGG---       VAWNSLGQP            252

Qy        305 WSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQLKPFLLSVPQVT 364
                                  |   ||           ||::|  :||   |:                  ::: |:
Db        253 -----  ----------HVNGR-------LAMIRSIGDLDLKISG       --  VIAEPEIK 281

Qy        365 VLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSKLAQMLIHST 424
                :      :|     :|   :|: |||:   :::::::      |              ||                   |
Db        282 RI---KLHHADDSFLVLTTDGINFMVNSQEICDFV------NQ-------------CHDP 319

Qy        425 QGKEDSLTEEGQVSY---DDVSVFVIPLHSQGQ 454
                        ::||:   :  |     |:  :    |:|    :  |:
Db        320 NEAAHAVTEQA-IQYGTEDNSTAVVVPFGAWGK 351


RESULT 11
US-09-973-064-4
; Sequence 4, Application US/09973064
; Patent No. US20020106773A1
; GENERAL INFORMATION:
;  APPLICANT: Roch, Jean-Marc
;  APPLICANT:  Bartel, Paul L.
;  APPLICANT:  Heichman, Karen
;  TITLE OF INVENTION: Protein-Protein Interactions in Neurodegenerative
;  TITLE OF INVENTION:  Diseases
;  FILE REFERENCE: Protein Interactions in ND
;  CURRENT APPLICATION NUMBER: US/09/973,064
;  CURRENT FILING DATE:  2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/240,790
;  PRIOR FILING DATE: 2000-10-17
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 372
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-973-064-4

  Query Match              8.2%;  Score 197.5;  DB 10;  Length 372;
  Best Local Similarity   22.7%;  Pred. No. 3.86e-09;
  Matches  103;  Conservative   60;  Mismatches  133;  Indels  157;  Gaps   21;

Qy         22 PGPHASPVPYRRPRFLRGSSSSPGAADASRRPDSR    PVRSPAR    GRILP     WNA 71
              |   |:|      |  ||      | ||    |       |:|     |:   |      |: :|       |
Db         36 PICHSSISEPRCSRFDPDGSGSPATWDNPGIWDNRIDEPILLPPSIKYGKPIPKISLENV 95

Qy         72 GYAEIINAEKSEFNEDQAACGKLCIRRCEFGAEEEWLILCPEEFLIGHYWALFDGHGGPA 131
              | |   |    |     |||:     :|                          :| |     |:|::||||||
Db         96 GCASQIGKRKE--NEDRFDFAQL------ --  -----  IDEVL-  YFAVYDGHGGPA 133

Qy        132 AAILAANILHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEEKGIRAEDLVIGA 191
              ||        :   |:    |                                      :||  :
Db        134 AADFCHIHMEKCIMDLLP------------------     --  KEKNLEI-    - L 159
```

```
Qy        227 KLYMANAGDSRAILVRRDEIRPLSFEFTPETERQRIQQLAFVYPELLAGEFTRLEFPRRL 286
              ||:|: |||||| | :|               | |:   :       |: |    :: |:
Db        228 ILYIANLGDCRAILCRYNE -- --  -    ESQKHAALS -     LSKEHNPTQYEERM 269

Qy        287 KGDDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRV 346
                                      |::|:          |  |  |:|| | ||| :|| | :
Db        270 ----------          ----RIQKAG       -GNVRDGRVLGVLEVSRSIGDGQYK   299

Qy        347 LDTNIQLKPFLLSVPQVTVLDVDQLELQEDD-VVVMATDGLWDVLSNEQVAWLVRSFLPG 405
                       :  : |||     |: : :|  :|  :::| |||: | : |:     : | |
Db        300 -------RCGVISVP-----DIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCL-- 345

Qy        406 NQEDPHRFSKLAQMLIHSTQGKE-- ---          DSLTEEGQVSYDDVSVPVI 447
                ||              | : :||                 :   : |   | |:|:| |:
Db        346 --EDEK---------IQTREGKSAADARYEAAGNRLANKAVQRG- SADNVTVMVV 389


RESULT 7
US-10-147-874-3
; Sequence 3, Application US/10147874
; Publication No. US20030027237A1
; GENERAL INFORMATION:
;  APPLICANT: TARDIEUX, ISABELLE
;  APPLICANT:  DELORME, VIOLAINE
;  TITLE OF INVENTION: SERINE THREONINE PHOSPHATASE PROTEIN OF A PARASITIC ORGANISM OF T
;  TITLE OF INVENTION:  APICOMPLEXA PHYLUM, APPLICATIONS IN THERAPEUTICS
;  FILE REFERENCE: 223316US0
;  CURRENT APPLICATION NUMBER: US/10/147,874
;  CURRENT FILING DATE:  2002-05-20
;  PRIOR APPLICATION NUMBER: US 60/291,609
;  PRIOR FILING DATE: 2001-05-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 248
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-147-874-3

  Query Match              8.3%;  Score 200;  DB 9;  Length 248;
  Best Local Similarity   25.1%;  Pred. No. 1.4e-05;
  Matches   87;  Conservative   45;  Mismatches   91;  Indels  124;  Gaps   14;

Qy        120 YWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEE 179
              |:|:||||||  |:  ||  ||  | |                             :| :
Db          7 YFAVFDGHGGTRASKFAAQNLHQNLIR---------------            -KFPKG 38

Qy        180 KGIRAEDLVICALESAFQECDEVIGRELEASGQ----MGGCTALVAVSLQGKLYMANAGD 235
                 |  :  |    |    |:  ||    :   :|||       | ||   :::   ||:|| ||
Db         39 DVISVEKTVKRCLLDTFKHTDEEFLK--QASSQKPAWKDGSTATCVLAVDNILYIANLGD 96

Qy        236 SRAILVRRDEIRPLSFEFTPETERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKV 295
              ||||| | :|                  | ::   |:        |: |     :: |:
Db         97 SRAILCRYNE             -- ESQKHAALS       -LSKEHNPTQYEERM--------- 129

Qy        296 LFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQLKP 355
                                 |::|:          |  |   |:|| | ||| :|| | :           :
Db        130 ----- --------RIQKAG-------GNVRDGRVLGVLEVSRSIGDGQYK---------RC 161

Qy        356 FLLSVPQVTVLDVDQLELQEDD VVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFS 414
                :  ||       |: : :|  :|  :::| |||: | : |:      : | |      ||
Db        162 GVISVP       DIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCL      EDEK      209

Qy        415 KLAQMLIHSTQGKE---------------DSLTEEGQVSYDDVSVPVI 447
                        | : :||                :   :  ,  ' |:|:| |:
Db        210 ------IQTREGKSAADARYEAAGNRLANKAVQRG  SADNVTVMVV 248


RESULT 8
US-09-973-941-4
; Sequence 4, Application US/09973941
; Patent No. US20020164655A1
; GENERAL INFORMATION:
;  APPLICANT: Roch, Jean-Marc
;  APPLICANT:  Bartel, Paul L.
;  APPLICANT:  Heichman, Karen
;  TITLE OF INVENTION: Protein Protein Interactions in Neurodegenerative
;  TITLE OF INVENTION:  Diseases
;  FILE REFERENCE: Protein Interactions in ND
;  CURRENT APPLICATION NUMBER: US/09/973,941
;  CURRENT FILING DATE:  2001-10-11
;  PRIOR APPLICATION NUMBER: US 60/240,790
;  PRIOR FILING DATE: 2000-10-17
;  PRIOR APPLICATION NUMBER: US 60/304,775
;  PRIOR FILING DATE: 2001-07-13
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 372
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-973-941-4

  Query Match              8.2%;  Score 197.5;  DB 9;  Length 372;
  Best Local Similarity   22.7%;  Pred. No. 3.8e-09;
  Matches  103;  Conservative   60;  Mismatches  133;  Indels  157;  Gaps   21;

Qy         22 FCPHASPVPYRRLSLLRGSSSPGAALAASRFLSR    VRSTSR    GRTLP  - WNA 71
              |   |:|      |  ||      | ||     |       |:|    |:   |       |: :|        |
Db         36 PTCHSSTSLFRCSKFDFDGSGSIATWENFGIWDNKIDEPLLLASIKYGKLIKISLENV 95

Qy         72 GYALLNALRSEENGGQAAGGRLSIRRCDPGAHEWHTPSPEELLGHYWALFDGHGGPA 131
              |  |   |    |   |||:     :|                    :|  |     |:|:||||||||
Db         96 GCASQIGKRKE--NEDRFDFAQL-------------------TDEVL---YFAVYDGHGGPA 133

Qy        132 AAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEEKGIRAEDLVICA 191
              ||        :   |:    |                              :||  :
Db        134 AADFCHTHMEKCIMDLLP------------------------------KEKNLET------L 159

Qy        192 LESAFQECDEVIGRELEASGQ    MGGCTALVAVSLQGKLYMANAGDSRAILVRRDEI 246
              |   || | |:           |          | || ||:     | :| :|: ||||||| |: :
Db        160 LTLAFLETDKAFSSHARLSADATLLISGTTATVALLRDGIELVVASVGDSRAILCRKGKP 219

Qy        247 RPLSFEFTPE  TERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKVLFRDHHMSG 304
                 |: : | |     |::||::              | |            :   : |||
Db        220 MKLTIPHTPERKPEKERIKK             GGCF           VAWNSLGQP---  ------ 252

Qy        305 WSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNIQLKPFLLSVPQVT 364
                                  |   ||          ||::| :||   |:                   ::: |:
Db        253 -----------------HVNGR--------LAMIRSIGDLDLKISG---------VIAEPEIK 281

Qy        365 VLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSKLAQMLIHST 424
                :      :|      :|    :|: |||:   :::::::       |           ||                    !
Db        282 RI---KLHHADDSFLVLTTDGINFMVNSQEICDFV        NQ---------------CHDP 319

Qy        425 QGKEDSLTEEGQVSY     DDVSVPVIPLHSQGG 454
                      ::||:   :  |      |:  :   |:|    :  |:
Db        320 NEAAHAVTEQA IQYGTEDNSTAVVVPFGAWGK 351


RESULT 9
US-09-986-992-2
; Sequence 2, Application US/09986992
; Publication No. US20030027308A1
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY D.
;  APPLICANT:  WHYTE, DAVID
;  APPLICANT:  MANNING, GERARD
;  TITLE OF INVENTION: NOVEL HUMAN PROTEIN PHOSPHATASES IDENTIFIED FROM
;  TITLE OF INVENTION:  GENOMIC SEQUENCING
;  FILE REFERENCE: 038602/1277
;  CURRENT APPLICATION NUMBER: US/09/986,992
;  CURRENT FILING DATE:  2001-11-13
;  PRIOR APPLICATION NUMBER: 60/246,974
;  PRIOR FILING DATE: 2000-11-13
;  PRIOR APPLICATION NUMBER: 60/208,291
;  APPLICANT:  HILL, RON
;  APPLICANT:  FLANAGAN, PETER
;  TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
;  FILE REFERENCE: 038602/1180
;  CURRENT APPLICATION NUMBER: US/09/866,987
;  CURRENT FILING DATE:  2001-05-30
;  PRIOR APPLICATION NUMBER: 60/208,291
;  PRIOR FILING DATE: 2000-05-30
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 487
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;    OTHER INFORMATION: phosphatase polypeptide
US-09-866-987-6

  Query Match              8.7%;  Score 210.5;  DB 10;  Length 487;
  Best Local Similarity   27.0%;  Pred. No. 3.1e-10;
  Matches   79;  Conservative   30;  Mismatches   75;  Indels  105;  Gaps    9;

Qy        121 WALF    DGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFV 177
              |:||    ||:||  ||    |                              || |  :    |:
Db         53 WALFAVLDGHGGARAARFGAK                              HLEGHVLQELAGEEPS 88

Qy        178 EEKGIRAEDLVIGALESAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSR 237
               | :::.          ||   ||    ||: : | |      : || ||:| :    |:|:| |||
Db         89 EPEGVRE  -      ALRRAFLSADERL-RSLWPRVETGGPTAVVLLVSPRFLYLAHCGDSR 141

Qy        238 AILVR          RDEIRPLSFEEIPETERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDD 290
               |:||          :: |||            ||:||
Db        142 AVLCEAGAVAFSTEDHRPLR       FRERERI          -          -          ---- 168

Qy        291 LGKKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTN 350
                           | :|                      |  :: |: |:|||:|| ||    :
Db        169              HAAG                      IIRPERVEGSLAVSRALGDFTYKEAPGR 201

Qy        351 IQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFL 403
                      : : |:|  |          ||: :::|:||:|| :|    :| || | |
Db        202 PPEQLVSARPEVAAL       AELAPEEFMLLASDGVWDVVSAAALAGLVASRL 250


RESULT 7
US-09-801-368-278
; Sequence 278, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
;  APPLICANT: Busby, Robert
;  APPLICANT:  Dill, Brian
;  APPLICANT:  Hecht, Peter
;  APPLICANT:  Holtzman, Dean
;  APPLICANT:  Madden, Kevin
;  APPLICANT:  Maxon, Mary
;  APPLICANT:  Milne, Todd
;  APPLICANT:  No. US20020128250Alman, Theo
;  APPLICANT:  Royer, John
;  APPLICANT:  Salama, Sofie
;  APPLICANT:  Sherman, Amir
;  APPLICANT:  Silva, Jeff
;  APPLICANT:  Summers, Eric
;  TITLE OF INVENTION: Methods for Improved Secondary Metabolite Production in Fungi
;  FILE REFERENCE: 109272.117
;  CURRENT APPLICATION NUMBER: US/09/801,368
;  CURRENT FILING DATE:  2001-03-07
;  PRIOR APPLICATION NUMBER: US 09/487,558
;  PRIOR FILING DATE: 2000-01-19
;  PRIOR APPLICATION NUMBER: US 60/160,587
;  PRIOR FILING DATE: 1999-10-20
;  NUMBER OF SEQ ID NOS: 440
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 278
;   LENGTH: 281
;   TYPE: PRT
;   ORGANISM: Saccharomyces cerevisiae
US-09-801-368-278

  Query Match              8.4%;  Score 202;  DB 10;  Length 281;
  Best Local Similarity   22.5%;  Pred. No. 1.1e-09;
  Matches   93;  Conservative   48;  Mismatches  114;  Indels  158;  Gaps   15;

Qy         55 SRPVRSFARGRTLPWNAGYAETINAEKSEFNEDQAACGKLCIRRCEFGAEEEWLTLCPEE 114
                |  :  |        : :  | ||  |::        ||      |      | ::|
Db          5 SEILERPETPYPITYRVCVAENENSKFRPTMEDVHTYVKNFASRLDWG  -    -   -   52

Qy        115 FLTGHYWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDP 174
                     |:|:|||| |   |:          ||: :
Db         53 -----YFAVFDGHAGIQASKWCGKHLHTI                                77

Qy        175 QFVEEKGIRAEDL- VIGALESAFQECDEVIGRELEASGQMGGCTALVAV     -      222
                  |: | |::      |       |   :|      || |   :|    :        |||| : |
Db         78   ---EQNILADLIRDVRDVLNDSTLAIDEEINTKLVGN     SGCTAAVCVLRWELPDSVS 130

Qy        223 --    ---SLQGKLYMANAGDSRAILVRRDEIRPLSFEEIPETERQRIQQLAFVYPELLAG 275
                          |  |||  ||  ||||  :|  |                                   |
Db        131 DDSMDLAQHQKKLYTANVGDSRIVLFRN---------   -   ---  --  ---  ---   - G 159

Qy        276 FFTRLEFPRRLKGDDLGKKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLA 334
                     ||  :                 ||    |          :|||::             |      ::|:  |  ||
Db        160 NSIKLTY        -    -      -RPASPEIMQKVLQAG              GLIMKSRVNGMLA 196

Qy        335 VSRGLGDHQLRVLDTNIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQ 394
              |:| |||      :    |:  :        ||    || ::|                        ||      :::|  |||||||: ::
Db        197 VIRSLGD     KPFDSLVVGSPFTTSV EIT              SEDKFLILACDGLWDVIDDQD 243

Qy        395 VAWLVRSLLTDNQLDPHRLSKLAQMLIHRIQGRLDSLTEDDQVGYDDVGVFVI 447
                   |::         |:                  |::|:                 |  |      :  |:|:|  |:
Db        244 ACELIKDTLEPNE              AAKVLVRYA              LENG    TTDNVIVMVV 279


RESULT 6
US-09-935-124A-2
; Sequence 2, Application US/09935124A
; Patent No. US20020156003A1
; GENERAL INFORMATION:
;  APPLICANT: Lorens, James
;  APPLICANT:  Xu, Weiduan
;  APPLICANT:  Atchison, Robert
;  APPLICANT:  Bogenberger, Jakob
;  TITLE OF INVENTION: Modulators of Angiogenesis
;  FILE REFERENCE: 021044-000210us
;  CURRENT APPLICATION NUMBER: US/09/935,124A
;  CURRENT FILING DATE:  2002-05-21
;  PRIOR APPLICATION NUMBER: 60/284,760
;  PRIOR FILING DATE: 2001-04-18
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 392
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-935-124A-2

  Query Match              8.3%;  Score 200.5;  DB 9;  Length 392;
  Best Local Similarity   25.0%;  Pred. No. 2.3e-09;
  Matches   89;  Conservative   46;  Mismatches   96;  Indels  125;  Gaps   15;

Qy        112 PEEFLTG HYWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCIC 170
                 |      :|      |:|:|||||||  |:   ||   ||   | |
Db        138 PSSLITRVSYFAVFDGHGGIRASKFAAQNLHQNLIR--     ---   -   --     --- -  173

Qy        171 PSDPQFVEEKGIRAEDLVIGALESAFQECDEVIGRELEASGQ     MGGCTALVAVSLQG 226
                       :| :      |    |    |     |    |:   ||     :    :|| |            | ||      :::
Db        174     --KIIKQVISVEKIVKECLLPIEKHIPKEFL   QASSQKFAWKDGSIATCVLAVDN 227
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Qy        121 WALFPWHGCPAAAIIAANTIHSCLRPQIFAVVPGIVATQPPMHLNGRCICPSDPQFVEEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WALFPWHGCPAAAIIAANTIHSCLRPQIFAVVPGIVATQPPMHLNGRCICPSDPQFVEEK 180

Qy        181 GIRAFDLVIGALESAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAIL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GIRAFDLVIGALESAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAIL 240

Qy        241 VRRDEIRPLSPEETPETERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKVLFRDH 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VRRDEIRPLSPEETPETERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKVLFRDH 300

Qy        301 HMSGWSYKRVFKSDLKYPLIHGQGRQAFLLGTLAVSRGLGDHQLRVLDTNIQLKPFLLSV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 HMSGWSYKRVFKSDLKYPLIHGQGRQAFLLGTLAVSRGLGDHQLRVLDTNIQLKPFLLSV 360

Qy        361 PQVTVIDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSKLAQML 420
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSKLAQML 420

Qy        421 IHSTQGKEDSLTEEGQVSYDDVSVFVIPLHSQGQESSDH 459
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RESULT 2
US-09-860-351-4
; Sequence 4, Application US/09860351
; Patent No. US20020077463A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc.
;  APPLICANT:  Meyers, Rachel
;  TITLE OF INVENTION: 16105, A NOVEL PROTEIN HUMAN PHOSPHATASE
;  TITLE OF INVENTION:  AND USES THEREFOR
;  FILE REFERENCE: 38155-20013.00
;  CURRENT APPLICATION NUMBER: US/09/860,351
;  CURRENT FILING DATE:  2001-05-17
;  PRIOR APPLICATION NUMBER: US 60/205,260
;  PRIOR FILING DATE: 2000-05-19
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 274
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Consensus amino acid
US-09-860-351-4

  Query Match             10.1%;  Score 244;  DB 10;  Length 274;
  Best Local Similarity   28.1%;  Pred. No. 2.6e-13;
  Matches   91;  Conservative   40;  Mismatches   81;  Indels  112;  Gaps   11;

Qy        120 YWALFPWHGCPAAAIIAANTIHSCLRPQIFAVVPGIVATQPPMHLNGRCICPSDPQFVEE 179
              ::|:||||||   ||   |    ||   :   : ::   ||                 ||   |
Db         26 TFAVFPGHGGSQAAFYA[illegible]AFKKSPPES                  --  DFW  FM 65

Qy        180 KGIRAFDLVIGALESAFQECD    EVIGRELEASGQM         GGCTALVAVSLQGKLY 229
              |       |       ||:  :|  |  |      |:      |    |:  ::          |  ||:||:        |||
Db         66 KLSDLED----ALKESFLEADTDEELPSAEASAANKVLIKFDLSSGSTAVVALIRGNKLY 121

Qy        230 MANAGDSRAILVRRDEIRPLSPEETP          ETERQRIQQLAFVYPELLAGEFTRLEFP 283
              :||  |:||||:|  |            :       |      | ||:||:               ||  |
Db        122 VANVGDSRAVLCRNGNAIKWAVTLIHDHKPSNEDERERIE----------AAGGFV----- 167

Qy        294 RRLKGDDLGQKVLFRDHHMSGWSYKRVFKSDLKYPLIHGQGRQAFLLGTLAVSRGLGDHQ 343
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Db        168 -----------------------SRVS--------------NGRVNGVLAVSRAFGDFE 189

Qy        344 LR---------VLDTNIQLKPFLLSVPQVTVLDVD-----QLELQEDDVVVMATDGLWDV 389
              |:                 |:  |  :     ::  |   |:      :  |          |      :|:  :::| ||||||
Db        190 LKPGSKLGPEESLFANYE---YIKSPEQLVTAEPDVTSSTDLTPDKDEFLILACDGLWDV 246
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Qy        390 LSNEQVAWLVRSFLPGNQ---EDP 410
              :|:::|  :|||  |   ||:   |||
Db        247 VSDQEVVDIVRGHLSDGNKSAEDL 270


RESULT 3
US-09-828-302-14
; Sequence 14, Application US/09828302
; Patent No. US20020152502A1
; GENERAL INFORMATION:
;  APPLICANT: COSTA E SILVA, OSWALDO DA
;  APPLICANT:  VAN THIELEN, NOCHA
;  APPLICANT:  CHEN, ROUYING
;  APPLICANT:  ISHITANI, MANABU
;  TITLE OF INVENTION: PHOSPHATASE STRESS RELATED PROTEINS AND METHODS OF USE
;  TITLE OF INVENTION:  IN PLANTS
;  FILE REFERENCE: 16313 0029
;  CURRENT APPLICATION NUMBER: US/09/828,302
;  CURRENT FILING DATE:  2001 08 20
;  PRIOR APPLICATION NUMBER: 60/196,001
;  PRIOR FILING DATE: 2000-04-07
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 353
;   TYPE: PRT
;   ORGANISM: Physcomitrella patens
US-09-828-302-14

  Query Match             9.1%;  Score 220;  DB 10;  Length 353;
  Best Local Similarity   22.8%;  Pred. No. 4.2e-11;
  Matches   87;  Conservative   55;  Mismatches  109;  Indels  130;  Gaps   12;

Qy        121 WALFPWHGCPAAAIIAANTIHSCLRPQIFAVVPGIVATQPPMHLNGRCICPSDPQFVEEK 180
              : :|||||    |    |    ||   :  :   ||   :|  :                     :|
Db        [illegible] [illegible]                                          LLYS 96

Qy        181 GIRAFDLVIGA            LESAFQECDEV          IGRELEAS   --      -    210
              :| :::: ||            ||     : |::          ||  :  |
Db         97 [illegible] 156

Qy        211 -              GQMGGCTALVAVSLQGKLYMANAGDSRAILVRRDEIRPLSPEETPETER 259
                             |  :  |  ||:||:      ||::|||||||  |:  ||  |      ||  :   |    |
Db        157 ATKKHKYSDLQGPIYGSTAVVALIRGNKLFVANAGDSRCIMSRRGEAVNLSIDHKPNLEH 216

Qy        260 QRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKVLFRDHHMSGWSYKRVFKSDLKYPL 319
              :|                                                   ||:|  :
Db        217 ER-----------------------------------------------KRIESAG---GF 227

Qy        320 IHGQGRQAFLLGTLAVSRGLGDHQLRVLDTNIQLKPFLLSVPQVTVLDVDQLELQ--  ED 376
              :||     |:  |:|  ::|  :||  :  :              :|  |        |      |  :|:         |
Db        228 [illegible] 276

Qy        377 DVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSKLAQMLIHSTQGKEDSLTEEGQ 436
              :  :|:|  ||:|||:|::  |    |:|  ||   :          |  |  :  ::             |  |     |
Db        277 EPIVLACDGIWDVMSSQAVVDFVKSRLPTIK     TLSSLCEEILDYCL    SGTTRQQ 328

Qy        437 VSYDDVSVFVIPLHSQGQESS 457
                 |::|:  ::        |   :|
Db        329 EGCDNMSIIIVQPKQSGVAAS 349


RESULT 4
US-09-866-987-9
; Sequence 9, Application US/09866987
; Patent No. US20020002733A1
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY D.
;  APPLICANT:  MARTINEZ, RICARDO
;  APPLICANT:  WHYTE, DAVID
;  APPLICANT:  MANNING, GERARD
;  APPLICANT:  SUDARSANAM, SUCHA
;  APPLICANT:  CAENEPEEL, SEAN
```

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                    GenCore version 5.1.3
            Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:          February 24, 2003, 14:36:36 ; Search time 13 Seconds
                                            (without alignments)
                                            1097.004 Million cell updates/sec

Title:           US-09-866-987-8
Perfect score:   2415
Sequence:        1 MSAGWFRRRFLPGEPLPAPR..........IDVSVFVIPLHSQGQESSDH 459

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        156504 seqs, 31069816 residues

Total number of hits satisfying chosen parameters:      156504

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Published_Applications_AA:*
                1: [illegible]_NEW_PUB.pep:*
                2: [illegible]_NEW_PUB.pep:*
                3: [illegible] NEW_PUB.pep:*
                4: [illegible]COMB.pep:*
                5: [illegible] NEW_PUB.pep:*
                6: [illegible]PUBCOMB.pep:*
                7: [illegible]COMB.pep:*
                8: [illegible]PUBCOMB.pep:*
                9: [illegible]_NEW_PUB.pep:*
               10: [illegible]COMB.pep:*
               11: [illegible]_NEW_PUB.pep:*
               12: [illegible]COMB.pep:*
               13: [illegible]_NEW_PUB.pep:*
               14: [illegible]COMB.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                   SUMMARIES
                     %
Result               Query
  No.      Score   Match Length DB  ID                           Description
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    1      2415    100.0    459  10  US-09-866-987-8             Sequence 8, Appli
    2       244     10.1    254  10  US-09-860-351-4             Sequence 4, Appli
    3       220      9.1    353  10  US-09-828-302-14            Sequence 14, Appl
    4     210.5      8.7    387  10  US-09-866-987-9             Sequence 9, Appli
    5       202      8.4    281  10  US-09-801-368-278           Sequence 278, App
    6  [illegible]   8.3 [illegible] 9  US-09-935-[illegible]4A-2  Sequence 2, Appli
    7       200      8.3    248   9  US-10-147-874-3            Sequence 3, Appli
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   10     197.5      8.2    372  10  US-09-973-[illegible]-4    Sequence 4, Appli
   11     197.5      8.2    372  10  US-09-973-064-4            Sequence 4, Appli
   12     197.5      8.2    372  10  US-09-973-077-4            Sequence 4, Appli
   13     197.5      8.2    372  10  US-09-973-063-4            Sequence 4, Appli
   14     197.5      8.2    372  10  US-09-973-964-4            Sequence 4, Appli
   15     197.5      8.2    372  10  US-09-975-072-4            Sequence 4, Appli
   16     197.5      8.2    372  10  US-09-972-[illegible]-4    Sequence 4, Appli
   17     197.5      8.2    372  10  US-09-972-757-4            Sequence 4, Appli
   18     197.5      8.2    372  10  US-09-973-[illegible]-4    Sequence 4, Appli
   19       195      8.1    361   9  US-10-178-977A-2           Sequence 2, Appli
   20       195      8.1    361   9  US-10-178-977A-4           Sequence 4, Appli
   21       195      8.1    361   9  US-10-178-977A-6           Sequence 6, Appli
   22     191.5      7.9    352  10  US-09-860-351-2            Sequence 2, Appli
   23     191.5      7.9    373  10  US-09-925-300-1655         Sequence 1655, Ap
   24     191.5      7.9    390   9  US-10-072-130-3            Sequence 3, Appli
   25     187.5      7.8    400  10  US-09-925-300-1254         Sequence 1254, Ap
   26     186.5      7.7    265   9  US-10-147-874-4            Sequence 4, Appli
   27     186.5      7.7    478   9  US-10-072-130-1            Sequence 1, Appli
   28     186.5      7.7    478   9  US-10-072-130-4            Sequence 4, Appli
   29     184.5      7.6    382  10  US-09-972-741-2            Sequence 2, Appli
   30     178.5      7.4    371  10  US-09-828-302-15           Sequence 15, Appl
   31       178      7.4    228  10  US-09-900-715-2            Sequence 2, Appli
   32     170.5      7.1    196   9  US-10-147-874-8            Sequence 8, Appli
   33     160.5      6.6    605   9  US-10-073-123-2            Sequence 2, Appli
   34       149      6.2    491   9  US-10-114-893-69           Sequence 69, Appl
   35       147      6.1    186   9  US-10-147-874-5            Sequence 5, Appli
   36     139.5      5.8    151   9  US-10-147-874-6            Sequence 6, Appli
   37     136.5      5.7    114  10  US-09-860-351-5            Sequence 5, Appli
   38     135.5      5.6    150   9  US-10-147-874-7            Sequence 7, Appli
   39     133.5      5.5    149  10  US-09-860-351-6            Sequence 6, Appli
   40     126.5      5.2    232   9  US-10-147-874-11           Sequence 11, Appl
   41       126      5.2    200   9  US-10-147-874-10           Sequence 10, Appl
   42     119.5      4.9    331   9  US-10-147-874-2            Sequence 2, Appli
   43     117.5      4.9    504   9  US-10-158-895-2            Sequence 2, Appli
   44     117.5      4.9    504  12  US-10-123-427-2            Sequence 2, Appli
   45     117.5      4.9    504  12  US-10-123-427-6            Sequence 6, Appli

                                   ALIGNMENTS

RESULT 1
US-09-866-987-8
; Sequence 8, Application US/09866987
; Patent No. US20020[illegible]703A1
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY D.
;  APPLICANT:  MARTINEZ, RICARDO
;  APPLICANT:  WHYTE, DAVID
;  APPLICANT:  MANNING, GERARD
;  APPLICANT:  SUDARSANAM, SUCHA
;  APPLICANT:  CAENEPEEL, SEAN
;  APPLICANT:  HILL, RON
;  APPLICANT:  FLANAGAN, PETER
;  TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
;  FILE REFERENCE: 038602/1180
;  CURRENT APPLICATION NUMBER: US/09/866,987
;  CURRENT FILING DATE:  2001-05-30
;  PRIOR APPLICATION NUMBER: 60/208,291
;  PRIOR FILING DATE: 2000-05-30
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 459
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: phosphatase polypeptide
US-09-866-987-8

  Query Match              100.0%;  Score 2415;  DB 10;  Length 459;
  Best Local Similarity    100.0%;  Pred. No. 1.9e-198;
  Matches  459;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MSAGWFRRRFLPGEPLPAPRPPGPHASPVPYRRPRFLRGSSSSPGAADASRRPDSRPVRS 60

Qy         61 PARGRTLFWNAGYAETINAEKSEFNEDQAACGKLCIRRCEFGAEEEWLTLCPEEFLTGHY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PARGRTLFWNAGYAETINAEKSEFNEDQAACGKLCIRRCEFGAEEEWLTLCPEEFLTGHY 120
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Qy       407 QED 409
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Db       411 DEN 413


Search completed: February 24, 2003, 14:39:57
Job time : 26 secs
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Db     177 ---NAGGSVMIQ---------------------------------KVNGSLAVSKALGDFDYKC 204

Qy     347 LDINIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGN 406
           :     :   |   |:  | |::: | ::|  :::| ||:|||: ||::    ||| |
Db     205 VHGKCPTFQ--IVSPFPEVHDIERSE-EDDQFIILACDGIWDVMGNEELCDFVRSRL--- 258

Qy     407 QEDPHRFSKLAQMLIHSTQGKEDSLTEEGQVSYDDVSVFVI 447
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Db     259 -EVTDDLEKVCNEVV-------DTCLYKG--SRDNMSVILI 289


RESULT 14
US-08-822-701-2
; Sequence 2, Application US/08822701
; Patent No. 5976853
;  GENERAL INFORMATION:
;    APPLICANT:  Guthridge, Mark
;    APPLICANT:  Basilico, Claudio
;    TITLE OF INVENTION:  NOVEL GROWTH FACTOR INDUCIBLE
;    TITLE OF INVENTION:  SERINE/THREONINE PHOSPHATASE, FIN13
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David A. Jackson, Esq.
;      STREET:  411 Hackensack Ave, Continental Plaza, 4th
;      STREET:  Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/822,701
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  1049-1-002 N
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  392 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:  N-terminal
US-08-822-701-2

  Query Match             6.4%;  Score 154;  DB 2;  Length 392;
  Best Local Similarity   24.3%;  Pred. No. 2.4e-06;
  Matches   59;  Conservative   42;  Mismatches   72;  Indels   70;  Gaps    9;

Qy     178 EEKCIRAFDIVIGALFSAFQECDEVIGPELEASGQMG---------CCTALVAVSLQGKLY 229
           :| |  :|:       |    :| :|     |:   |  |          | ||:||:    :|
Db     130 DEDGYSSEEAFNEFDEDDTEEAEEDDDEEMMVPGMEGKEEPGSDSGTTAVVALIRGKQLI 189

Qy     230 MANAGDSKAILVRRDEIRPLSFEETPETEPQRIQQLAFVYPELLACEETRLEEPPRLKGD 289
           :|||||| ::       :     :|::  || |       :||                |:|
Db     190 VANAGDSRCVVSEAGKALDMSYDHKPEDE----VELA-------------------RIK- 225

Qy     290 DEGQKVIERRDHHMSCWSYKEVEKSDIKYPLIHQQGRQARLLGTLAVSRGLGDHQLRVLDT 349
           : | ||        | |                           |: | | :|| :|||  :
Db     226 NAGGKVI----MEG------------------------KVNGCLNLSRAIGDHFYK---R 254

Qy     350 NIQLKP---FLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGN 406
           |  | |     : ::| : || :         : : :|:| ||:|:|:|:::|    ::| :
Db     255 NKNLPPQEQMISALPDIKVLTI----TPDHEFMVIACDGIWNVMSSQEVVDFIQSKISQR 310

Qy     407 QED 409
            |:
Db     311 DEN 313


RESULT 15
US-08-935-855-2
; Sequence 2, Application US/08935855
; Patent No. 6066485
;  GENERAL INFORMATION:
;    APPLICANT:  Guthridge, Mark
;    APPLICANT:  Basilico, Claudio
;    TITLE OF INVENTION:  NOVEL GROWTH FACTOR INDUCIBLE
;    TITLE OF INVENTION:  SERINE/THREONINE PHOSPHATASE, FIN13
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David A. Jackson, Esq.
;      STREET:  411 Hackensack Ave, Continental Plaza, 4th
;      STREET:  Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/935,855
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  1049-1-002 CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  392 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:  N-terminal
US-08-935-855-2

  Query Match             6.4%;  Score 154;  DB 3;  Length 392;
  Best Local Similarity   24.3%;  Pred. No. 2.4e-06;
  Matches   59;  Conservative   42;  Mismatches   72;  Indels   70;  Gaps    9;

Qy     178 EEKCIRAFDIVIGALFSAFQECDEVIGPELEASGQMG---------CCTALVAVSLQGKLY 229
           :| |  :|:       |    :| :|     |:   |  |          | ||:||:    :|
Db     130 DEDGYSSEEAFNEFDEDDTEEAEEDDDEEMMVPGMEGKEEPGSDSGTTAVVALIRGKQLI 189

Qy     230 MANAGDSKAILVRRDEIRPLSFEETPETEPQRIQQLAFVYPELLACEETRLEEPPRLKGD 289
           :|||||| ::       :     :|::  || |       :||                |:|
Db     190 VANAGDSRCVVSEAGKALDMSYDHKPEDE----VELA-------------------RIK- 225

Qy     290 DEGQKVIERRDHHMSCWSYKEVEKSDIKYPLIHQQGRQARLLGTLAVSRGLGDHQLRVLDT 349
           : | ||        | |                           |: | | :|| :|||  :
Db     226 NAGGKVI----MEG------------------------KVNGCLNLSRAIGDHFYK---R 254

Qy     350 NIQLKP---FLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGN 406
           |  | |     : ::| : || :         : : :|:| ||:|:|:|:::|    ::| :
Db     255 NKNLPPQEQMISALPDIKVLTI----TPDHEFMVIACDGIWNVMSSQEVVDFIQSKISQR 310
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Qy        388 LVEGELTGNLEDPHRFSKLAQMLIHSTQGKEDSLT 432
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Db        257 YVKGEEEVSGEEENVCNWVVEETGH  KGSRDNMS 289


RESULT 12
US-08-822-761-8
; Sequence 8, Application US/08822761
; Patent No. 5976853
;  GENERAL INFORMATION:
;     APPLICANT:  Guthridge, Mark
;     APPLICANT:  Basilico, Claudio
;     TITLE OF INVENTION:  NOVEL GROWTH FACTOR INDUCIBLE
;     TITLE OF INVENTION:  SERINE/THREONINE PHOSPHATASE, FIN13
;     NUMBER OF SEQUENCES:  18
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  David A. Jackson, Esq.
;       STREET:  411 Hackensack Ave, Continental Plaza, 4th
;       STREET:  Floor
;       CITY:  Hackensack
;       STATE:  New Jersey
;       COUNTRY:  USA
;       ZIP:  07601
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/822,761
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jackson Esq., David A.
;       REGISTRATION NUMBER:  26,742
;       REFERENCE/DOCKET NUMBER:  1049-1-002 N
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201-487-5800
;       TELEFAX:  201-343-1684
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  306 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:
;     ORIGINAL SOURCE:
;       ORGANISM:  Rattus
US-08-822-761-8

  Query Match              7.6%;  Score 183.5;  DB 2;  Length 306;
  Best Local Similarity   21.7%;  Pred. No. 2.7e-09;
  Matches   74;  Conservative   53;  Mismatches  111;  Indels  103;  Gaps   12;

Qy        112 PEEFLTGHYWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICP 171
                        ::  ::|||  |     |                 |      |:  :
Db         47 PSGLETWSFFAVYDGHAGSQVA         KYCCEHLLDHIT              -  -  -  80

Qy        172 SDPQFVEEKGIRAEDLVIGALESAFQECDE    VIGRELEASGQMGGCTALVAVSLQGKL 228
                 ::    .     .  :  :  |     :  :  |  |  ||     |:  :    :  :  |        |  :  |
Db         81 NNQDFKGSAGAPSVENVKNGIRTGFLEIDEHMRVMSLKKHGADRSGSTAVGVLISPQ HT 139

Qy        229 YMANAGDSRAILVRRDEIRPLSFEFTPET   ERQRIQQLAFVYPELLAGEFTRLEFPRRL 286
                  |    |  ||||  :|  |    ::        :  :    |        |::|||
Db        140 YFINCGDSRGLLCRNRKVHFFTQDHKPSNPLEKERIQ                 -             -  176

Qy        287 KGPDLGQKVLFRDHHMSGWSYKEVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRV 346
                     :  |    |:  :                                      |:  |:||||| |||       :
Db        177      NAGGSVMIQ                                  -RVNGSLAVSRALGDFDYKC 204

Qy        347 LDINIQLKPFLLSVPQVTVLDVDQLELQEEDVVVMATDGLWDVLSNEQVAWLVRGFLEGN 406
```

```
              :         :       |   |:    |  |:::  |  ::|    :::|  ||:|||:  ||::      |||  |
Db        205 VHGKGPTEQ   LVSPEPEVHDIERSE-EDDQFIILACDGIWDVMGNEELCDFVRSRL  -  258

Qy        407 QEDPHRFSKLAQMLIHSTQGKEDSLTEEGQVSYDDVSVFVI 447
                |      :  :    ::             |:      :|    |  |::|' :|
Db        259  EVIDDLEKVCNEVV           DTCLYKG  GKDNMSVILI 289


RESULT 13
US-08-935-855-8
; Sequence 8, Application US/08935855
; Patent No. 6066485
;  GENERAL INFORMATION:
;     APPLICANT:  Guthridge, Mark
;     APPLICANT:  Basilico, Claudio
;     TITLE OF INVENTION:  NOVEL GROWTH FACTOR INDUCIBLE
;     TITLE OF INVENTION:  SERINE/THREONINE PHOSPHATASE, FIN13
;     NUMBER OF SEQUENCES:  22
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  David A. Jackson, Esq.
;       STREET:  411 Hackensack Ave, Continental Plaza, 4th
;       STREET:  Floor
;       CITY:  Hackensack
;       STATE:  New Jersey
;       COUNTRY:  USA
;       ZIP:  07601
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/935,855
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jackson Esq., David A.
;       REGISTRATION NUMBER:  26,742
;       REFERENCE/DOCKET NUMBER:  1049-1-002 CIP
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201-487-5800
;       TELEFAX:  201-343-1684
;   INFORMATION FOR SEQ ID NO:  8:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  306 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:
;     ORIGINAL SOURCE:
;       ORGANISM:  Rattus
US-08-935-855-8

  Query Match              7.6%;  Score 183.5;  DB 3;  Length 306;
  Best Local Similarity   21.7%;  Pred. No. 2.7e-09;
  Matches   71;  Conservative   53;  Mismatches  111;  Indels  103;  Gaps   12;

Qy        112 PEEFLTGHYWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICP 171
              |      |    ::|::|||  |     |                 |      |:  :
Db         47 PSGLETWSFFAVYDGHAGSQVA- ---  -KYCCEHLLDHIT-- ---  --  -------   80

Qy        172 SDPQFVEEKGIRAEDLVIGALESAFQECDE   -VIGRELEASGQMGGCTALVAVSLQGKL 228
              ::    |         |    :    :    |        :    :  |  |  ||       |:     :          :    :    |            |  :  |  |
Db         81 NNQDFKGSAGAPSVENVKNGIRTGFLEIDEHMRVMSLKKHGADRSGSTAVGVLISPQ-HT 139

Qy        229 YMANAGDSRAILVRRDEIRPLSFEFTPET   ERQRIQQLAFVYPELLAGEFTRLEFPRRL 286
              |    |  ||||  :/  |    ::        :  :    |        |::/||
Db        140 YFINCGDSRGLLCRNRKVHFFTQDHKPSNPLEKERIQ--   -   --    -     - ---   176

Qy        287 KGPDLGQKVLFRDHHMSGWSYKEVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRV 346
                 :  |    |:  :                                       |:  |:||||| |||       :
                      | :     : |     |     : |     : : | : || :      :|         | ||:
Db         83 -------EDFRAAGKSCSALFLSVENVKNGIRTGFLKIDFYMRNFSDLRNGMDRSGSTAV 135

Qy        220 VAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEFTP--ETERQRIQQLAFVYPELLAGEF 277
                 :      :|   | ||||||:| |   ::    : :   |     |::|||
Db        136 GVMISPKHIYFINCGDSRAVLYRNGQVCFSTQDHKPCNPREKERIQ-------------- 181

Qy        278 TRLEFPRRLKGDDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSR 337
                          : |   |: :                               |: |:|||||
Db        182 ------------NAGGSVMIQ------------------------------FVNGSLAVSR 200

Qy        338 GLGDHQLRVLDTNIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAW 397
                |||:   : :|        :   :    |:|       : |   :||: :::| ||:|||:|||::
Db        201 ALGDYDYKCVDGKGPTEQLVSPEPEV----YEILRAEEDEFIILACDGIWDVMSNEELCE 256

Qy        398 LVRSFLPGNQEDPHRFSKLAQMLIHSTQGKEDSLT 432
                |:| |   : :   :   :  :      :|   :|   |:::
Db        257 YVKSRLEVSDDLENVCNWVVDTCLH--KGSRDNMS 289


RESULT 10
US-08-873-093-4
; Sequence 4, Application US/08873093
; Patent No. 5853997
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Goli, Surya K.
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Corley, Neil C.
;    APPLICANT:  Zhang, Hong
;    TITLE OF INVENTION:  NEW PROTEIN PHOSPHATASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/873,093
;      FILING DATE:  Filed Herewith
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0319 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-0555
;      TELEFAX:  415-845-4166
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  478 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  1452526
US-08-873-093-4

  Query Match              7.7%;  Score 186.5;  DB 2;  Length 478;
  Best Local Similarity   20.6%;  Pred. No. 2.7e-09;
  Matches   69;  Conservative   57;  Mismatches  106;  Indels  103;  Gaps   10;

Qy        105 EEWLILCPEEFLTGHYWALFDGHGGPAAAILAANTLHSCLRRQLEAVVECLVATQPPMHL 164
              |:|            ::|::||| |     |              : |     || :
Db         51 EDW------------SFFAVYDGHAGSRVA------NYCSTHLLEHITTN----------- 82

Qy        165 NGRCICPSDPQFVEEKGIRAE---DLVIGALESAFQECDEVIGR--ELEASGQMGGCTAL 219
                      | :     : |     |     : |     : : | : || :      :|         | ||:
Db         83 -------EDFRAAGKSCSALFLSVENVKNGIRTGFLKIDFYMRNFSDLRNGMDRSGSTAV 135

Qy        220 VAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEFTP--ETERQRIQQLAFVYPELLAGEF 277
                 :      :|   | ||||||:| |   ::    : :   |     |::|||
Db        136 GVMISPKHIYFINCGDSRAVLYRNGQVCFSTQDHKPCNPREKERIQ-------------- 181

Qy        278 TRLEFPRRLKGDDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSR 337
                          : |   |: :                               |: |:|||||
Db        182 ------------NAGGSVMIQ------------------------------FVNGSLAVSR 200

Qy        338 GLGDHQLRVLDTNIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAW 397
                |||:   : :|        :   :    |:|       : |   :||: :::| ||:|||:|||::
Db        201 ALGDYDYKCVDGKGPTEQLVSPEPEV----YEILRAEEDEFIILACDGIWDVMSNEELCE 256

Qy        398 LVRSFLPGNQEDPHRFSKLAQMLIHSTQGKEDSLT 432
                |:| |   : :   :   :  :      :|   :|   |:::
Db        257 YVKSRLEVSDDLENVCNWVVDTCLH--KGSRDNMS 289


RESULT 11
US-09-206-646-1
; Sequence 1, Application US/09206646
; Patent No. 6436637
; GENERAL INFORMATION:
;  APPLICANT: Bandman, Olga
;  APPLICANT:  Goli, Surya K.
;  APPLICANT:  Lal, Preeti G.
;  APPLICANT:  Corley, Neil C.
;  APPLICANT:  Zhang, Hong
;  TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
;  FILE REFERENCE: PF-0319-1 DIV
;  CURRENT APPLICATION NUMBER: US/09/206,646
;  CURRENT FILING DATE:  2001-12-07
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PERL Program
; SEQ ID NO 1
;   LENGTH: 479
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. 6436637 013177CI1
US-09-206-646-1

  Query Match              7.7%;  Score 186.5;  DB 4;  Length 479;
  Best Local Similarity   20.6%;  Pred. No. 2.7e-09;
  Matches   69;  Conservative   57;  Mismatches  106;  Indels  103;  Gaps   10;

Qy        105 EEWLILCPEEFLTGHYWALFDGHGGPAAAILAANTLHSCLRRQLEAVVECLVATQPPMHL 164
              |:|            ::|::||| |     |              : |     || :
Db         51 EDW------------SFFAVYDGHAGSRVA------NYCSTHLLEHITTN----------- 82

Qy        165 NGRCICPSDPQFVEEKGIRAE---DLVIGALESAFQECDEVIGR--ELEASGQMGGCTAL 219
                      | :     : |     |     : |     : : | : || :      :|         | ||:
Db         83 -------EDFRAAGKSCSALFLSVENVKNGIRTGFLKIDFYMRNFSDLRNGMDRSGSTAV 135

Qy        220 VAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEFTP--ETERQRIQQLAFVYPELLAGEF 277
                 :      :|   | ||||||:| |   ::    : :   |     |::|||
Db        136 GVMISPKHIYFINCGDSRAVLYRNGQVCFSTQDHKPCNPREKERIQ-------------- 181

Qy        278 TRLEFPRRLKGDDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSR 337
                          : |   |: :                               |: |:|||||
Db        182 ------------NAGGSVMIQ------------------------------FVNGSLAVSR 200

Qy        338 GLGDHQLRVLDTNIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAW 397
                |||:   : :|        :   :    |:|       : |   :||: :::| ||:|||:|||::
Db        201 ALGDYDYKCVDGKGPTEQLVSPEPEV----YEILRAEEDEFIILACDGIWDVMSNEELCE 256
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Qy        286 LKCDDLGQKVLFEDHHMSGWSYKRVEKSDLKYPLIHGQGPQARLLGILAVSPGLGDHQLR 345
                    : |  |: :                                 |: |:||||| |||:  :
Db        181     NAGGSVMIQ                                   RVNGSLAVSRALGDYDYK 207

Qy        346 VLDINIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPG 405
                 :|      :  :    |:|        : :  :||:  ||:| ||:|||:|||::    |:| |
Db        208 CVDGKGPIEQLVSPEPEV    YEIVRAEEDEFVVLACDGIWDVMSNEELCEFVKSRLEV 263

Qy        406 NQEDPHRFSKLAQMLIHSTQGKEDSLI 432
               :  :  :  :  :     :|   :|  |:::
Db        264 SDDLENVCNWVVDTCLH  KGSRDNMS 288


RESULT 8
US-08-935-855-7
; Sequence 7, Application US/08935855
; Patent No. [illegible]
;  GENERAL INFORMATION:
;     APPLICANT:  Gathridge, Mark
;     APPLICANT:  Basilico, Claudio
;     TITLE OF INVENTION:  NOVEL GROWTH FACTOR INDUCIBLE
;     TITLE OF INVENTION:  SERINE/THREONINE PHOSPHATASE, FIN13
;     NUMBER OF SEQUENCES:  22
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  David A. Jackson, Esq.
;       STREET:  411 Hackensack Ave, Continental Plaza, 4th
;       STREET:  Floor
;       CITY:  Hackensack
;       STATE:  New Jersey
;       COUNTRY:  USA
;       ZIP:  07601
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/935,855
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Jackson, Esq., David A.
;       REGISTRATION NUMBER:  26,742
;       REFERENCE/DOCKET NUMBER:  1049 1 002 CIP
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201 487 5800
;       TELEFAX:  201 343 1684
;   INFORMATION FOR SEQ ID NO:  7:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  309 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:  NO
;     FRAGMENT TYPE:
;     ORIGINAL SOURCE:
;       ORGANISM:  Mus musculus
US-08-935-855-7

  Query Match             7.8%;  Score 188.5;  DB 3;  Length 309;
  Best Local Similarity   21.4%;  Pred. No. 9.1e-10;
  Matches   70;  Conservative   52;  Mismatches   98;  Indels  107;  Gaps    9;

Qy        120 YWALFDGHGGPAAAILAANILHSCLRRQLEAVVEGLVATQPPMHLNGRCICESHEQFVEE 179
                :|::::||  |     |               : |      || :
Db         65 FFAVYDGHAGSRVA        NYCSTHLLEHI                      -      TIN 82

Qy        180 KGIRAEDLVIGALE              SAFQECDEVIGR  ELEASGQMGGCIALVAVSLQGK 227
                :  |   |     | |                : | : || :      :|             | ||:  :
Db         83 EDFRAADKSGSALEPDVEQVKKGFEDPLKIFFYMPNFLLERNIMEGGCAVCVMVGPIH 142

Qy        228 LYMANAGDSRAILVRRDEIRPLSFEFTP  ETERQRIQQLAFVYPELLAGEFTRLEFPRR 285
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              :;  | ||||||:| |   ::   : :  |    |::|||
Db        143 MYFINCGDSRAVLCRNGQVCFSTQDHKPCNPVEKERIQ--- ---- ------------ - 180

Qy        286 LKCDDLGQKVLFEDHHMSGWSYKRVEKSDLKYPLIHGQGPQARLLGILAVSPGLGDHQLR 345
                    : |  |: :                                 |: |:||||| |||:  :
Db        181   ---NAGGSVMIQ--    - - -   - - - - - -- --      ---RVNGSLAVSRALGDYDYK 207

Qy        346 VLDINIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPG 405
                 :|      :  :    |:|        : :  :||:  ||:| ||:|||:|||::    |:| |
Db        208 CVDGKGPIEQLVSPEPEV----YEIVRAEEDEFVVLACDGIWDVMSNEELCEFVKSRLEV 263

Qy        406 NQEDPHRFSKLAQMLIHSTQGKEDSLI 432
               :  :  :  :  :     :|   :|  |:::
Db        264 SDDLENVCNWVVDTCLH--KGSRDNMS 288


RESULT 9
US-08-873-093-1
; Sequence 1, Application US/08873093
; Patent No. 5853997
;  GENERAL INFORMATION:
;     APPLICANT:  Bandman, Olga
;     APPLICANT:  Goli, Surya K.
;     APPLICANT:  Lal, Preeti
;     APPLICANT:  Corley, Neil C.
;     APPLICANT:  Zhang, Hong
;     TITLE OF INVENTION:  NEW PROTEIN PHOSPHATASE
;     NUMBER OF SEQUENCES:  4
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;       STREET:  3174 Porter Drive
;       CITY:  Palo Alto
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  94304
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/873,093
;       FILING DATE:  Filed Herewith
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Billings, Lucy J.
;       REGISTRATION NUMBER:  36,749
;       REFERENCE/DOCKET NUMBER:  PF-0319 US
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415-855-0555
;       TELEFAX:  415-845-4166
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  478 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     IMMEDIATE SOURCE:
;       LIBRARY:  THP1PLB01
;       CLONE:  13177
US-08-873-093-1

  Query Match             7.7%;  Score 186.5;  DB 2;  Length 478;
  Best Local Similarity   20.6%;  Pred. No. 2.7e-09;
  Matches   69;  Conservative   57;  Mismatches  106;  Indels  103;  Gaps   10;

Qy        105 EEWLIISPEEFLIGHYWALFDGHGGPAAAILAANILHSCLRRQLEAVVEGLVATQPPMHL 164
                 |:|                  ::|::|||  |    |              :  |     || :
Db         51 EDW               GFFAVYDGHAGSRVA         NYCSTHLLEHITTN ---   ---  82

Qy        165 NGRCICESHEQFVEEKGIRAE--DLVIGALESAFQECDEVIGR--ELEASGQMGGCTAL 219
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  Query Match             7.9%;  Score 191.5;  DB 4;  Length 390;
  Best Local Similarity   21.2%;  Pred. No. 6.7e-10;
  Matches   71;  Conservative   55;  Mismatches  106;  Indels  103;  Gaps   10;

Qy        105 EEWLILCPEEFLIGHYWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHL 164
              |:|            ::|::||| |   |       : |    || :
Db         51 EDW-----------SFFAVYDGHAGSRVA-------NYCSTHLLEHITTN---------- 82

Qy        165 NGRCICPSDPQFVEEKGIRAE---DLVIGALESAFQECDEVIGR--ELEASGQMGGCTAL 219
                      | :  :: |   |   : |   : : | : || :    :|       | ||:
Db         83 -------EDFRAADKSCFALEPSVENVKTGIRTGFLKIDEYMRNFSDLRNGMDRSCSTAV 135

Qy        220 VAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEFTP--ETERQRIQQLAFVYPELLAGEF 277
                :     :|  | |||||:| |  ::  : :    |    |::|||
Db        136 GVMVSPTHMYFINCGDSRAVLCRNGQVCFSTQDHKPCNPMEKERIQ-------------- 181

Qy        278 TRLEFPRRLKGDDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSR 337
                          : |  |: :                             |: |:|||||
Db        182 ------------NAGGSVMIQ-----------------------------RVNGSLAVSR 200

Qy        338 GLGDHQLRVLDTNIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAW 397
               |||:  : :|     :  :   |:|     : |  :||: ||:| ||:|||:|||::
Db        201 ALGDYDYKCVDGKGPTEQLVSPEPEV----YEIIRAEEDEFVVLACDGIWDVMSNEELCE 256

Qy        398 LVRSFLPGNQEDPHRFSKLAQMLIHSTQGKEDSLT 432
               | | |  :  :  :  : :    :|  :|  |:::
Db        257 FVNSRLEVSDDLENVCNWVVDTCLH--KCSRDNMS 289


RESULT 6
US-09-206-646-4
; Sequence 4, Application US/09206646
; Patent No. 6436637
; GENERAL INFORMATION:
;  APPLICANT: Bandman, Olga
;  APPLICANT:  Goli, Surya K.
;  APPLICANT:  Lal, Preeti G.
;  APPLICANT:  Corley, Neil C.
;  APPLICANT:  Zhang, Hong
;  TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
;  FILE REFERENCE: PF-0319-1 DIV
;  CURRENT APPLICATION NUMBER: US/09/206,646
;  CURRENT FILING DATE:  2001-12-07
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PERL Program
; SEQ ID NO 4
;   LENGTH: 390
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: ID No. 6436637 g452526
US-09-206-646-4

  Query Match             7.9%;  Score 190;  DB 4;  Length 390;
  Best Local Similarity   23.1%;  Pred. No. 9.3e-10;
  Matches   74;  Conservative   54;  Mismatches   99;  Indels   94;  Gaps   12;

Qy        120 YWALFDGHGGPAAAILAANTLHSCLRRQLEAVV--EGLVATQPPMHLNGRCICPSDPQFV 177
              ::|::||| |   |       : |    || :   |   |       :|  : ||    |
Db         55 FFAVYDGHAGSRVA-------NYCSTHLLEHITTNEDFRAADK----SGSALEPS----V 99

Qy        178 E--EKGIRAEDLVIGALESAFQECDEVIGR--ELEASGQMGGCTALVAVSLQGKLYMANA 233
              |  : |||          : | : || :    :|       | ||:  :     :|  |
Db        100 ESVKTCIR----------TGFLKIDEYMRNFSDLRNGMDRSGSTAVGVMVSPTHMYFINC 149

Qy        234 GDSRAILVRRDEIRPLSFEFTP--ETERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDL 291
              |||||:| |  ::   : :  |    |::|||                          :
Db        150 GDSRAVLCRNGQVCFSTQDHKPCNPVEKERIQ--------------------------NA 183

Qy        292 GQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDTNI 351
              |  |: :                             |: |:||||| |||:  : :|
Db        184 GGSVMIQ-----------------------------RVNGSLAVSRALGDYDYKCVDGKG 214

Qy        352 QLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPH 411
                :  :   |:|     : :  :||: ||:| ||:|||:|||::   |:| |  : :  :
Db        215 PTEQLVSPEPEV----YEIVRAEEDEFVVLACDGIWDVMSNEELCEFVKSRLEVSDDLEN 270

Qy        412 RFSKLAQMLIHSTQGKEDSLT 432
                : :    :|  :|  |:::
Db        271 VCNWVVDTCLH--KCSRDNMS 289


RESULT 7
US-08-822-701-7
; Sequence 7, Application US/08822701
; Patent No. 5976853
;  GENERAL INFORMATION:
;    APPLICANT:  Guthridge, Mark
;    APPLICANT:  Basilico, Claudio
;    TITLE OF INVENTION:  NOVEL GROWTH FACTOR INDUCIBLE
;    TITLE OF INVENTION:  SERINE/THREONINE PHOSPHATASE, FIN13
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David A. Jackson, Esq.
;      STREET:  411 Hackensack Ave, Continental Plaza, 4th
;      STREET:  Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/822,701
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  1049 1-002 N
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 487-5800
;      TELEFAX:  201-343-1684
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  309 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:  Mus musculus
US-08-822-701-7

  Query Match             7.8%;  Score 188.5;  DB 2;  Length 309;
  Best Local Similarity   21.4%;  Pred. No. 9.1e-10;
  Matches   70;  Conservative   52;  Mismatches   98;  Indels  107;  Gaps    9;

Qy        120 YWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEE 179
              ::|::||| |   |       : |    || :
Db         55 FFAVYDGHAGSRVA-------NYCSTHLLEHI-------------------------TTN 82

Qy        180 KGIRAEDLVIGALE----------SAFQECDEVIGR--ELEASGQMGGCTALVAVSLQGK 227
              :  || |    |||          : | : || :    :|       | ||:  :
Db         83 EDFRAADKSCSALEPSVESVKTCRTGFLKIDEYMRNFSDLRNGMDRSGSTAVGVMVSPTH 142

Qy        228 LYMANAGDSRAILVRRDEIRPLSFEFTP--ETERQRIQQLAFVYPELLAGEFTRLEFPRR 285
              :|  | |||||:| |  ::   : :  |    |::|||
Db        143 MYFINCGDSRAVLCRNGQVCFSTQDHKPCNPVEKERIQ---------------------- 180
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;      TELECOMMUNICATION INFORMATION:
;        TELEPHONE: 650-855-0555
;        TELEFAX: 650-845-4166
;        TELEX:
;   INFORMATION FOR SEQ ID NO: 2:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH: 392 amino acids
;        TYPE: amino acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;      IMMEDIATE SOURCE:
;        LIBRARY: KIDNNOT02
;        CLONE: 195647
US-08-673-881-2

  Query Match             8.3%;  Score 200.5;  DB 4;  Length 392;
  Best Local Similarity   15.0%;  Pred. No. 9.4e-11;
  Matches   89;  Conservative   46;  Mismatches   96;  Indels  125;  Gaps   15;

Qy        112 PEEELIC HYWALPDCHGGPAAAILAANTLHSCLPRQLEAVVEGLVATQPPMHLNGRCIC 179
Db        138 PSSLTFRVSYFAVPASHGGTRASKPAAQNLHQNLIR                       173

Qy        173 PSDPQFVEEKGIRAEDLVIGALESAFQECDEVIGRELEASGQ    MGGCIALVAVSLQG 226
Db        174       KEPKGDVISVEEKIVKPCLLPIPKHIPEEPLE  QASSQEPAWEDGSIAPCVLAVGN 227

Qy        227 KLYMANAGDSRAILVRRDEIRPLSFEFTPETERQRIQQLAFVYPELLAGEFTRLEFPRRL 286
Db        228 [illegible]                 [illegible]               [illegible]NFIQYEERM 2[illegible]

Qy        [illegible] [illegible]QEVLI[illegible]HM[illegible]W[illegible]VLSNEQVAWLVESIE[illegible] [illegible]
Db        [illegible]                    [illegible]FAG       GNVEGGSVLGVLEVTPC[illegible]TK  [illegible]

Qy        347 LDINIQLKPPLLSVPQVTVLEVLDLPDQPDDVVVMATDGLWDVLSNEQVAWLVRSFLPG 407
Db        [illegible]            RGGVISVP    DIRRCQLTPNDRFILLACDGLFKVFTPEEAVNFILSCL     345

Qy        408 NQEDPHRFSKLAQMLIHSTQGKE                   DSLIEEEQVSYDDVSVPVI 447
Db        346    EEEK           IQTREGKPAALARYEAA NRLANKAVQRG  SALNVIVMSV 388


RESULT 4
US-08-873-093-3
; Sequence 3, Application US/08873093
; Patent No. 5955[illegible]
;   GENERAL INFORMATION:
;      APPLICANT: Bandman, Olga
;      APPLICANT: Goli, Surya K.
;      APPLICANT: Lal, Preeti
;      APPLICANT: Corley, Neil C.
;      APPLICANT: Zhang, Hong
;      TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
;      NUMBER OF SEQUENCES: 4
;      CORRESPONDENCE ADDRESS:
;        ADDRESSEE: Incyte Pharmaceuticals, Inc.
;        STREET: 3174 Porter Drive
;        CITY: Palo Alto
;        STATE: CA
;        COUNTRY: USA
;        ZIP: 94304
;      COMPUTER READABLE FORM:
;        MEDIUM TYPE: Diskette
;        COMPUTER: IBM Compatible
;        OPERATING SYSTEM: DOS
;        SOFTWARE: FastSEQ for Windows Version 2.0
;      CURRENT APPLICATION DATA:
;        APPLICATION NUMBER: US/08/873,093
;        FILING DATE: Filed Herewith
;      PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:
;        FILING DATE:
;      ATTORNEY/AGENT INFORMATION:
;        NAME: Billings, Lucy J.
;        REGISTRATION NUMBER: 36,749
;        REFERENCE/DOCKET NUMBER: PF-0319 US
;      TELECOMMUNICATION INFORMATION:
;        TELEPHONE: 415-855-0555
;        TELEFAX: 415-845-4166
;   INFORMATION FOR SEQ ID NO: 3:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH: 390 amino acids
;        TYPE: amino acid
;        STRANDEDNESS: single
;        TOPOLOGY: linear
;      IMMEDIATE SOURCE:
;        LIBRARY: GenBank
;        CLONE: 1247927
US-08-873-093-3

  Query Match             7.9%;  Score 191.5;  DB 2;  Length 390;
  Best Local Similarity   21.2%;  Pred. No. 6.7e-10;
  Matches   71;  Conservative   55;  Mismatches  106;  Indels  103;  Gaps   10;

Qy        105 EEWLTLCPEEPLTGHYWALPDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHL 164
Db         51 EDW               SPTAVYDGHAGSEVA    -   NYCSTHLLEHITTN--------- - 82

Qy        165 NGRCICPSDPQFVEEKGIRAE---DLVIGALESAFQECDEVIGR--ELEASGQMGGCIAL 219
Db         83         [illegible]EAADEGGIALLEPVENVKI[illegible]LK[illegible]DLYMKNE[illegible]RNGMDRSGSTAV 135

Qy        220 VAV[illegible]LYMANAG[illegible]SRAILV[illegible]TFPETERQRIQQLAFVYPELLAGEF 277
Db        136 IVMI[illegible]NG[illegible]AV[illegible]ENG[illegible]ERIQ --- -------- - 181

Qy        278 TRLEFPRRLKGDDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSR 337
Db        182 --- -             NAGGSVMIQ                                   RVNGSLAVSR 200

Qy        338 GLGDHQLRVLDTNIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAW 397
Db        201 ALGDYDYK[illegible]VEGKGPTEQLVSPEPEV      YEILRAEEDEFVVLACDGIWDVMSNEELCE 256

Qy        398 LVRSFLPGNQEDPHRFSKLAQMLIHSTQGKEDSLI 432
Db        257 FVNSRLEVSDDLENVCNWVVDTCLH  KGSRDNMS 289


RESULT 5
US-09-206-646-3
; Sequence 3, Application US/09206646
; Patent No. 6436647
; GENERAL INFORMATION:
;  APPLICANT: Bandman, Olga
;  APPLICANT: Goli, Surya K.
;  APPLICANT: Lal, Preeti G.
;  APPLICANT: Corley, Neil C.
;  APPLICANT: Zhang, Hong
;  TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
;  FILE REFERENCE: PF-0319-1 DIV
;  CURRENT APPLICATION NUMBER: US/09/206,646
;  CURRENT FILING DATE: 2001-12-07
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PERL Program
; SEQ ID NO 3
;   LENGTH: 390
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: ID No. 6436647 g1247927
US-09-206-646-3
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Qy         55 SRPVRSPARCRTLPWNAGYARIINAEKSEPNEPQAACCKLCIPSCEPCASEEWLTLCPPE 114
              |  :  |     : :  | ||  |::     ||     |    | ::|
Db          5 SEILERPETPYDIIYRVGVAENKNSKFRRIMEDVHIYVKNFASRLDWG------------ 52

Qy        115 FLTGHYWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDP 174
                   |:|:|||| |  |:      ||: :
Db         53 -----YFAVFDGHAGIQASKWCGKHLHTII------------------------------ 77

Qy        175 QFVEEKGIRAEDL-VIGALESAFQECDEVIGRELEASGQMGGCIALVAV----------- 222
                  |: | |::   |   |  :|   || |  :|  :     |||| | |
Db         78 ----EQNILADETRDVRDVLNDSFLAIDEEINTKLVGN---SGCIAAVCVLRWELPDSVS 130

Qy        223 -------SLQGKLYMANAGDSRAILVRRDEIRPLSFEFTPETERQRIQQLAFVYPELLAG 275
                       | ||| || |||| :| |                                |
Db        131 DDSMDLAQHQRKLYTANVGDSRIVLFRN-------------------------------G 159

Qy        276 EFTELEEPRRLKCPILGQFVIPRPHHMSG-WSYKEVFFSSLFYPLIHGQGRQARLLGTLA 334
                 || :                ||  |     :||||::       |   ::|: | ||
Db        160 NSIRLTY----------------DHKASDTLEMQRVEQAG-------GLIMKSRVNGMLA 196

Qy        335 VSRGLGDHQLRVLDINIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQ 394
              |:| |||   :  |: :   ||  || ::|          ||  :::| ||||||: ::
Db        197 VTRSLGD---KFFDSLVVGSPFTTSV-EIT---------SEDKFLILACDGLWDVIDDQD 243

Qy        395 VAWLVRSFLPGNQEDPHRFSKLAQMLIHSTQGKEDSLTEEGQVSYDDVSVFVI 447
                 |::     |:         |::|:           ||   : |:|:|  :
Db        244 ACELIKDIIEPNE--------AAKVLVRYA-------LENG--TIDNVTVMVV 279

RESULT 2
US-08-935-855-9
; Sequence 9, Application US/08935855
; Patent No. 6066485
;  GENERAL INFORMATION:
;    APPLICANT:  Guthridge, Mark
;    APPLICANT:  Basilico, Claudio
;    TITLE OF INVENTION:  NOVEL GROWTH FACTOR INDUCIBLE
;    TITLE OF INVENTION:  SERINE/THREONINE PHOSPHATASE, FIN13
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David A. Jackson, Esq
;      STREET:  411 Hackensack Ave, Continental Plaza, 4th
;      STREET:  Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/935,855
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  1049-1-002 CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  281 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:  Saccharomyces cerevisiae
US-08-935-855-9

  Query Match             8.4%;  Score 202;  DB 3;  Length 281;
  Best Local Similarity   22.5%;  Pred. No. 4.1e-11;
  Matches   93;  Conservative   48;  Mismatches  114;  Indels  158;  Gaps   15;

Qy         55 SRPVRSPARCRTLPWNAGYARIINAEKSEPNEPQAACCKLCIPSCEPCASEEWLTLCPPE 114
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Db          5 SEILERPETPYDIIYRVGVAENKNSKFRRIMEDVHIYVKNFASRLDWG------------ 52

Qy        115 FLTGHYWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDP 174
                   |:|:|||| |  |:      ||: :
Db         53 -----YFAVFDGHAGIQASKWCGKHLHTII------------------------------ 77

Qy        175 QFVEEKGIRAEDL-VIGALESAFQECDEVIGRELEASGQMGGCIALVAV----------- 222
                  |: | |::   |   |  :|   || |  :|  :     |||| | |
Db         78 ----EQNILADETRDVRDVLNDSFLAIDEEINTKLVGN---SGCIAAVCVLRWELPDSVS 130

Qy        223 -------SLQGKLYMANAGDSRAILVRRDEIRPLSFEFTPETERQRIQQLAFVYPELLAG 275
                       | ||| || |||| :| |                                |
Db        131 DDSMDLAQHQRKLYTANVGDSRIVLFRN-------------------------------G 159

Qy        276 EFTELEEPRRLKCPILGQFVIPRPHHMSG-WSYKEVFFSSLFYPLIHGQGRQARLLGTLA 334
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Db        160 NSIRLTY----------------DHKASDTLEMQRVEQAG-------GLIMKSRVNGMLA 196

Qy        335 VSRGLGDHQLRVLDINIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQ 394
              |:| |||   :  |: :   ||  || ::|          ||  :::| ||||||: ::
Db        197 VTRSLGD---KFFDSLVVGSPFTTSV-EIT---------SEDKFLILACDGLWDVIDDQD 243

Qy        395 VAWLVRSFLPGNQEDPHRFSKLAQMLIHSTQGKEDSLTEEGQVSYDDVSVFVI 447
                 |::     |:         |::|:           ||   : |:|:|  :
Db        244 ACELIKDIIEPNE--------AAKVLVRYA-------LENG--TIDNVTVMVV 279

RESULT 3
US-09-013-881-2
; Sequence 2, Application US/09013881
; Patent No. 6132964
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Hillman, Jennifer L.
;    APPLICANT:  Corley, Neil C.
;    APPLICANT:  Guegler, Karl J.
;    APPLICANT:  Shah, Purvi
;    TITLE OF INVENTION:  HUMAN HYDROLASE LIKE MOLECULES
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Drive
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/013,881
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BILLINGS, LUCY J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0470 US
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                     GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:          February 24, 2003, 14:35:06 ; Search time 18 Seconds
                                          (without alignments)
                                          750.285 Million cell updates/sec

Title:           US-09-866-987-8
Perfect score:   2415
Sequence:        1 MSAGWFRRRFLPGEPLPAPR..........DDVSVFVIPLHSQGQESSDH 459

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters:       262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_AA:*
                 1:  /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
                 2:  /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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                 4:  /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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                 6:  /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES

                    %
Result            Query
   No.   Score    Match Length DB   ID                        Description
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     1     202     8.4     281  2  US-08-822-701-9           Sequence 9, Appli
     2     202     8.4     281  3  US-08-935-855-9           Sequence 9, Appli
     3   200.5     8.3     392  4  US-09-013-881-2           Sequence 2, Appli
     4   191.5     7.9     390  2  US-08-873-093-3           Sequence 3, Appli
     5   191.5     7.9     390  4  US-09-206-646-3           Sequence 3, Appli
     6     190     7.9     390  4  US-09-206-646-4           Sequence 4, Appli
     7   188.5     7.8     409  2  US-08-822-701-7           Sequence 7, Appli
     8   188.5     7.8     409  3  US-08-935-855-7           Sequence 7, Appli
     9   186.5     7.7     478  2  US-08-873-093-1           Sequence 1, Appli
    10   186.5     7.7     478  2  US-08-873-093-4           Sequence 4, Appli
    11   186.5     7.7     479  4  US-09-206-646-1           Sequence 1, Appli
    12   183.5     7.6     396  2  US-08-822-701-8           Sequence 8, Appli
    13   183.5     7.6     396  3  US-08-935-855-8           Sequence 8, Appli
    14     154     6.4     392  2  US-08-822-701-2           Sequence 2, Appli
    15     154     6.4     392  3  US-08-935-855-2           Sequence 2, Appli
    16     154     6.4     542  3  US-08-935-855-22          Sequence 22, Appl
    17   153.5     6.4     546  3  US-08-935-855-20          Sequence 20, Appl
    18     134     5.5     314  2  US-08-822-701-10          Sequence 10, Appl
    19     134     5.5     314  3  US-08-935-855-10          Sequence 10, Appl
    20   117.5     4.9     504  2  US-08-752-891-2           Sequence 2, Appli
    21   117.5     4.9     504  2  US-08-752-891-6           Sequence 6, Appli
    22   117.5     4.9     504  2  US-09-144-178-2           Sequence 2, Appli
    23   117.5     4.9     504  2  US-09-144-178-6           Sequence 6, Appli
    24   117.5     4.9     504  4  US-09-406-854-2           Sequence 2, Appli
    25   117.5     4.9     504  4  US-09-406-854-6           Sequence 6, Appli
    26   117.5     4.9     504  4  US-09-529-279-2           Sequence 2, Appli
    27   117.5     4.9     513  1  US-09-529-279-43          Sequence 43, Appl
    28   117.5     4.9     517  4  US-09-529-279-11          Sequence 11, Appl
    29   117.5     4.9    7257  3  US-09-335-409-5           Sequence 5, Appli
    30   117.5     4.9    7257  4  US-09-568-102-5           Sequence 5, Appli
    31   117.5     4.9    7257  4  US-09-567-969-5           Sequence 5, Appli
    32   117.5     4.9    7257  4  US-09-568-480-5           Sequence 5, Appli
    33   117.5     4.9    7257  4  US-09-568-486-5           Sequence 5, Appli
    34   117.5     4.9    7257  4  US-09-568-472-5           Sequence 5, Appli
    35   117.5     4.9    7257  4  US-09-567-899-5           Sequence 5, Appli
    36   103.5     4.3    2293  4  US-09-368-590-2           Sequence 2, Appli
    37     103     4.3     802  4  US-09-147-236-4           Sequence 4, Appli
    38    98.5     4.1    1005  2  US-08-935-450-2           Sequence 2, Appli
    39      98     4.1    3031  1  US-07-689-008-2           Sequence 2, Appli
    40    95.5     4.0     707  3  US-08-704-711A-19         Sequence 19, Appl
    41    95.5     4.0     707  4  US-09-521-220-19          Sequence 19, Appl
    42    95.5     4.0     707  4  US-09-391-104-20          Sequence 20, Appl
    43    95.5     4.0     708  4  US-08-448-489-16          Sequence 16, Appl
    44    93.5     3.9     983  4  US-09-311-236-2           Sequence 2, Appli
    45    92.5     3.8     841  4  US-09-413-814-107         Sequence 107, App

                              ALIGNMENTS

RESULT 1
US-08-822-701-9
; Sequence 9, Application US/08822701
; Patent No. 5976853
;  GENERAL INFORMATION:
;    APPLICANT:  Guthridge, Mark
;    APPLICANT:  Basilico, Claudio
;    TITLE OF INVENTION:  NOVEL GROWTH FACTOR INDUCIBLE
;    TITLE OF INVENTION:  SERINE/THREONINE PHOSPHATASE, FIN13
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  David A. Jackson, Esq.
;      STREET:  411 Hackensack Ave, Continental Plaza, 4th
;      STREET:  Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/822,701
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  1049-1-002 N
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  281 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
;      ORGANISM:  Saccharomyces cerevisiae
US-08-822-701-9

  Query Match             8.4%;  Score 202;  DB 2;  Length 281;
  Best Local Similarity   22.5%;  Pred. No. 4.1e-11;
  Matches   93;  Conservative   48;  Mismatches  114;  Indels  158;  Gaps   15;
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  Query Match             11.2%;  Score 271;  DB 21;  Length 442;
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Qy         88  QAACGKLCIRRCEEGAEEEWLTLCPE        - EE   LIGHYWALFDGHGGPAAAILAAN 138
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Qy        196 EQECDEVIGEELEASGQMGGCIALVAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEFTP 255
                    ::| |                      | :|:|:|      |:  :,  : :||:| |   :   |||  :   :
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Qy        256 E   TERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKVLFRDHHMSGWSYKPVEKS 310
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Search completed: February 24, 2003, 14:35:48
Job time : 44 secs
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Qy        374 QEDDVVVMATDGLWDVLSNEQVAWLVRSFL                  PGNQEDPHRFSKLAQ 418
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KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
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Qy      256 P--TPPQPIQLAFVYPELLAGPPTEIEEPKPIEKGI-QEVIPETGHHMSGWSTEEVLRP 313
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Qy      419 MLIHSTQGKEDSLTEE---------------GQVSYDDVSVFVIPL 449
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DT   17-OCT-2000  (first entry)
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KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
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PR   03-JUN-1999;   99US-0137528.
PR   04-JUN-1999;   99US-0137502.
PR   07-JUN-1999;   99US-0137724.
PR   08-JUN-1999;   99US-0138094.
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PR   29-OCT-1999;   99US-0162142.

  Query Match             11.2%;  Score 271;  DB 21;  Length 405;
  Best Local Similarity   24.7%;  Pred. No. 7.6e-17;
  Matches  115;  Conservative   65;  Mismatches  137;  Indels  148;  Gaps   19;

Qy         36 FLRGSSSSPGAADASRRPDSRPVR---     SPARGRILPWNAGYAEIINAEKSEFNED-  87
              |:   :||||   :         |:     |           | : | :     :        :|  ::|:      |
Db         29 FMNCASSSPSQSS ---PEEESVSLEDSDVSISDGNS-- SVNDVAVIPSKKIVKETDLR 81

Qy         88 -QAACGKLCIRRCEFGAEEEWLTLCPE- ----EF--LIGHYWALFDGHGGPAAAILAAN 138
               :        :| || :     |: : | |          ||        ||: ::||||       |
Db         82 FKYGVASVCDRRGM-- EDAVALHFGIVRKQIEISRIRWHYIGVYISGRGSHVAARCKE 138

Qy        139 ILHSCLRRQLLAVVEGLVATQPPMHLNGRCICPSDPQFVEEKGIRAEDLVIGA   LESA 195
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DE   Herbicidally active polypeptide SEQ ID NO 1489.
XX
KW   Herbicidal; plant; agriculture; herbicide.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200210210-A2.
XX
PD   07-FEB-2002.
XX
PF   28-AUG-2001; 2001WO-EP09892.
XX
PR   28-AUG-2001; 2001WO-EP09892.
XX
PA   (FARB ) BAYER AG.
XX
PI   Tietjen K,  Weidler M;
XX
DR   WPI; 2002-269010/31.
XX
PT   Identifying plant target proteins for herbicidally active compounds,
PT   comprising aligning and comparing nucleic acid or amino acid sequences
PT   from plant with nucleic acid or amino acid sequences from non plant
PT   organisms -
XX
PS   Claim 5; SEQ ID NO 1489; 261pp + Sequence Listing; English.
XX
CC   The invention relates to identifying target proteins
CC   (ABB90760-ABB94016) for herbicidally active compounds, comprising
CC   aligning and comparing nucleic acid or amino acid sequences from plant
CC   with nucleic acid or amino acid sequences from non-plant organisms using
CC   suitable search parameters, where plant sequences having an E-value
CC   greater by a factor of 3 than the E-value of most similar non-plant
CC   sequences are selected. The polypeptides or nucleic acids encoding them
CC   are useful for identifying modulators. The identified modulators are
CC   useful as herbicides.
XX
SQ   Sequence   399 AA;

  Query Match             11.4%;  Score 275;  DB 23;  Length 399;
  Best Local Similarity   25.2%;  Pred. No. 3.1e-17;
  Matches  120;  Conservative   69;  Mismatches  159;  Indels  128;  Gaps   20;

Qy          7 RRR--FLPGEPLPAPRPPGPHASPVPYRRPRRLRGSSSSPG  AADASRRPDSRPVRSPA 62
              |||     |    : |      |          |: |      |: ||     |:: | ::: ||
Db         27 RRRIDKIFSIKIVAFSAVAFPLFNTRRRQRRRIVVLFLFDNIIIDGNVRSFNKKARSAV 86

Qy         63 RGPTLPWNACYAEIINAEKSEFNEDQAACGKLCIRRCEFCAEHEWLTLCPEEPL-----T 117
                         :  ||     :   :      :| || :      |: ::: |  ||
Db         87 TNSN---------SVTFAFSFFSDVPKICTTSVCGRRPDM---FDAVSIHP-SPLQRNSPN 134

Qy        118 GHYWALFDCEGGPAAAILAANTLHSCLRRQLFAV-----VFGLVATQFPMHLNGRCICPS 172
                |:: : ||||      |         ||   :::::| :          | :| :     |
Db        135 HHFTGVHDGHGCSHVALKCRRRIHGIVNKEVEVMASDEWIEIMVKSFQKMD--------- 185

Qy        173 DPQFVEEKCIRAFPDVI-GALESAFQECD-EVIGKHLEASCQMGCCTALVAVSLQGKLYM 230
                       :: |  :::: ||  |     |  |:    : :| |      ||:|:|    |: :
Db        186 -----KPVSQFFCNLVVNGALRSMKNSCRCEIQSPLQCPAVCS     TAVVSVVIPEKLIV 236

Qy        231 ANAGDSRAILVRRDPIRPLSPPPPPP  TPRQRPQQLAPVYPHLLAGEFTRLEPPRRLKG 288
               :| |||||:' |          ||| :     |:      |   ||||
Db        237 SNCGDSRAVLCRNGVAIPLSVDHKPDRPDELIRIQQ     -            -  -- 272

Qy        289 PPI[illegible]PVIPPLHHMAGWSYFPVERSLPNYPPLHHN[illegible]PLAPPI[illegible]TLAVSPC[illegible]PHQLPVIP 348
                     | :|:: |                                      ||:|| ||:|| :||:
Db        273 --AGGRVIYWD        -- -- -- --               GARVLGVLAMSRAIGDN       298

Qy        349 INPQLKPPLLSVPPVTVLDVPQLHLQHDDVVVMAIDGLWDVLSNDQVAWLVRSPLPG--  405
                     |||::::    |:|||| |           ||: :::|:||||||: ||      :  |   | |
Db        299 ---YLEPYVIPDPEVIVID----RLDEDECLILASDGLWDVVPNETACGVARMCLRGACA 351

Qy        406 --N[illegible]PHRP[illegible]PLA[illegible]M[illegible]PRS[illegible]T[illegible]TPP[illegible]LVPTT[illegible]VSPVPIL[illegible]HPQ  [illegible]QHSS 457
                   :  :    |         |  :|:            :|    :      | |:|||  |:  |     :       |  ||
Db        352 GMDSDAAHNACLAALLLTKL     ALARQ    [illegible]NVSVVVV[illegible]LRKPRRLASS 399


RESULT 13
AAG14034
ID   AAG14034 standard; Protein; 405 AA.
XX
AC   AAG14034;
XX
DT   17-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 13746.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405 A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;    99US-0121825.
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PR   09-MAR-1999;    99US-0123548.
PR   23-MAR-1999;    99US-0125788.
PR   25-MAR-1999;    99US-0126264.
PR   29-MAR-1999;    99US-0126785.
PR   01-APR-1999;    99US-0127462.
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PR   30-APR-1999;    99US-0132048.
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PR   04-JUN-1999;    99US-0137502.
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PR   16-JUN-1999;    99US-0139452.
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PR   18-JUN-1999;    99US-0139455.
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Db         27 RRRIDLIPS-IPIVADSAVAPFLLNCPKRQKREIVVLSILPGNLDLDSNVRSENKKAPSAV 86

Qy         63 RGRILPWNAGYAEIINAEKSEFNEDQAACGKLCIRRCEFGAEEEWLTLCPEEFL-----I 117
                                    :    ||        :    :       :|  ||  :      |:  :::  |   ||
Db         87 INSN---------SVIEAESFFSDVPKIGTTSVCGRRRDM---EDAVSIHP-SFLQRNSEN 134

Qy        118 GHYWALFDGHGGPAAAILAANTLHSCLRRQLEAV-----VEGLVATQPPMHLNGRCICPS 172
                 |::  :|||||       |          ||   :::::|  :          |  :|  :      |
Db        135 HHFYGVFDGHGCSHVAEKCRERLHDIVKKEVEVMASDEWIEIMVKSFQKMD--------  185

Qy        173 DPQFVEEKGIRAEDLVI-GALESAFQECD-EVIGRELEASGQMGGCTALVAVSLQGKLYM 230
                           :|     |   :||:  ||   |         |   |:     :  :|  |         ||:|:|       |:  :
Db        186 -----KEVSQRPECNLVVNGATRSMKNSCRCELQSPQCDAVCS---IAVVSVVIPEKIIV 236

Qy        231 ANAGDSRAILVRRDEIRPLSPEFTPE-TERQRIQQLAFVYPELLAGEFTRLEFPRRLKG 288
               :|  ||||::|  |           |||  :      |:       |   ||||
Db        237 SNCGDSRAVLCRNGVAIPLSVDHKPDRPDELIRIQQ------------------------ 272

Qy        289 PDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLD 348
                   |  :|:::  |                                                   ||:||  ||:||  :||:
Db        273    AGGRVIYWD                                      GARVLGVLAMSRAIGDN       298

Qy        349 INIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPG--- 405
                       |||:::    |:|||  |               ||:   :::|:||||||:  :|          :   |     |   |
Db        299   --YLKPYVIPDPEVIVTD---RIDEDECLILASDGLWDVVPNETACGVARMCLRGAGA 351

Qy        406 --NQEDPHRFSKLAQMLIHSTQGKEDSLTEEGQVSYDDVSVFVIPLHSQ--GQESS 457
                      :   :     |          |  :|:                  :|     :        |   |:|||  |:   |     :       |  ||
Db        352 GDDSDAAHNACSDAALLLTKL        ALARQ     SSDNVSVVVVDLRKKRNNQASS 399


RESULT 11
AAU78803
ID   AAU78803 standard; Protein; 399 AA.
XX
AC   AAU78803;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human protein phosphatase II C-like (PPIIC) enzyme homologue.
XX
KW   Protein phosphatase II C like; agonist; antagonist; apoptosis; AIDS;
KW   Acquired immunodeficiency virus; genetic immunodeficiency; PPIIC;
KW   neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW   retinitis pigmentosa; amyotropic lateral sclerosis; myelodysplasia;
KW   aplastic anaemia; ischaemic injury; myocardial infarction; stroke;
KW   reperfusion injury; toxin induced disease; cirrhosis; wasting disease;
KW   cachexia; viral infection; hepatitis; osteoporosis; cancer; diabetes;
KW   central nervous system disorder; CNS disorder; cardiovascular disorder;
KW   inflammatory disorder; chronic obstructive pulmonary disease; COPD;
KW   enzyme; human.
XX
OS   Homo sapiens.
XX
PN   WO200218565-A2.
XX
PD   07-MAR-2002.
XX
PF   20-AUG-2001; 2001WO-EP09558.
XX
PR   30-AUG-2000; 2000US-228758P.
PR   02-APR-2001; 2001US-280115P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Xiao Y;
XX
DR   WPI; 2002-292201/33.
XX
PT   New protein phosphatase IIC like enzyme and polynucleotide, useful for
PT   treating a disease associated with an increase or decrease in
PT   apoptosis, e.g. neurodegenerative diseases, viral infections,
PT   myelodysplasia, cancer, diabetes
XX
PS   Disclosure; Fig 4; 125pp; English.
XX
CC   The invention describes an isolated polynucleotide (I) which encodes a
CC   protein phosphatase IIC (PPIIC)-like enzyme (II). (I) and (II) can be
CC   used in diagnostic assays for detecting diseases and abnormalities or
CC   susceptibility to diseases and abnormalities related to the presence of
CC   mutations in the nucleic acid sequences encoding the enzyme. (I) and (II)
CC   or its antagonists, agonists, or modulators are useful for treating a
CC   disease or disorder associated with an increase in apoptosis such as AIDS
CC   or other infectious or genetic immunodeficiencies, neurodegenerative
CC   diseases (e.g. Alzheimer's disease or Parkinson's disease, retinitis
CC   pigmentosa, or amyotropic lateral sclerosis), myelodysplasia (e.g.
CC   aplastic anaemia), ischaemic injuries (e.g. myocardial infarction, stroke
CC   or reperfusion injury), toxin induced diseases (e.g. alcohol-induced
CC   liver damage or cirrhosis), wasting diseases (e.g. cachexia), viral
CC   infections (e.g. hepatitis B or C), and osteoporosis; or a decrease in
CC   apoptosis such as cancer, diabetes, CNS disorders, cardiovascular
CC   disorders, chronic obstructive pulmonary disease (COPD), and inflammatory
CC   disorders. Regulation of human PPIIC-like enzyme can be used to treat
CC   disorders such as diabetes, CNS disorders, cardiovascular disorders,
CC   COPD, and cancers (e.g. leukaemia, lymphoma, or cancers of the organs).
CC   This is the amino acid sequence of the novel human protein phosphatase
CC   IIC-like enzyme homologue described in the invention.
XX
SQ   Sequence   399 AA;

  Query Match             11.4%;  Score 275;  DB 23;  Length 399;
  Best Local Similarity   25.2%;  Pred. No. 3.1e-17;
  Matches  120;  Conservative   69;  Mismatches  159;  Indels  128;  Gaps   20;

Qy          7 RRR--FLPCEPLPAPRPPCPHASPVPYRRPRFLRGSSSSPG-AADASRRPDSRPVRSPA 62
              |||    ||    :  |        |          |:  |        |:  ||      |::  | :::   ||
Db         27 RRRIDLIFS-IFIVADSAVAPFLLNCRKRQKREIVVLSILPGNLDLDSNVESENKKAESAV 86

Qy         63 RGRILPWNAGYAEIINAEKSEFNEDQAACGKLCIRRCEFGAEEEWLTLCPEEFL-----I 117
                                    :    ||        :    :       :|  ||  :      |:  :::  |   ||
Db         87 INSN---------SVIEAESFFSDVPKIGTTSVCGRRRDM---EDAVSIHP-SFLQRNSEN 134

Qy        118 GHYWALFDGHGGPAAAILAANTLHSCLRRQLEAV-----VEGLVATQPPMHLNGRCICPS 172
                 |::  :|||||       |          ||   :::::|  :          |  :|  :      |
Db        135 HHFYCVFDGHGCSHVAEKCRERLHDIVKKEVEVMASDEWIEIMVKSFQKMD--------  185

Qy        173 DPQFVEEKGIRAEDLVI-GALESAFQECD-EVIGRELEASGQMGGCTALVAVSLQGKLYM 230
                           :|     |   :||:  ||   |         |   |:     :  :|  |         ||:|:|       |:  :
Db        186 -----FFVSQRPECNLVVNGATRSMKNSCRCELQSPQCDAVCS---TAVVSVVIPEKIIV 236

Qy        231 ANAGDSRAILVRRDEIRPLSPEFTPE-TERQRIQQLAFVYPELLAGEFTRLEFPRRLKG 288
               :|  ||||::|  |           |||  :      |:       |   ||||
Db        237 SNCGDSRAVLCRNGVAIPLSVDHKPDRPDELIRIQQ------------------------ 272

Qy        289 PDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLD 348
                   |  :|:::  |                                                   ||:||  ||:||  :||:
Db        273    AGGRVIYWD                                      GARVLGVLAMSRAIGDN       298

Qy        349 INIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPG--- 405
                       |||:::    |:|||  |               ||:   :::|:||||||:  :|          :   |     |   |
Db        299   --YLKPYVIPDPEVIVTD---RIDEDECLILASDGLWDVVPNETACGVARMCLRGAGA 351

Qy        406 --NQEDPHRFSKLAQMLIHSTQGKEDSLTEEGQVSYDDVSVFVIPLHSQ--GQESS 457
                      :   :     |          |  :|:                  :|     :        |   |:|||  |:   |     :       |  ||
Db        352 GDDSDAAHNACSDAALLLTKL        ALARQ     SSDNVSVVVVDLRKKRNNQASS 399


RESULT 12
ABB92278
ID   ABB92278 standard; Protein; 399 AA.
XX
AC   ABB92278;
XX
DT   31-MAY-2002  (first entry)
XX
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PR   10-JUN-1999;   99US-0138540.
PR   10-JUN-1999;   99US-0138847.
PR   14-JUN-1999;   99US-0139119.
PR   16-JUN-1999;   99US-0139452.
PR   16-JUN-1999;   99US-0139453.
PR   17-JUN-1999;   99US-0139492.
PR   18-JUN-1999;   99US-0139454.
PR   18-JUN-1999;   99US-0139455.
PR   18-JUN-1999;   99US-0139456.
PR   18-JUN-1999;   99US-0139457.
PR   18-JUN-1999;   99US-0139458.
PR   18-JUN-1999;   99US-0139459.
PR   18-JUN-1999;   99US-0139460.
PR   18-JUN-1999;   99US-0139461.
PR   18-JUN-1999;   99US-0139462.
PR   18-JUN-1999;   99US-0139463.
PR   18-JUN-1999;   99US-0139750.
PR   18-JUN-1999;   99US-0139763.
PR   21-JUN-1999;   99US-0139817.
PR   22-JUN-1999;   99US-0139899.
PR   23-JUN-1999;   99US-0140353.
PR   23-JUN-1999;   99US-0140354.
PR   24-JUN-1999;   99US-0140695.
PR   28-JUN-1999;   99US-0140823.
PR   29-JUN-1999;   99US-0140991.
PR   30-JUN-1999;   99US-0141287.
PR   01-JUL-1999;   99US-0141842.
PR   01-JUL-1999;   99US-0142154.
PR   02-JUL-1999;   99US-0142055.
PR   06-JUL-1999;   99US-0142390.
PR   08-JUL-1999;   99US-0142803.
PR   09-JUL-1999;   99US-0142920.
PR   12-JUL-1999;   99US-0142977.
PR   13-JUL-1999;   99US-0143542.
PR   14-JUL-1999;   99US-0143624.
PR   15-JUL-1999;   99US-0144005.
PR   16-JUL-1999;   99US-0144085.
PR   16-JUL-1999;   99US-0144086.
PR   19-JUL-1999;   99US-0144325.
PR   19-JUL-1999;   99US-0144331.
PR   19-JUL-1999;   99US-0144332.
PR   19-JUL-1999;   99US-0144333.
PR   19-JUL-1999;   99US-0144334.
PR   19-JUL-1999;   99US-0144335.
PR   20-JUL-1999;   99US-0144352.
PR   20-JUL-1999;   99US-0144632.
PR   20-JUL-1999;   99US-0144884.
PR   21-JUL-1999;   99US-0144814.
PR   21-JUL-1999;   99US-0145086.
PR   21-JUL-1999;   99US-0145088.
PR   22-JUL-1999;   99US-0145085.
PR   22-JUL-1999;   99US-0145087.
PR   22-JUL-1999;   99US-0145089.
PR   22-JUL-1999;   99US-0145192.
PR   23-JUL-1999;   99US-0145145.
PR   23-JUL-1999;   99US-0145218.
PR   23-JUL-1999;   99US-0145224.
PR   26-JUL-1999;   99US-0145276.
PR   27-JUL-1999;   99US-0145913.
PR   27-JUL-1999;   99US-0145918.
PR   27-JUL-1999;   99US-0145919.
PR   28-JUL-1999;   99US-0145951.
PR   02-AUG-1999;   99US-0146386.
PR   02-AUG-1999;   99US-0146388.
PR   02-AUG-1999;   99US-0146389.
PR   04-AUG-1999;   99US-0147048.
PR   04-AUG-1999;   99US-0147204.
PR   04-AUG-1999;   99US-0147302.
PR   05-AUG-1999;   99US-0147192.
PR   05-AUG-1999;   99US-0147260.
PR   06-AUG-1999;   99US-0147303.
PR   06-AUG-1999;   99US-0147416.
PR   09-AUG-1999;   99US-0147493.
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PR   09-AUG-1999;   99US-0147935.
PR   10-AUG-1999;   99US-0148171.
PR   11-AUG-1999;   99US-0148319.
PR   12-AUG-1999;   99US-0148341.
PR   13-AUG-1999;   99US-0148565.
PR   13-AUG-1999;   99US-0148684.
PR   16-AUG-1999;   99US-0149368.
PR   17-AUG-1999;   99US-0149175.
PR   18-AUG-1999;   99US-0149426.
PR   20-AUG-1999;   99US-0149722.
PR   20-AUG-1999;   99US-0149723.
PR   20-AUG-1999;   99US-0149929.
PR   23-AUG-1999;   99US-0149902.
PR   23-AUG-1999;   99US-0149930.
PR   25-AUG-1999;   99US-0150566.
PR   26-AUG-1999;   99US-0150884.
PR   27-AUG-1999;   99US-0151065.
PR   27-AUG-1999;   99US-0151066.
PR   27-AUG-1999;   99US-0151080.
PR   30-AUG-1999;   99US-0151303.
PR   31-AUG-1999;   99US-0151438.
PR   01-SEP-1999;   99US-0151930.
PR   07-SEP-1999;   99US-0152463.
PR   10-SEP-1999;   99US-0153070.
PR   13-SEP-1999;   99US-0153758.
PR   15-SEP-1999;   99US-0154018.
PR   16-SEP-1999;   99US-0154039.
PR   20-SEP-1999;   99US-0154779.
PR   22-SEP-1999;   99US-0155139.
PR   23-SEP-1999;   99US-0155486.
PR   24-SEP-1999;   99US-0155659.
PR   28-SEP-1999;   99US-0156458.
PR   29-SEP-1999;   99US-0156596.
PR   04-OCT-1999;   99US-0157117.
PR   05-OCT-1999;   99US-0157753.
PR   06-OCT-1999;   99US-0157865.
PR   07-OCT-1999;   99US-0158029.
PR   08-OCT-1999;   99US-0158232.
PR   12-OCT-1999;   99US-0158369.
PR   13-OCT-1999;   99US-0159293.
PR   13-OCT-1999;   99US-0159294.
PR   13-OCT-1999;   99US-0159295.
PR   14-OCT-1999;   99US-0159329.
PR   14-OCT-1999;   99US-0159330.
PR   14-OCT-1999;   99US-0159331.
PR   14-OCT-1999;   99US-0159637.
PR   14-OCT-1999;   99US-0159638.
PR   18-OCT-1999;   99US-0159584.
PR   21-OCT-1999;   99US-0160741.
PR   21-OCT-1999;   99US-0160767.
PR   21-OCT-1999;   99US-0160768.
PR   21-OCT-1999;   99US-0160770.
PR   21-OCT-1999;   99US-0160814.
PR   21-OCT-1999;   99US-0160815.
PR   22-OCT-1999;   99US-0160980.
PR   22-OCT-1999;   99US-0160981.
PR   22-OCT-1999;   99US-0160989.
PR   25-OCT-1999;   99US-0161404.
PR   25-OCT-1999;   99US-0161405.
PR   25-OCT-1999;   99US-0161406.
PR   26-OCT-1999;   99US-0161359.
PR   26-OCT-1999;   99US-0161360.
PR   26-OCT-1999;   99US-0161361.
PR   28-OCT-1999;   99US-0161920.
PR   28-OCT-1999;   99US-0161992.
PR   28-OCT-1999;   99US-0161993.
PR   29-OCT-1999;   99US-0162142.

  Query Match             11.1%;  Score 275;  DB 21;  Length 399;
  Best Local Similarity   25.2%;  Pred. No. 3.1e-17;
  Matches  120;  Conservative   69;  Mismatches  159;  Indels  128;  Gaps   30;

Qy          7 RRR  FLPGEPLPAPRPPGPHASPVPYRRPRFLRGSSSSPG  AAPASPRRQSRPVRSPA 62
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RESULT 9
ABB90804
ID   ABB90804 standard; Protein; 442 AA.
XX
AC   ABB90804;
XX
DT   31 MAY 2002  (first entry)
XX
DE   Herbicidally active polypeptide SEQ ID NO 105.
XX
KW   Herbicidal; plant; agriculture; herbicide.
XX
OS   Arabidopsis thaliana.
XX
PN   WO200210210-A2.
XX
PD   07-FEB-2002.
XX
PF   28-AUG-2001; 2001WO-EP09802.
XX
PR   28-AUG-2001; 2001WO-EP09802.
XX
PA   (FARB ) BAYER AG.
XX
PI   Tietjen K,  Wendler M;
XX
DR   WPI; 2002-269710/31.
XX
PT   Identifying plant target proteins for herbicidally active compounds,
PT   comprising aligning and comparing nucleic acid or amino acid sequences
PT   from plant with nucleic acid or amino acid sequences from non plant
PT   organisms
XX
PS   Claim 5; SEQ ID NO 105; 261pp + Sequence Listing; English.
XX
CC   The invention relates to identifying target proteins
CC   (ABB90790-ABB94016) for herbicidally active compounds, comprising
CC   aligning and comparing nucleic acid or amino acid sequences from plant
CC   with nucleic acid or amino acid sequences from non-plant organisms using
CC   suitable search parameters, where plant sequences having an E-value
CC   greater by a factor of 3 than the E-value of most similar non-plant
CC   sequences are selected. The polypeptides or nucleic acids encoding them
CC   are useful for identifying modulators. The identified modulators are
CC   useful as herbicides.
XX
SQ   Sequence   442 AA;

  Query Match             11.5%;  Score 278;  DB 23;  Length 442;
  Best Local Similarity   24.9%;  Pred. No. 1.9e-17;
  Matches  116;  Conservative   65;  Mismatches  136;  Indels  148;  Gaps   19;

Qy         39 FLPGSSSSPGAADASRPPLSRFVR         GFARGRLLWNAGYAEIINADRGEPNEL  87
                 :  :||||  :        |:     |            | : | :      :  :| ::|:       |
Db         66 FMNCASSSPSQSS      PEEFSVSLEDSDVSISDGNS     SVNDVAVIPSKKIVKDDDLF 118

Qy         88  QAACGKIETRRCTFGAEPEWLLLCPE          EF   LLGHYWALPDGHGGPAAAILAAN 138
                   :       :|  |  :        |  :  | |             ||        ||:  ::||||       |
Db        119 PRYGVASVCGRRREM     EDAVALHPSFVRRQILLGKIRWHYPGVYDGHGCSHVAARCKE 175

Qy        139 LLHSCLRRQLEAVVEGLVALQPPMHLNGRCLCPSDPQPVEEKGIFADDLVIGA     LESA 195
                |    :   | ||: :          :  |       |         | : |        |  : |: |        |
Db        176 KLHELV    QEEALSDKKEEWKKMME      RCFTRMDKEVV        RWGESVMCANCRCELQ 225

Qy        196 FQEGDEVIGREELEASGQMGGCIALVAVSLQGKLYMANAGDCRAIIVRPDEIRPLCPEPTP 255
                  :||  :                    | :||:|:|       |: :|: ||||:|:| |    :    |||  :   |
Db        226 IEDCDAV                    GGTAVVGVIIPEKIIVANCGDSRAVLCRNGKAVPLSTDHKP 274

Qy        256 E    EEPLEILLAPVYEEELACRPCRLEPERLK      EVLPEGHHMGGWGYRRVERQ 313
                :     |     |||                                    :  |  :| : :  :
Db        274 DRPDELDRIQ                                  EAGGRVIYWD--              293

Qy        314 DEKYPEGRPQGPQARLDGLLAVCRGLGDHQLRVLLLNIGLKPFLLSVPQVIVLDVGQLEL 373
                               ||:||  ||:||  :||:                    |||::  |  |:|||  |
Db        294       ---  -   --GARVLGVLAMSRAIGDN--    --    YLKPYVTSEPEVTVTD-      RI 328

Qy        374 QEDDVVVMAIDGLWDVLSNEQVAWLVRSFL-------              PGNQEDPHRESKLAQ 418
                :||:  :::|||||||||:::||      :||     |                   |;  :  :          :    :
Db        329 EEDEFLILAIDGLWDVVTNEAACIMVRMCLNRKSGRGRRRGLIQIPCRRGLLGKLEEEK 388

Qy        419 MLIHSTQGKEDSLTEE                          GQVSYDDVSVFVIPL 449
                ::           ||      :|::                          :  |    |:|||  || |
Db        389 VVGSRKNGRPPRLLTEATLLASVLLEKLAGAKRRSGNVSVVVIDL 433


RESULT 10
AAG35799
ID   AAG35799 standard; Protein; 399 AA.
XX
AC   AAG35799;
XX
DT   18-OCT-2000  (first entry)
XX
DE   Arabidopsis thaliana protein fragment SEQ ID NO: 43784.
XX
KW   Protein identification; signal transduction pathway; metabolic pathway;
KW   hybridisation assay; genetic mapping; gene expression control; promoter;
KW   termination sequence.
XX
OS   Arabidopsis thaliana.
XX
PN   EP1033405-A2.
XX
PD   06-SEP-2000.
XX
PF   25-FEB-2000; 2000EP-0301439.
XX
PR   25-FEB-1999;    99US-0121825.
PR   05-MAR-1999;    99US-0123180.
PR   09-MAR-1999;    99US-0123548.
PR   23-MAR-1999;    99US-0125788.
PR   25-MAR-1999;    99US-0126264.
PR   29-MAR-1999;    99US-0126785.
PR   01-APR-1999;    99US-0127462.
PR   06-APR-1999;    99US-0128234.
PR   08-APR-1999;    99US-0128714.
PR   16-APR-1999;    99US-0129845.
PR   19-APR-1999;    99US-0130077.
PR   21-APR-1999;    99US-0130449.
PR   23-APR-1999;    99US-0130510.
PR   23-APR-1999;    99US-0130891.
PR   28-APR-1999;    99US-0131449.
PR   30-APR-1999;    99US-0132048.
PR   30-APR-1999;    99US-0132407.
PR   04-MAY-1999;    99US-0132484.
PR   05-MAY-1999;    99US-0132485.
PR   06-MAY-1999;    99US-0132486.
PR   06-MAY-1999;    99US-0132487.
PR   07-MAY-1999;    99US-0132863.
PR   11-MAY-1999;    99US-0134256.
PR   14-MAY-1999;    99US-0134218.
PR   14-MAY-1999;    99US-0134219.
PR   14-MAY-1999;    99US-0134221.
PR   14-MAY-1999;    99US-0134370.
PR   18-MAY-1999;    99US-0134768.
PR   19-MAY-1999;    99US-0134941.
PR   20-MAY-1999;    99US-0135124.
PR   21-MAY-1999;    99US-0135353.
PR   24-MAY-1999;    99US-0135629.
PR   25-MAY-1999;    99US-0136021.
PR   27-MAY-1999;    99US-0136392.
PR   28-MAY-1999;    99US-0136782.
PR   01-JUN-1999;    99US-0137222.
PR   03-JUN-1999;    99US-0137528.
PR   04-JUN-1999;    99US-0137502.
PR   07-JUN-1999;    99US-0137724.
PR   08-JUN-1999;    99US-0138094.
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CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   614 AA;

  Query Match             28.9%;  Score 697;  DB 22;  Length 614;
  Best Local Similarity   35.3%;  Pred. No. 5.5e-57;
  Matches  179;  Conservative   87;  Mismatches  155;  Indels   70;  Gaps   15;

Qy         13 GPPLPAPPPPGPHASPVPYRRPPPLRGSSSSPGAAPASRRPPSRPVRSPARGRPLPWNAG 72
              |:|:|                 || || ||:      :|     ||    : ||:  |      ||| |
Db         50 GQPMP---------DKFPYARPPFLQ--LLTPDEIRASADHNVRPIIVPRDINLLPWGTG 98

Qy         73 YAEIINAEKSEENEDQAACGKICIRRCEEGAFEEWITIGPEEELTGHYWALFDGHGGPAA 132
              ||| :|: |||:||||     |   |  |:        | :       |:  |     |:  :||||  |   |
Db         99 YAECVNSGKSEWNEDQ---GAFC-RQVLSDPEHKH----PD--LPYTYPGIFDCHAGYGA 148

Qy        133 AILAANTLHSCLRRQLEAVVEGLVATQPPMHLN-------GRCICPSDPQFVE-EKGIRA 184
              |: |::  |   |  :|   :| |:    |    :       |  : |:| |   :  :: :
Db        149 ALAASHQFHHIIHEKIVDCLELLI----PRDADATNQQQCNKINPTEPHPIYEQREVTK 204

Qy        185 EDLVIGALESAFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAILVRR- 243
              ::|:||||||||    | :| :: :        ||||| |: : ||:|:||||||||:| :|
Db        205 PEILICALESAFENMDGLIAQDCTRYEDAGGCTACVSLFIIGKMYVANAGDSRAVLCQRP 264

Qy        244 -------------------DEIR      PLSFEETPETERQRIQQLAFVYPELLAGEFTRLE 281
                                 | :       | | : ||||||:|:  :| : | |.   .  |
Db        265 AIPERPQINTESGIPEEIEASTYEVPESADHTEETLEEEINVAELFPHLMGEHYVAMD 324

Qy        282 EFPRRLKGDDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLG 341
              : :|      |:||:| |     | ||:||  :     ||   |:::|:|:::|||||  |:|| ||
Db        325 YAKKEHIKDMIQEIICSHQTIMEGWTYKTILMEIKMEVVNGDGKKSEIIGTICVIECRGD 384

Qy        342 DHQLKVLDTNIQLKPFLLSVPQVTVLDVDQLELQ------VVVMATDGLWDVLSNE 393
              |:|   ::: ||:||||     | |     |: | : : ::|        |:||||||||||   |:
Db        385 HELLAINPGIQTKPPLLTPHPDVRQRPLTQVVSIPDPDNRDCTYCVLVMATDGLWDVSEND 444

Qy        394 QVAWLVRSFLPGNQEDPHRFSKLAQMLIHSTQGKEDS      LTEEGQVSYDDVSVFVI 447
               |:  |    |         : ||:: :|| |:    :||  ||               :    : ||:|| ||
Db        445 AVSRIVFQTLSKYSTEKHRYTMVAQFLVARARGKINDSCHWRLADSKAAATVDDISVIVI 504

Qy        448 PL 449
              |:
Db        505 PV 506


RESULT 8
AAU78802
ID   AAU78802 standard; Protein; 299 AA.
XX
AC   AAU78802;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human protein phosphatase II C-like (PPIIC) enzyme.
XX
KW   Protein phosphatase II C like; agonist; antagonist; apoptosis, AIDS;
KW   Acquired immunodeficiency virus, genetic immunodeficiency, viral,
KW   neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW   retinitis pigmentosa; amyotropic lateral sclerosis, myelodysplasia,
KW   aplastic anaemia, ischaemic injury; myocardial infarction; stroke;
KW   reperfusion injury; toxin induced disease, cirrhosis, wasting disease,
KW   cachexia; viral infection; hepatitis, osteoporosis; cancer; diabetes;
KW   central nervous system disorder, CNS disorder, cardiovascular disorder,
KW   inflammatory disorder; chronic obstructive pulmonary disease; COPD;
KW   enzyme; human
XX
OS   Homo sapiens.
XX
PN   WO200219555-A2.
XX
PD   07-MAR-2002.
XX
PF   29-AUG-2001; 2001WO-EP09558.
XX
PR   30-AUG-2000; 2000US-228758P.
PR   02-APR-2001; 2001US-280115P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Xiao Y;
XX
DR   WPI; 2002-290201/33.
DR   N-PSDB; ABK47452.
XX
PT   New protein phosphatase IIC like enzyme and polynucleotide, useful for
PT   treating a disease associated with an increase or decrease in
PT   apoptosis, e.g. neurodegenerative diseases, viral infections,
PT   myelodysplasia, cancer, diabetes  -
XX
PS   Claim 18; Fig 2; 125pp; English.
XX
CC   The invention describes an isolated polynucleotide (I) which encodes a
CC   protein phosphatase IIC (PPIIC) like enzyme (II). (I) and (II) can be
CC   used in diagnostic assays for detecting diseases and abnormalities or
CC   susceptibility to diseases and abnormalities related to the presence of
CC   mutations in the nucleic acid sequences encoding the enzyme. (I) and (II)
CC   or its antagonists, agonists, or modulators are useful for treating a
CC   disease or disorder associated with an increase in apoptosis such as AIDS
CC   or other infectious or genetic immunodeficiencies, neurodegenerative
CC   diseases (e.g. Alzheimer's disease or Parkinson's disease, retinitis
CC   pigmentosa, or amyotropic lateral sclerosis), myelodysplasia (e.g.
CC   aplastic anaemia), ischaemic injuries (e.g. myocardial infarction, stroke
CC   or reperfusion injury), toxin-induced diseases (e.g. alcohol-induced
CC   liver damage or cirrhosis), wasting diseases (e.g. cachexia), viral
CC   infections (e.g. hepatitis B or C), and osteoporosis; or a decrease in
CC   apoptosis such as cancer, diabetes, CNS disorders, cardiovascular
CC   disorders, chronic obstructive pulmonary disease (COPD), and inflammatory
CC   disorders. Regulation of human PPIIC-like enzyme can be used to treat
CC   disorders such as diabetes, CNS disorders, cardiovascular disorders,
CC   COPD, and cancers (e.g. leukaemia, lymphoma, or cancers of the organs).
CC   This is the amino acid sequence of the novel human protein phosphatase
CC   IIC-like enzyme described in the invention.
XX
SQ   Sequence   299 AA;

  Query Match             28.6%;  Score 691.5;  DB 23;  Length 299;
  Best Local Similarity   44.6%;  Pred. No. 6.3e-57;
  Matches  146;  Conservative   55;  Mismatches   93;  Indels   33;  Gaps    3;

Qy        135 LAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEEKGIRAEDLVIGALES 194
              :|:  ||  :| ||:                                  : |  :  | ||:|||::
Db          1 MASRLLHRHIREQLA--------------------------------PLKEVSHESLVVCAIEN 32

Qy        195 AFQECDEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEET 254
              |||  || : ||          ||| |||  : | ||:|:|||||||||:||  |: :|| |||
Db         33 AFQLMLEQMAREEEGHQVEESGGGALVVIYLLDGKVYVANAGDSEAIIVRNGEIIPMSREFT 92

Qy        255 PETERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKV-LFRDHHMSGWSYKRVEKSD 314
              ||||||:  | |: ||||  ||| ||||||:   :|||::|:|: :|:||:|||::|  |
Db         93 PETERQRLQLLGFLKPELLGSEFTHLEFPRRVLPKELGQRMLYRDQNMTGWAYKKIELED 152

Qy        315 LKYPLIHGQGRQARLLGTLAVSRGLGDHQLKVLDTNIQLKPFLLSVPQVTVLDVDQLELQ 374
              |::||: |:|::||:: |: |:|||||| |:|   : : :||||    |:| | |: | |
Db        153 LRFPLVCGEGKKARVMATIGVTRGLGDHSLKVCSSTLPIKPFLSCFPEVRVYDLTQYEHC 212

Qy        375 EDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSKLAQMLIHSTQGKEDS--- 430
               |||:|: ||||||| :: :||  |    |     : : | |:: ||| |:    :|
Db        213 PDDVLVLGTDGLWDVTTDCEVAATVDRVLSAYEPNDHSRYTALAQALVLGARGTPRDRGW 272

Qy        431 -LTEEGQVSYDDVSVFVIPLHSQGQES 456
               |         | ||:|||||||    |  |
Db        273 RLPNNKLGSGDDISVFVIPLGGPGSYS 299
Db        360 FEEVQEKEEDKKMLYEEENMPCWAYKEIEPEDLKEELLYYEEKKARVMAIIGVIRGLGDH 419

Qy        343 QLRVLDTNIQLKPFLLSVPQVIVLDVDQLELQEDDVVVMAIDGLWDVLSNEQVAWLVRSF 402
              |:|  |:||  :||||  |:|  :  |:  :  :     ||::::||||||||:|:||     :    |
Db        420 DLKVHESNIYIKPFLSSAPLVEIYFLSKYDHGSDDVLLLAIDGLWDVLSNEEVAEAIQF 479

Qy        403 LPG NQEDPHRFSKLAQMLIHSTQG     KEDSLTEEQQVSYDDVSVFVIPL 449
              ||   :::|||::   ||:   :|     :    ::  :    :  ||:||:||||
Db        480 LPNCDPDEPHRYILAAQLLVMKARGVLKDRGWKISNDRLGSGDDISVYVIPL 531


RESULT 6
AAB95300
ID   AAB95300 standard; Protein; 263 AA.
XX
AC   AAB95300;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human protein sequence SEQ ID NO:17738.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;    99JP-0248036.
PR   27-AUG-1999;    99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full length cDNAs
XX
PS   Claim 8; SEQ ID 17738; 2537pp + CD-ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5' end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3' end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5' end sequence/3' end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full length cDNAs. The primers allow obtaining of the full length
CC   cDNAs easily without any specialised methods. AAH02166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95843 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
```

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XX
SQ   Sequence   263 AA;

  Query Match              29.0%;  Score 701.5;  DB 22;  Length 263;
  Best Local Similarity   52.9%;  Pred. No. 5.9e-58;
  Matches  135;  Conservative   52;  Mismatches   63;  Indels    5;  Gaps    2;

Qy        200 DEVIGRELEASGQMGGCTALVAVSLQGKLYMANAGDSRAILVRRDEIRPLSFEFTPETER 259
              |  |  ||    :      ||||||: : |  ||||:||||||||||::|   ||  |:| |||||||
Db          2 DLQIERERSSYNISGGCTALIVICLLGKLYVANAGDSRAIIIRNGEIIPMSSEFTPETER 61

Qy        260 QRIQQLAFVYPELLAGEFTRLEFPRRLKCPDLCQKVLLPEPHHMSCWSYKKVEKSPLKYPL 319
              ||:| |||: | ||   ||| ||||||::   :||:|:|:||  :|:||:|| :|   |||:||
Db         62 QRLQYLAEMQPHLLGNEPIHLEPPRRVQKKLKKKMLYEEENMPCWAYKEIEPEDLKEPL 121

Qy        320 IHGQGRQARLLGILAVSRGLGDHQLRVLDTNIQLKPFLLSVPQVIVLDVDQLELQEDDVV 379
              |:|:|::||:: |: |:|||||| |:| |:|| :||||| | |:|  : |: :  :   |||:
Db        122 IYCEEKKARVMAIIGVIRGLGDHDLKVHESNIYIKEPLLSSAPLVEIYFLEKYDHGSDDVL 181

Qy        380 VMAIDGLWDVLSNEQVAWLVRSFLPG NQEDPHRFSKLAQMLIHSTQG     KEDSLTEE 434
              ::||||||||||||:||   :   |||   : :||||::   ||  |      :|      :    : : :
Db        182 ILAIDGLWDVLSNEEVAEAIQFLPNCDPDEPHRYILAAQLLAMKARGVLKDRGWKISND 241

Qy        435 GQVSYDDVSVFVIPL 449
                 |  ||:||:||||
Db        242 RLGSGDDISVYVIPL 256


RESULT 7
ABB69591
ID   ABB69591 standard; Protein; 614 AA.
XX
AC   ABB69591;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster polypeptide SEQ ID NO 35565.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE-) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   N-PSDB; ABL13694.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Disclosure; SEQ ID NO 35565; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
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PS   Example 4; SEQ ID NO 2155; 10078pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC   the encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: Immune system suppression,
CC   Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence   502 AA;

  Query Match             40.0%;  Score 967;  DB 22;  Length 502;
  Best Local Similarity   45.1%;  Pred. No. 1e-82;
  Matches  213;  Conservative   75;  Mismatches  128;  Indels   56;  Gaps   10;

Qy       30 PYRPPPELPGSSSSPGAADASPPPDSPPVPSPAPGPTLPWNAGYAELINAEKSPPNEDQA 89
            || |  ||        |     : |       :||:          | |||  ||||:||| ||   |||||
Db       28 PYCRPEEL---CLSQDEVECSADHIARPILILKETRRLPWATGYAEVINACKSTHNEDQA 84

Qy       90 ACGKLCIRRCEEGA------------------EEEWLTL---CPEEELTCHYWALFDGHGG 129
            :|   | ::: : ||                     |   |        | :: |||:||||| |
Db       85 SCEVLTVKK-KAGAVTSTPNRNSSKRRSSLPNGEGLQLKENSESEGVSCHYWSLFDGHAG 143

Qy      130 PAAAILAANTLHSCLRRQLEAVVEGL--VATQPPMHL--------NGRCL---------- 169
                ||::::  |     :  ||: :|: |     |   ||   |              | | :
Db      144 SGAAVVASRLLQHHITEQLQDIVDILKNSAVLPPTCLGEEPENTPANSETLTPAASLPGG 203

Qy      170 --    CPSDP--QEVEEKCIRAEDLVIGALESAPQECDEVIGPELEASGQMGGCTALVAV 222
                   || |   :|   || |    | |||||||||||:| |   | ||    :        ||||||: :
Db      204 VGAPGSPSTPPTRFFTEKKIPHECLVIGALESAPKEMDLQIERERSSYNISGGCTALIVI 263

Qy      223 SLQCKLYMANAGDSRAILVRRDEIRPLSPEPTPETERQRIQQLAFVYPELLAGEFTRLEF 282
              | |||:|||||||||||::|    ||  |:| ||||||||||:| |||: | ||   ||| |||
Db      264 CLLCKLYVANAGDSRAILIRNGEIIPMSSEFTPETERQRLQYLAFMQPHLLGNEFTHLEF 323

Qy      283 PRRLKGDDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDH 342
            ||||::    :|  :|:|:||  :|:||:||  :|    |||:|||:|:|::||:: |: |:||||||
Db      324 PRRVQRKELGKKMLYRDHNMTGWAYKTIEDEDLKFPLIYGEGKKARVMATIGVTRGLGDH 383

Qy      343 QLRVLDTNIQLKPFLLSVPQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSF 402
              |:|  |:||  :|||  |  |:|  : |:  : :    |||::::|||||||||||:||    :   |
Db      384 DLEVHDSNIYIKPFLSSAPEVRIYDLSKYEHGSDDVLILATDGLWDVLSNEEVAEAITQF 443

Qy      403 LPG-NQEDPHRFSKLAQMLIHSTQGK----KEDSLTEEGQVSYDDVSVFVIPL 449
            ||    : :||||::   || |:     :|       :       :: :    | ||:|||:||||
Db      444 LPNCDPDDPHRYTLAAQDLVMRARGVLKDRGWRISNDRLGSGDDISVYVIPL 495


RESULT 5
ABG29453
ID   ABG29453 standard; Protein; 538 AA.
XX
AC   ABG29453;
XX
DT   18-FEB-2002  (first entry)
XX
DE   Novel human diagnostic protein #29444.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; protein; disorder.
XX
OS   Homo sapiens
XX
PN   WO200175067 A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   N-PSDB; AAS93640.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 20; SEQ ID NO 59812; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits, to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. ABG00010-ABG30377 represent novel human
CC   diagnostic amino acid sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence   538 AA;

  Query Match             40.0%;  Score 967;  DB 22;  Length 538;
  Best Local Similarity   45.1%;  Pred. No. 1.1e-82;
  Matches  213;  Conservative   75;  Mismatches  128;  Indels   56;  Gaps   10;

Qy       30 PYRPPPELPGSSSSPGAADASPPPDSPPVPSPAPGPTLPWNAGYAELINAEKSPPNEDQA 89
            || ||  ||        |     : |       :||:          | |||  ||||:||| ||   |||||
Db       64 PYCRPEEL---CLSQDEVECSADHIARPILILKETRRLPWATGYAEVINACKSTHNEDQA 120

Qy       90 ACGKLCIRRCEEGA------------------EEEWLTL---CPEEELTCHYWALFDGHGG 129
            :|   | ::: : ||                     |   |        | :: :| :||||| |
Db      121 SCEVLTVKK-KAGAVTSTPNRNSSKRRSSLPNGEGLQLKENSESEGVSCHYWSLFDGHAG 179

Qy      130 PAAAILAANTLHSCLRRQLEAVVEGL--VATQPPMHL--------NGRCL---------- 169
                ||::|:  |     :  ||: :|: |     |   ||   |              | | :
Db      180 SGAAVVASRLLQHHITEQLQDIVDILKNSAVLPPTCLGEEPENTPANSETLTRAASLRGG 239

Qy      170 --    CPSDP--QEVEEKCIRAEDLVIGALESAPQECDEVIGPELEASGQMGGCTALVAV 222
                   || |   :|   || |    | |||||||||||:| |   | ||    :        ||||||: :
Db      240 VGAPGSPSTPPTRFFTEKKIPHECLVIGALESAPKEMDLQIERERSSYNISGGCTALIVI 299

Qy      223 SLQCKLYMANAGDSRAILVRRDEIRPLSPEPTPETERQRIQQLAFVYPELLAGEFTRLEF 282
              | ||||:|||||||||||::|    ||  |:| ||||||||||:| |||: | |    |:| | |
Db      300 CLLCKLYVANAGDSRAILIRNGEIIPMSSEFTPETERQRLQYLAFMQPHLLGNEFTHLEF 359

Qy      283 PRRLKGDDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDH 342
            ||||::    :|  :|:|:||  :|:||:||  :|    |||:|||:|:|::||:: |: |:||||||
Qy        241 VRRLEIEPLSEEPIPEIERQRIQQLAFVYPELLAGEFIRLEFPRRLKGDDLGQKVLFRDH 300
              |:| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 VRRLEIEPLSEEPIPEIERQRIQQLAFVYPELLAGEFIRLEFPRRLKGDDLGQKVLFRDH 300

Qy        301 HMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDINIQLKPFLLSV 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 HMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQLRVLDINIQLKPFLLSV 360

Qy        361 PQVIVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSK 415
              |||||| || ||||||||||||||||||||||||||||||||||||||||:: :  |
Db        361 PQVIVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEEPTQVLK 415


RESULT 3
AAW04327
ID   AAW04327 standard; Protein; 647 AA.
XX
AC   AAW04327;
XX
DT   16-JAN-1997  (first entry)
XX
DE   Rat petrin.
XX
KW   Petrin; neurite outgrowth associated protein; CNS;
KW   central nervous system; myelin; protein phosphatase 2C; stroke;
KW   neurodegeneration.
XX
OS   Rattus sp.
XX
PN   WO9632476-A1.
XX
PD   17-OCT-1996.
XX
PF   12-APR-1996;   96WO-CA00234.
XX
PR   13-APR-1995;   95US-0421701.
XX
PA   (MOUN-) MOUNT SINAI HOSPITAL CORP.
XX
PI   Labes M,  Lozano A,  Roach A,  Roder J;
XX
DR   WPI; 1996-477127/47
DR   N-PSDB; AAT38486.
XX
PT   Assay for substance that modulates response of neuronal cells  and
PT   neurite growth associated protein, Petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 10; Fig 24; 119pp; English.
XX
CC   Rat petrin (AAW04327) is a protein involved in modulating neurite
CC   growth inhibition. Its amino sequence was deduced from a
CC   cDNA sequence (AAT38486) derived from an adult rat brain cDNA
CC   library. Petrin is a new member of the protein phosphatase 2C
CC   family, and is expressed in neurons in brain tissue, partic. in
CC   the Purkinje cells of the cerebellum. Petrin, and antibodies
CC   raised against it, can be used to modulate neurite growth and
CC   axonal regeneration.
XX
SQ   Sequence  647 AA;

  Query Match             40.5%;  Score 977.5;  DB 17;  Length 647;
  Best Local Similarity   46.1%;  Pred. No. 1.5e-83;
  Matches  217;  Conservative   72;  Mismatches  127;  Indels   55;  Gaps   10;

Qy         36 PYRRFFFLRGSSSSLGAADASRRDSRRVRSFARGRLEFWNAGYALLINALKGEENLQA 89
              || |: ||      |      : |       :||:         | |||  ||||:||| ||  |||||
Db        174 PYGRPPFL---GLSQDEVSCADHIARPLLLKEIRRLEWAPGYAEVINAGKSHNEQA 230

Qy         90 ACGKDCIRRCEGA                    EEEWLLD----CPEEFLGHYWALFDGHGGP 130
              ::  | ::: : |                     | | :         | :: |||:||||| |
Db        231 SCEVLTVEE EVCTITSTPNRNSERRSSLPNCECLQLEENSESEGISCHYWSLFDGHAGS 289

Qy        131 AAAILAANTLHSCLRRQLEAVVEGL--VATQPPMHL-   ---  - NGRCT-    ---      169
               ||::|:   |     :  :||: :;| |     |   ||   |               :||  :
Db        290 GAAVVASRLLQHHITQQLQDIVEILKNSAILPPTCLGEEPESTPAHGRTLTRAASLRGGV 349

Qy        170 ----CPSDP--QFVEEKGIRAEDLVIGALESAFQECDEVIGRELEASGQMGGCTALVAVS 223
                        |   |   :|   || |   | ||||||||||:|  |    | ||   |      ||||||: |
Db        350 GAPGSPSTPPTRFFTEKKIPHECLVIGALESAFKEMDLQIERERSAYNISGGCTALIVVC 409

Qy        224 LQGKLYMANAGDSRAILVRRDEIRPLSFEPTPETERQRIQQLAFVYPELLAGEFTRLEFP 283
              |  |||:|||||||||||::|    || |:| ||||||||||:| |||: |  ||   ||| ||||
Db        410 LLGKLYVANAGDSRAIIIRNGEIIPMSSEFTPETERQRLQYLAFMQPHLLGNEFTHLEFP 469

Qy        284 RRLKGDDLGQKVLFRDHHMSGWSYKRVEKSDLKYPLIHGQGRQARLLGTLAVSRGLGDHQ 343
              ||::   :|||:|:|:||  :|:|||:||  :|    |||:|||:|:|::|||::  |:  |:||||||
Db        470 RRVQRRLLGRRMLYRDNMRWAYRLEDDCFFRLLYGLCRKARVMATTGVIRGLGDHD 529

Qy        344 LRVLDINIQLKPFLLSVPQVTVIDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFL 403
              |:| |:||  :|||| | |:| | |: : |    |||::::|||||||||||||:||  :  ||
Db        530 LEVHDSNIYIKPFLSSAPEVRVYDLSKYEHGADDVLILATDGLWDVLSNEEVAEAIFQFL 589

Qy        404 PG-NQEDPHRFSKLAQMLTHSTQG---KEDSLTEEGQVSYDDVSVFVIPL 449
              |  : :|||||::  || |:    :|     :     :: :     |  ||:|||:||||
Db        590 PNCDPDDPHRYTLAAQELVMRARGVLKDRGWRISNDRLGSGDDISVYVIPL 640


RESULT 4
AAM39010
ID   AAM39010 standard; Protein; 502 AA.
XX
AC   AAM39010;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polypeptide SEQ ID NO 2155.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US34263.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUL-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0653450.
PR   14-SEP-2000; 2000US-0662191.
PR   19-OCT-2000; 2000US-0693036.
PR   29-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J;
PI   Zhao QA,  Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   N-PSDB; AAI58166.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries
XX
```

```
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman GD,  Whyte D,  Sudarsanam S,  Manning G,  Caenepeel S;
PI   Martinez R,  Hill RJ,  Flanagan P;
XX
DR   WPI; 2002-114340/15.
DR   N-PSDB; ABA94426.
XX
PT   New phosphatase polypeptides for treating e.g., cancers, immune-related
PT   diseases and disorders, cardiovascular diseases, or brain or
PT   neuronal-associated diseases  -
XX
PS   Claim 6; Fig 2; 161pp; English.
XX
CC   The invention relates to human protein phosphatase polypeptides and
CC   polynucleotides. The phosphatase polypeptides are useful for diagnosing
CC   and treating various phosphatase-related diseases and conditions, such as
CC   cancers, immune-related diseases and disorders, cardiovascular diseases
CC   (e.g., reperfusion restenosis), brain or neuronal-associated diseases,
CC   metabolic disorders (e.g., diabetes or obesity), central or peripheral
CC   nervous system diseases and conditions (e.g., pain, migraine, mood
CC   disorders, hypotension, or hypertension), psychotic and neurological
CC   disorders (e.g., anxiety, schizophrenia), neurodegenerative diseases
CC   (e.g., Alzheimer's or Parkinson's disease), infections caused by viral
CC   (e.g., human immunodeficiency virus (HIV)), bacterial, fungal or prion-
CC   agents, ocular diseases, macular degeneration, and inflammatory disorders
CC   (e.g., rheumatoid arthritis, multiple sclerosis, osteoarthritis). The
CC   polypeptides may also be used for screening for small molecule compounds
CC   that inhibit the catalytic activity of the encoded protein phosphatase
CC   with potential use for treating the above-mentioned diseases, for
CC   generating antibodies or hybridomas, and as a diagnostic tool for
CC   detecting a disease or disorder. Genetic sequences of phosphatases are
CC   useful in gene therapy. The present sequence represents a novel human
CC   serine threonine phosphatase (STP) like phosphatase polypeptide SGP050.
XX
SQ   Sequence   459 AA;

  Query Match             100.0%;  Score 2415;  DB 23;  Length 459;
  Best Local Similarity   100.0%;  Pred. No. 4e-220;
  Matches  459;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MSAGWFRRRFLPGEPLPAPRPPGPHASPVPYRRPRFLRGSSSSPGAADASRRPDSRPVRS 60

Qy         61 PARGRTLPWNAGYAPIINALKSEFNEDQAACGKLCIRRCEEGAEEEWLTLCPEEFLTGHY 120
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Db         61 PARGRTLPWNAGYAPIINALKSEFNEDQAACGKLCIRRCEEGAEEEWLTLCPEEFLTGHY 120

Qy        121 WALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEEK 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEEK 180

Qy        181 GIRAFDLVIGALESAFQECDEVICRELEASCQMGGCTALVAVSLQCKLYMANAGDSRAIL 240
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Db        181 GIRAFDLVIGALESAFQECDEVICRELEASCQMGGCTALVAVSLQCKLYMANAGDSRAIL 240

Qy        241 VRRDEIRPLSFEFTPETERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKVLFRDH 300
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Db        241 VRRDEIRPLSFEFTPETERQRIQQLAFVYPELLAGEFTRLEFPRRLKGDDLGQKVLFRDH 300

Qy        301 HMSGWSYKRVFEKSDLKYPLIHCQQRQAPLLGTLAVSRGLGDHQLRVLDTNIQLKPFLLSV 360
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Db        301 HMSGWSYKRVFEKSDLKYPLIHCQQRQAPLLGTLAVSRGLGDHQLRVLDTNIQLKPFLLSV 360

Qy        361 PQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSKLAQML 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 PQVTVLDVDQLELQEDDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSKLAQML 420

Qy        421 IHSTQGKEDSLTEEGQVSYDDVSVFVIPLHSQGQESSDH 459
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RESULT 2
AAB85358
ID   AAB85358 standard; Protein; 440 AA.
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AC   AAB85358;
XX
DT   17-SEP-2001  (first entry)
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DE   Human phosphatase (PP) (clone ID 1723447CD1).
XX
KW   Phosphatase; PP; Alzheimer's disease; Huntington's disease; human;
KW   immune disorder; cancer; nootropic; immunomodulatory; cytostatic;
KW   neuroprotective; anticonvulsant.
XX
OS   Homo sapiens.
XX
PN   WO200153469-A2.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US02088.
XX
PR   21-JAN-2000; 2000US-0177719.
PR   28-JAN-2000; 2000US-0178988.
PR   25-FEB-2000; 2000US-0184959.
PR   17-MAR-2000; 2000US-0190142.
XX
PA   (INCY ) INCYTE GENOMICS INC.
XX
PI   Bandman O,  Tang YT,  Azimzai Y,  Yue H,  Baughn MR,  Hillman JL;
PI   Lal P,  Wang E,  Gandhi AR,  Policky JL,  Mathur P;
XX
DR   WPI; 2001-451905/48.
DR   N-PSDB; AAH22961.
XX
PT   Novel phosphatases useful for treating diseases associated with
PT   decreased expression of functional phosphatases, e.g., Alzheimer's
PT   disease, Huntington's disease, immune disorders, and cancers -
XX
PS   Claim 1; Page 93-94; 103pp; English.
XX
CC   The invention provides human phosphatases (PP) and polynucleotides
CC   encoding the phosphatases. The polypeptides can be expressed by standard
CC   recombinant methodology. The PP are useful for treating a disease or
CC   condition associated with decreased expression of functional
CC   phosphatases. Compositions containing agonists or antagonists of PP may
CC   be used to treat a disease associated with decreased expression or
CC   overexpression of PP, respectively. Such diseases may include
CC   Alzheimer's disease, Huntington's disease, immune disorders, and
CC   cancers. The present sequence represents a human phosphatase.
XX
SQ   Sequence   440 AA;

  Query Match             89.5%;  Score 2161;  DB 22;  Length 440;
  Best Local Similarity   98.8%;  Pred. No. 4.7e-196;
  Matches  410;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 MSAGWFRRRFLPGEPLPAPRPPGPHASPVPYRRPRFLRGSSSSPGAADASRRPDSRPVRS 60
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Db          1 MSAGWFRRRFLPGEPLPAPRPPGPHASPVPYRRPRFLRGSSSSPGAADASRRPDSRPVRS 60

Qy         61 PARGRTLPWNAGYAPIINALKSEFNEDQAACGKLCIRRCEEGAEEEWLTLCPEEFLTGHY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 PARGRTLPWNAGYAPIINALKSEFNEDQAACGKLCIRRCEEGAEEEWLTLCPEEFLTGHY 120

Qy        121 WALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEEK 180
              |||||||| |||||:||||||||||||||||||||||||||||: ||||||||||||||
Db        121 WALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGLVATQPPMHLNGRCICPSDPQFVEEK 180

Qy        181 GIRAFDLVIGALESAFQECDEVICRELEASCQMGGCTALVAVSLQCKLYMANAGDSRAIL 240
              |||||||||||||| ||||||||||||||||||||||||||||| |||||||||||||||
Db        181 GIRAFDLVIGALESAFQECDEVICRELEASCQMGGCTALVAVSLQCKLYMANAGDSRAIL 240
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                       GenCore version 5.1.3
              Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:          February 24, 2003, 14:34:37 ; Search time 41 Seconds
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Title:           US-09-866-987-8
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Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters:       908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                  2:  [illegible]
                  3:  [illegible]AA1982.DAT:*
                  4:  [illegible]
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                  6:  [illegible]AA1985.DAT:*
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                  9:  [illegible]AA1988.DAT:*
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                 21:  [illegible]
                 22:  [illegible]
                 23:  [illegible]

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
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   No.    Score   Match Length DB  ID                           Description
                                                         ------------------------
     1     2415   100.0    459  23  ABB07304                     Human protein phos
     2    [illegible]   [illegible]     44  22  AAB85358                     Human phosphatase
     3    [illegible]    40.5    647  17  AAW04327                     Rat petrin.  Rattu
     4      967    40.0    502  22  AAM39010                     Human polypeptide
     5      967    40.0    538  22  ABG29453                     Novel human diagno
     6    701.5    29.0    263  22  AAB95390                     Human protein sequ
     7      697    28.9    614  22  ABB69591                     Drosophila melanog
     8    691.5    28.6    299  23  AAU78802                     Human protein phos
     9      278    11.5    442  23  ABB90894                     Herbicidally activ
    10      275    11.4    399  21  AAG35799                     Arabidopsis thalia
    11      275    11.4    399  23  AAU78803                     Human protein phos
    12      275    11.4    399  23  ABB92278                     Herbicidally activ
    13      271    11.2    405  21  AAG14034                     Arabidopsis thalia
    14      271    11.2    410  21  AAG14033                     Arabidopsis thalia
    15      271    11.2    442  21  AAG14032                     Arabidopsis thalia
    16    270.5    11.2    362  23  ABB91924                     Herbicidally activ
    17      266    11.0    416  23  ABB93786                     Herbicidally activ
    18    263.5    10.9    283  21  AAG35800                     Arabidopsis thalia
    19    257.5    10.7    527  23  ABB91043                     Herbicidally activ
    20      255    10.6    438  22  AAB82980                     Trichoderma reesei
    21      255    10.6    438  23  AAE15376                     Trichoderma reesei
    22      251    10.4    423  22  AAE01345                     Arabidopsis thalia
    23      251    10.4    423  23  ABB07400                     Amino acid sequenc
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    27      233     9.6    352  22  ABB59269                     Drosophila melanog
    28      231     9.6    371  22  ABB58533                     Drosophila melanog
    29      231     9.6    371  22  ABB66446                     Drosophila melanog
    30      230     9.5    360  21  AAG16902                     Arabidopsis thalia
    31    224.5     9.3    232  21  AAG35801                     Arabidopsis thalia
    32    223.5     9.3    454  23  ABB08398                     Human-derived prot
    33      220     9.1    353  23  ABB77579                     Physcomitrella pat
    34      217     9.0    360  22  AAE04841                     Human SGP039 phosp
    35      217     9.0    360  23  AAU75784                     Human protein phos
    36    216.5     9.0    377  23  AAM49271                     Human protein phos
    37    216.5     9.0    377  23  ABB10093                     Protein phosphatas
    38    216.5     9.0    441  22  AAU23566                     Novel human enzyme
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                              ALIGNMENTS


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ID   ABB07304 standard; protein; 459 AA.
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AC   ABB07304;
XX
DT   [illegible] MAR 2002  (first entry)
XX
DE   Human protein phosphatase SGP050.
XX
KW   Protein phosphatase; serine threonine phosphatase; PTP; STP; SGP050;
KW   [illegible] hypotensive;
KW   [illegible] antibacterial; human;
KW   fungicide; ophthalmological; antiinflammatory; cardiant; antimigraine;
KW   antiarthritic; muscular; antiasthmatic; osteopathic; antipsoriatic;
KW   antiarteriosclerotic; antiallergic; antidiabetic; tranquilizer; cancer;
KW   neuroleptic; antiparkinsonian; anorectic; gene therapy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                          printed in the corresponding DNA sequence"
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PN   WO200192491-A2.
XX
PD   06-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US17305.
XX
PR   30-MAY-2000; 2000US-208291P.
XX
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Qy      711 GGCCATCTTG[illegible] 770
Db      481 GGCCATCTTGCTGCGGAGGATGAGGTACGG[illegible]CAGAGA 540

Qy      771 TGAGGGGCAGCGGATC[illegible]TGA 827
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RESULT 14
BI847199
LOCUS       BI847199                550 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  384149 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BI847199
VERSION     BI847199.1  GI:15959718
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 550)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the  minscore 18
            and  minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
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ORIGIN

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Qy      648 CACA[illegible]GCAGGAAA[illegible] 707
Db      181 [illegible] 240

Qy      708 CAGGGCCATCTTGCTG[illegible] 767
Db      241 CAGGGCCATCTTGCTGCGGAGGATGAGGTA[illegible] 300

Qy      768 GACTGAGCGGCAGCGGATCTAGCAGCTGGGCTTTGTCTATCCTGA[illegible] 827
Db      301 GACTGAGCGGCAGCGGAT[illegible] 360

Qy      828 GTTCACCCGACTGGAG[illegible] 887
Db      361 GTTCAC[illegible] 420

Qy      888 [illegible] 947
Db      421 [illegible] 480

Qy      948 GTACC[illegible] 1007
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Db      541 [illegible] 549


RESULT 15
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LOCUS       BF415112                58? bp    mRNA    linear   EST [illegible]
DEFINITION  UI-R-BJ2-bou-h-04-0-UI.s1 UI-R-BJ2 Rattus norvegicus cDNA clone
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ACCESSION   BF415112
VERSION     BF415112.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 58?)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Oligo-dT track not found. Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab Clone distribution: clones will be available through
            Research Genetics (www.resgen.com)
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            POLYA No.
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                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D Pac (Pharmacia) with a modified
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                     library is a subtracted library derived from the following
                     tissues: heart, atrium at 15 dpc, ventricle at 15.5 dpc,
                     atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15
            DNA Sequencing by: Washington University Genome Sequencing Center
            [illegible] NCI CGAP [illegible] information can be
            found through the I.M.A.G.E. Consortium/LLNL. Send email to:
            [illegible]
            Seq primer: -40UP from Gibco
            High quality sequence stop: [illegible]
FEATURES             Location/Qualifiers
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                     [illegible] were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of [illegible] clones made from the same library, [illegible]
                     [illegible], and [illegible].
                     Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT     [illegible]
ORIGIN

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ACCESSION   BF[illegible]
VERSION     BF[illegible]  GI:[illegible]
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished ([illegible])
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            P.O. Box [illegible], Clay Center, NE [illegible], USA
            Tel: 402 762 4[illegible]
            Fax: 4[illegible]
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and qual trimmed with phred
            v0.980904.e. Vector identified by cross_match with the [illegible]
            and [illegible] options.
            PCR Primers
            FORWARD: A[illegible]GAAA[illegible]
            BACKWARD: [illegible]CCAGTCACGAC[illegible]
            Plate: [illegible] row: [illegible] column: [illegible]
            Seq primer: A[illegible]TAGGGGA[illegible]
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 2PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from testis, ovary,
                     endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT     [illegible] a    [illegible] c    [illegible] g    [illegible] t
ORIGIN

  Query Match             [illegible];  Score 490.6;  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  [illegible];  Conservative    [illegible];  Mismatches   [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy     [illegible] AGAGAAA[illegible]
Db       1 AGAGAAA[illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
```

```
Db      181 CCCTTCTTGCTCTCTGTGCCACAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAG 240

Qy     1123 [illegible] 1182

Db      241 GAGGATGATGTGGTTGTCATGGCAACTGATGGACTCTGGGATGTACTGTCCAAGGAGGAG 300

Qy     1183 [illegible] 1242

Db      301 [illegible]

Qy     1243 [illegible]

Db      361 [illegible]

Qy     1303 [illegible] 1362

Db      421 GGCCAGGTGTGCTACGATGACGTCTCTGTGTTCGTGATTCCCTTGCACAGTCAGGGCCAA 480

Qy     1363 GAGAGCAGTGACCACTGA 1380

Db      481 GAGAGCAGTGACCACTGA 498


RESULT 11
AW742365
LOCUS       AW742365                 639 bp    mRNA    linear   EST [illegible]
DEFINITION  up56to5.y1 Soares_mouse_NMIL Mus musculus cDNA clone IMAGE:2780049
            5' similar to WP:C42C1.2 CE16908 PROTEIN PHOSPHATASE ;, mRNA
            sequence.
ACCESSION   AW742365
VERSION     AW742365.1  GI:7654152
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 639)
  AUTHORS   NCI-CGAP [illegible]
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40RP from Gibco
            High quality sequence stop: 400.
FEATURES             Location/Qualifiers
     source          1..639
                     /organism "Mus musculus"
                     /strain "C58 x 131 F1"
                     /db_xref "taxon:10090"
                     /clone "IMAGE:2780049"
                     /clone_lib "Soares_mouse_NMIL"
                     /sex="male"
                     /dev_stage "newborn"
                     /lab_host "DH10B"
                     /note "Organ: inner ear, 17 pooled. Vector: pT7T3 Pac,
                     Site_1: Not I, Site_2. Eco RI. 1st strand cDNA was primed
                     with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCACACTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not
                     I and Eco RI sites of the modified pT7T3 vector. Library
                     is normalized, and was constructed and donated by Bento
                     Soares and M.Fatima Bonaldo (University of Iowa) and R.
                     Hardisty, A. Varela-Carver, P. Mburu and S.D.M. Brown (MRC
                     UK Mouse Genome Centre and Mammalian Genetics Unit,
                     Harwell, UK)."
BASE COUNT      142 a    151 c    205 g    141 t
ORIGIN
```

```
  Query Match             [illegible];  Score 496.6;  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  550;  Conservative    0;  Mismatches   89;  Indels  [illegible];  Gaps  [illegible];

Qy      562 [illegible]

Db        1 GTGATCGGGCTCTGGAGAAGGCCTTCCAGGAAATGTGATGATGTGAT[illegible]

Qy      622 [illegible]

Db       61 [illegible]

Qy      682 [illegible]

Db      121 [illegible]

Qy      742 [illegible]

Db      181 [illegible]

Qy      802 [illegible]

Db      241 [illegible]

Qy      862 [illegible] 921

Db      301 [illegible]

Qy      922 [illegible] 981

Db      361 [illegible]

Qy      982 [illegible]

Db      421 [illegible]

Qy     1042 [illegible]

Db      481 [illegible]

Qy     1102 [illegible]

Db      541 [illegible]

Qy     1162 GATGTACTGTCCAAGGAGCAGGTGGCATGGCTGGTGCGG 1200

Db      601 [illegible] 639


RESULT 12
BF059521
LOCUS       BF059521                 494 bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible]
            similar to TR:Q9ULK3 Q9ULK3 KIAA1157 PROTEIN ;, mRNA sequence.
ACCESSION   BF059521
VERSION     BF059521.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 494)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
            5', mRNA sequence.
ACCESSION   BM[illegible]
VERSION     BM[illegible]  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM[illegible]  row: [illegible]  column: [illegible]
            High quality sequence stop: [illegible].
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:[illegible]"
                     /clone_lib="NIH_MGC_98"
                     /tissue_type="astrocytoma grade IV, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Library constructed by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT    [illegible] a   [illegible] c   [illegible] g   [illegible] t
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   421 [illegible]

Qy   [illegible] GAGAGCAGGACTATGA [illegible]
Db   481 GAGAGCAGGACTATGA 498


RESULT [illegible]
BM[illegible]
LOCUS       BM[illegible]              1018 bp    mRNA    linear   EST [illegible]
DEFINITION  AGENCOURT_[illegible] NIH_MGC_98 Homo sapiens cDNA clone IMAGE:[illegible]
            5', mRNA sequence.
ACCESSION   BM[illegible]
VERSION     BM[illegible]  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM[illegible]  row: [illegible]  column: 14
            High quality sequence stop: [illegible].
FEATURES             Location/Qualifiers
     source          1..1018
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:[illegible]"
                     /clone_lib="NIH_MGC_98"
                     /tissue_type="astrocytoma grade IV, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Library constructed by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT    [illegible] a   [illegible] c   [illegible] g   [illegible] t
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Qy        972 TAGGCAGGCTGGGTTACTAGCAACACTGGCTGT[illegible]GGAGACCATCAGCT 1031
              [illegible]
Db        181 TAGGCAGGCTGGGTTACTAGGAA[illegible]GGAGACCATCAGCT 240

Qy       1032 [illegible] 1091
              [illegible]
Db        241 [illegible] 300

Qy       1092 [illegible] 1151
              [illegible]
Db        301 [illegible] 360

Qy       1152 [illegible] 1211
              [illegible]
Db        361 [illegible] 41[illegible]

Qy       1212 [illegible] 12[illegible]
              [illegible]
Db        42[illegible] [illegible] 479

Qy       1272 ACA[illegible]GAAAGTAAGACAGCTCACAGAGGAAG[illegible]GATGACGTCTCTGT 1331
              [illegible]
Db        480 ACAGGGAAAGTAAGACAGCTCACAGAGGAAG[illegible]GATGACGTCTCTGT 539

Qy       1332 GTTCGTGA 1339
              [illegible]
Db        540 GTTCGTGA 547


RESULT 8
BG079142
LOCUS       BG079142                 631 bp    mRNA    linear   EST 26-JAN-2001
DEFINITION  H3036C10-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
            H3036C10 5', mRNA sequence.
ACCESSION   BG079142
VERSION     BG079142.1  GI:12561710
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 631)
  AUTHORS   Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka
            ,T.S., Carter,M.G. and Ko,M.S.H.
  TITLE     Verification and initial annotation of NIA mouse 15K cDNA clone set
  JOURNAL   Unpublished (2001)
COMMENT     Other_ESTs: H3036C10-3
            Contact: George J. Kargul
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: cdna@lgsun.grc.nia.nih.gov
            This clone set has been freely distributed to the community. Please
            visit [illegible] for details.
            Plate: H3036  row: C  column: 10
            Seq primer: -21M13 Reverse
            High quality sequence stop: 631
            POLYA No.
FEATURES             Location/Qualifiers
     source          1..631
                     /organism "Mus musculus"
                     /strain "C57BL/6J"
                     /db_xref="niaEST:H3036C10-5"
                     /db_xref="taxon:10090"
                     /clone "H3036C10"
                     /clone_lib "NIA Mouse 15K cDNA Clone Set"
                     /sex="Clones arrayed from a variety of cDNA libraries"
                     /dev_stage "Clones arrayed from a variety of cDNA
                     libraries"
                     /lab_host "DH10B"
                     /note "Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
                     clone is among a rearrayed set of 15,247 clones from 11
                     embryo cDNA libraries (including preimplantation stage
                     embryos from unfertilized egg to blastocyst, embryonic
                     part of E7.5 embryos, extraembryonic part of E7.5 embryos
                     , and E12.5 female mesonephros/gonad, [illegible]
                     ovary cDNA library. Average insert size 1.5 kb. All
                     [illegible]
                     )-NotI primers. References include: (1) Genome-wide
                     expression profiling of mid-gestation placenta and embryo
                     using a 15,000 mouse developmental cDNA microarray. [illegible]
                     Proc. Natl. Acad. Sci. U S A. 97: 9127-9132; (2)
                     Large scale cDNA analysis reveals phased gene expression
                     patterns during preimplantation mouse development. [illegible]
                     Development, 127: 1737-1748; (3) Genome-wide mapping of
                     unselected transcripts from extraembryonic tissue of
                     7.5-day mouse embryos reveals enrichment in the t-complex
                     and under-representation on the X chromosome. 1998. Hum
                     Mol Genet 7: 1967-1978."
BASE COUNT      138 a    154 c    214 g    125 t
ORIGIN

  Query Match             [illegible]%;  Score [illegible];  DB 12;  Length [illegible];
  Best Local Similarity   89.1%;  Pred. No. 3.8e-108;
  Matches  562;  Conservative    [illegible];  Mismatches   69;  Indels    [illegible];  Gaps    [illegible];

Qy        436 [illegible] 495
              [illegible]
Db          1 [illegible] 60

Qy        496 GCCCGCTGCATCTGCCCCAGTGA[illegible]GGAGGAAAAGG[illegible]CAGAA 555
              [illegible]
Db         61 GCCCGCTGTGTCTGCCCCAGTGA[illegible]GGAGGAAAAGG[illegible]CAGAA 120

Qy        556 [illegible] 615
              [illegible]
Db        121 [illegible] 180

Qy        616 [illegible] 675
              [illegible]
Db        181 [illegible] 240

Qy        676 [illegible] 735
              [illegible]
Db        241 [illegible] 300

Qy        736 [illegible] 795
              [illegible]
Db        301 [illegible] 360

Qy        796 [illegible] 855
              [illegible]
Db        361 [illegible] 420

Qy        856 [illegible] 915
              [illegible]
Db        421 [illegible] 480

Qy        916 [illegible] 975
              [illegible]
Db        481 [illegible] 540

Qy        976 [illegible]
              [illegible]
Db        541 [illegible]

Qy       1036 [illegible] 1066
              [illegible]
Db        601 [illegible] 631


RESULT 9
BM56[illegible]7
LOCUS       [illegible]    [illegible] bp    mRNA    linear   EST [illegible]-FEB-[illegible]
DEFINITION  AGENCOURT_[illegible] NIH_MGC_98 Homo sapiens cDNA clone IMAGE:[illegible]
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FEATURES             Location/Qualifiers
     source          [illegible]
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     [illegible]
                     /clone_lib="[illegible]"
                     /tissue_type="[illegible] retina, retinal [illegible] and Macular, [illegible] and
                     [illegible]"
                     /dev_stage="[illegible]"
                     /lab_host="[illegible] (Life Technologies) ([illegible] phage resistant)"
                     /note="[illegible] Vector: pT7T3[illegible] ([illegible]), with a
                     modified polylinker; Site_1: [illegible]; Site_2: Not I;
                     [illegible] subtracted cDNA library [illegible]
                     [illegible] Soares, Genome Research,
                     [illegible] 1996. First strand cDNA synthesis was primed
                     with an [illegible] primer containing a Not I site. Double
                     stranded cDNA was ligated to an [illegible] adaptor, digested
                     with Not I and cloned directionally into [illegible]
                     [illegible] used to prime the synthesis of
                     first strand cDNA [illegible] library tag sequence that is
                     located between the Not I site and the (dT)[illegible]. The
                     sequence tags for this library are: fetal eyes, AGAAT[illegible]
                     [illegible] eye anterior segment, AAT[illegible]
                     optic nerve, [illegible]; retina, [illegible]; retina foveal and
                     Macular, [illegible] and [illegible]. This library was
                     created for the program [illegible] in the Vision
                     [illegible] supported by National Eye Institute (NEI)."
BASE COUNT     [illegible]
ORIGIN

  Query Match             [illegible]  Score [illegible]  DB [illegible]  Length [illegible]
  Best Local Similarity   [illegible]  Pred. No. [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

[illegible]

RESULT 7
AA[illegible]
LOCUS       AA[illegible]            [illegible] bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible] Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGE:[illegible] 5' similar to SW:[illegible] ARATH [illegible]
            [illegible] mRNA sequence.
ACCESSION   AA[illegible]
VERSION     AA[illegible]  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
            ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
            ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
            Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
            Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   [illegible]
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: [illegible]
            Fax: [illegible]
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: [illegible]   Std Error: [illegible]
            Seq primer: [illegible] from Amersham
            High quality sequence stop: [illegible].
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:[illegible]"
                     /clone_lib="Soares ovary tumor NbHOT"
                     /sex="female"
                     /tissue_type="ovarian tumor"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     [illegible] 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT     [illegible] a   [illegible] c   [illegible] g   [illegible] t
ORIGIN

  Query Match             [illegible]  Score [illegible]  DB [illegible]  Length [illegible]
  Best Local Similarity   [illegible]  Pred. No. [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

[illegible]
```

```
Qy       [illegible]
             [illegible]
Db        481 [illegible] 540

Qy       1158 CTGGGATGTACTGTCCAAGGAGCAGGTGGCATGGCTGGTGCGGAGCTTCCTCCCTGGGAA 1217
             [illegible]
Db        541 CTGGGATGTCCTGTCCAATGAGCAGGTGGCACTGCTTGTGCGGAGCTTCCTCACCGGGAA 600

Qy       1218 [illegible]
             [illegible]
Db        601 [illegible]

Qy       1275 [illegible]
             [illegible]
Db        661 [illegible] 720

Qy       1335 [illegible] 1380
             [illegible]
Db        721 TGTGATTCCTTTGCACAGCCAGG[illegible]CAAGAAGGCAGTG[illegible]CA[illegible]TGA 766


RESULT [illegible]
BI909341
LOCUS       BI909341                760 bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible] NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214292 5',
            mRNA sequence.
ACCESSION   BI909341
VERSION     BI909341.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 760)
  AUTHORS   NIH [illegible]
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
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            High quality sequence stop: 754.
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                     /db_xref="taxon:9606"
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                     /clone_lib "NIH_MGC_118"
                     /tissue_type "leukocyte"
                     /lab_host "DH10B"
                     /note "Vector: [illegible]
                     (destroyed); RNA source leukocytes from anonymous pool [illegible]
                     non activated adult donors. Library is oligo dT primed
                     and directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.7 kb, insert size range
                     1.2-[illegible] kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 827. Note:
                     this is a NIH MGC Library."
BASE COUNT      179 a    202 c    218 g    161 t
ORIGIN

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  Best Local Similarity    [illegible];  Pred. No. [illegible];
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Db         61 [illegible]

Qy        908 [illegible]
             [illegible]
Db        120 [illegible]

Qy        968 [illegible]
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Qy       1028 [illegible]
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Qy       1088 [illegible]
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Qy       1207 [illegible]
             [illegible]
Db        420 [illegible] 479

Qy       1267 AGCACACAGGGAAAGGAAGACAGTCTCACAGAGGAAGGGCAGGT[illegible]TAGGATCAGGTC 1326
             [illegible]
Db        480 AGCACACAGGGAAAGGAAGACAGTC[illegible]

Qy       1327 [illegible] 1371
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Db        540 [illegible]AAGAGAGCAGT 584


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DEFINITION  UI-E-EJ1-ajt-m-[illegible] UI-E-EJ1 Homo sapiens cDNA clone
            UI-E-EJ1-ajt-m-[illegible] 5', mRNA sequence.
ACCESSION   BM719494
VERSION     BM719494.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 547)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: [illegible]
            Tissue Procurement: Dr. Gregg Hageman.
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   [illegible]
   PUBMED   [illegible]
REFERENCE   [illegible]
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   [illegible]
   PUBMED   [illegible]
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   [illegible]
   PUBMED   [illegible]
REFERENCE   5  (bases 1 to 1182)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,H., Arai,A.,
            Arakawa,T., [illegible]
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kondo,S., Koya,S.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,K., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A.,
            Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa [illegible], Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [illegible]. cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length cDNA by cap trapper. cDNA went
            through one round of normalization to Rot = [illegible] and subtraction to
            Rot = [illegible]. Second strand cDNA was prepared with the primer
            adapter of sequence [illegible]
            [illegible]. cDNA was cleaved
            with BamHI and XhoI. Vector: a modified pBluescript KS(+) after
            bulk excision from lambda FLC I. Cloning sites, 5' end: SalI; 3'
            end: BamHI. Host: DH10B.
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                     /db_xref="MGI:MGI:[illegible]"
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                     /clone="[illegible]"
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                     /dev_stage="[illegible] days neonate"
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                     data source:[illegible], source key:[illegible], evidence:ISS
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                     [illegible]
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     polyA_site      [illegible]
                     /note="putative"
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Db          1 [illegible]

Qy        [illegible]
              [illegible]
Db        [illegible]

Qy        [illegible]
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Db        [illegible]

Qy        [illegible]
              [illegible]
Db        181 [illegible]

Qy        858 [illegible]
              [illegible]
Db        241 [illegible]

Qy        [illegible]
              [illegible]
Db        [illegible]

Qy        978 [illegible]
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Db        [illegible]

Qy        [illegible]
              [illegible]
Db        [illegible]
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Qy        683 TGTACATGG[illegible]TACGGC 742
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        743 CACTGAGCTTCGAGTTCACCCCAGAGACTGAGCGGCAGC-GGATCCAGCAGCTGGCCTTT 801
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Db        693 CACTGAGCTTCGAGTTCACCCCAGAGACTGAGCGGCAGCGGGATCCAGCAGCTGGCCTTT 752

Qy        802 GTCTATCCTGAGCTTCTGGCTGG-TGAGTTCACCCGACTGGAGTTCCCTCG-GCGGCTGA 859
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Db        753 GTCTATCCTGAGCTTCTGGCTGGTTGAGTTCACCCGACTGGAGTTCCCTCGTGCGGCTGA 812

Qy        860 AGGGGG-ATGACTTGGGACAGAAGGTTTTGTTCAGGGATCACCACATG-AGTGGCTGGA 916
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Db        813 [illegible]GAA 872

Qy        917 GCTACAAAGTGTTGGAGAAATCGGATCTCAAGTACC 952
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Db        873 GCTACAAAGTGTTGGAGAAATCGGATCTCAAGTACC 908


RESULT 3
AW960759
LOCUS       AW960759                 796 bp    mRNA    linear   EST [illegible]
DEFINITION  EST372830 MAGE resequences, MAGF Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW960759
VERSION     AW960759.1  GI:8150443
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 796)
  AUTHORS   Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Hughes
            ,J.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
  TITLE     Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
  JOURNAL   Unpublished (2000)
COMMENT     Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: [illegible]
            Seq primer: Reverse.
FEATURES             Location/Qualifiers
     source          1..796
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /note="Vector: pBluescriptSKm"
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ORIGIN

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  Matches  76[illegible];  Conservative    0;  Mismatches   27;  Indels    2;  Gaps    2;

Qy        245 [illegible] 304
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 [illegible] 120

Qy        365 [illegible] 424
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACTGTTCGATGGGCACGGCGGTCCTGCAGGAGCTA[illegible] 180

Qy        425 CCTGCTTGCGGCGGCAGCTGGAGG[illegible]GGTGGCTACTCAG[illegible]A 484
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        485 TGCACTCAATG[illegible]TCAGTTTGTGGAGGAAAAGGGA 544
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Db        241 TGCACTCAATG[illegible]CAGTTTGTGGAGGAAAAGGGA 300

Qy        545 TCAGG[illegible] 604
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCAGGGCAGAAGACTTGGTGATGGGGCATTGGAGAGTGCCTTCAGGAATGTGATGATG 360

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Qy        665 [illegible] 724
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Db        421 TGTCCCTGCAGGGAAAGCTGTACATGGCCAATGCTGGGGATAGCAGGGCCATCCTGGTG 480

Qy        725 GGAGAGAT[illegible] 784
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Db        481 GGAGAGAT[illegible] 540

Qy        785 [illegible] 844
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Db        541 [illegible] 600

Qy        845 [illegible] 904
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Qy        905 [illegible] 964
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Qy        965 [illegible]TGTCTCCC-G[illegible]GA 1022
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Qy       1023 [illegible] 1038
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Db        781 [illegible] 796


RESULT 4
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LOCUS       AK017245                1162 bp    mRNA    linear   HTC [illegible]
DEFINITION  Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched
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            protein, full insert sequence.
ACCESSION   AK017245
VERSION     AK017245.1  GI:[illegible]
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) 6 days neonate head cDNA to mRNA,
            clone_lib:RIKEN full-length enriched mouse cDNA library
            clone:5430400J23.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
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ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished ([illegible])
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM[illegible]  row: [illegible]  column: [illegible]
            High quality sequence start: [illegible]
            High quality sequence stop: 841.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_118"
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                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     unactivated adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.5 kb.  Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code [illegible]. Note:
                     this is a NIH_MGC Library."
BASE COUNT      178 a    252 c    307 g    171 t
ORIGIN

  Query Match             52.5%;  Score 793.2;  DB 13;  Length 908;
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Qy      [illegible]
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REFERENCE   3
  AUTHORS   [illegible]
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., [illegible]
            Yoneda,Y., Ishikawa,T., Ozawa,K., [illegible]
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., [illegible]
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., [illegible]
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5  (bases 1 to 1787)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., [illegible]
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., [illegible]
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN [illegible]
            RIKEN Yokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://[illegible]-9222,
            Fax:81-45-503-9216)
COMMENT     [illegible]
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' [illegible] 3'] cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap trapper. cDNA went
            through one round of normalization to Rot = 7.5 and subtraction to
            Rot = 37.5. Second strand cDNA was prepared with the primer adapter
            of sequence [5'
            GAGAGAGAGA[illegible] 3']. cDNA was cleaved
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                     /db_xref="GI:128[illegible]"
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                     SSH"
BASE COUNT      [illegible] a    [illegible] c    [illegible] g    [illegible] t
ORIGIN

  Query Match             71.1%;  Score [illegible];  DB 11;  Length 1787;
  Best Local Similarity   85.[illegible]%;  Pred. No. [illegible];
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Db          2 [illegible]

Qy         89 [illegible]
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Db        122 [illegible] 181

Qy        209 [illegible]
Db        182 [illegible] 241

Qy        269 [illegible]
Db        242 [illegible]

Qy        323 [illegible]
Db        302 [illegible]

Qy        383 [illegible]
Db        362 [illegible] 421

Qy        443 [illegible]
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Qy        503 [illegible]
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        Copyright (c) [illegible] Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:           February 24, 2003, 11:42:10 ; Search time 2411 Seconds
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                                        [illegible] Million cell updates/sec

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Perfect score:    [illegible]
Sequence:         [illegible]

Scoring table:    IDENTITY_NUC
                  Gapop [illegible] , Gapext [illegible]

Searched:         [illegible]

Total number of hits satisfying chosen parameters:        [illegible]

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Maximum DB seq length: [illegible]

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 6:  em_estpl:*
                 7:  em_estro:*
                 8:  em_htc:*
                 9:  gb_est1:*
                 10:  gb_est2:*
                 11:  gb_htc:*
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   Pred. No. is the number of results predicted by chance to have a
   score greater than or equal to the score of the result being printed,
   and is derived by analysis of the total score distribution.

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   14    483.1  [illegible]  [illegible]  13  BG[illegible]   BG[illegible] MA
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                              ALIGNMENTS

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DEFINITION  Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
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            containing protein, full insert sequence.
ACCESSION   AK013149
VERSION     AK013149.1  GI:12850[illegible]
KEYWORDS    HTC; CAP trapper.
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REFERENCE   1
  AUTHORS   [illegible] and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. [illegible] (1999)
  MEDLINE   [illegible]
   PUBMED   [illegible]
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
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  JOURNAL   Genome Res. [illegible] (2000)
  MEDLINE   20499374
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; Sequence [illegible], Application PCT/US[illegible]
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT: KAR[illegible], Amy [illegible]
;  APPLICANT: CHIEN, [illegible]
;  APPLICANT: W[illegible]N, Amy [illegible]
;  APPLICANT: SWARNAKAR, Anita
;  APPLICANT: [illegible]EVAL, Ann [illegible]
;  APPLICANT: HAFALIA, April J.A.
;  APPLICANT: EMERLING, Brooke M.
;  APPLICANT: SANKUMAR, [illegible]
;  APPLICANT: [illegible]IN, [illegible]
;  APPLICANT: GRIFFIN, Jennifer A.
;  APPLICANT: MARQUIS, Joseph P.
;  APPLICANT: [illegible]HIN, [illegible]
;  APPLICANT: CHAWLA, Narinder K.
;  APPLICANT: [illegible]MAN, Patricia M.
;  APPLICANT: KHARE, Reena
;  APPLICANT: LEE, [illegible]
;  APPLICANT: HAWKINS, Phillip R.
;  APPLICANT: BECHA, [illegible]
;  APPLICANT: LEE, [illegible] Yeun
;  APPLICANT: SPRAGUE, William W.
;  APPLICANT: [illegible]IAN, [illegible]
;  TITLE OF INVENTION: KINASES AND PHOSPHATASES
;  FILE REFERENCE: PF[illegible] PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/[illegible]
;  CURRENT FILING DATE: 2002-12-[illegible]
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: 2001-12-[illegible]
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;  PRIOR FILING DATE: 2001-12-[illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PERL Program
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
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;   OTHER INFORMATION: Incyte ID No: [illegible]
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; Sequence 4[illegible], Application US/10349781
; GENERAL INFORMATION:
;  APPLICANT: [illegible], Jeffrey [illegible]; [illegible], Aimee M.
;  APPLICANT: Stuart, Susan G.; [illegible], Laura [illegible]
;  APPLICANT: M[illegible], Sara [illegible]; [illegible], [illegible]
;  TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIV
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/10/349,781
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]/[illegible]40,764
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;  PRIOR APPLICATION NUMBER: [illegible]/992,868
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;  PRIOR APPLICATION NUMBER: 60/032,808
;  PRIOR FILING DATE: 1996-12-13
;  PRIOR APPLICATION NUMBER: [illegible]/7[illegible]4,050
;  PRIOR FILING DATE: 1996-10-18
;  PRIOR APPLICATION NUMBER: [illegible]/00[illegible],111
;  PRIOR FILING DATE: 1995-10-24
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;  PRIOR APPLICATION NUMBER: [illegible],804
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: [illegible]/7[illegible],42[illegible]
;  PRIOR FILING DATE: 1996-12-11
;  PRIOR APPLICATION NUMBER: [illegible],794
;  PRIOR FILING DATE: 1995-12-14
;  PRIOR APPLICATION NUMBER: [illegible]/7[illegible],783
;  PRIOR FILING DATE: 1996-12-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PERL Program
; SEQ ID NO 4[illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: [illegible]
US-10-349-781-4[illegible]

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  Best Local Similarity   [illegible]%;  Pred. No. 1.[illegible];
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Qy        736 [illegible]

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;  PRIOR FILING DATE: 1995-12-14
;  PRIOR APPLICATION NUMBER: 60/772,785
;  PRIOR FILING DATE: 1996-12-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 61458
;  SOFTWARE: PERL Program
; SEQ ID NO 23865
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;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: ha00909709
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 236
;   OTHER INFORMATION: a, t, c, g, or other
US-10-349-781-23865

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Qy      945 CAAGTACCCACTGATCCATGGACAGGGTAGGCAGGCTCGTTTATTAGGAACACTGGCTGT 1004
            |||||||||||||||||||||||||||||||||||||||.||||||||||||||||||||
Db       61 CAAGTACCCACTGATCCATGGACAGGGTAGGCAGGCTCTTTTATTAGGAACACTGGCTGT 120

Qy     1005 CTCCGGGGGCCTGGGAGACCATCAGCTCAGAGTCCTGGACACAAACATCCAGTCCAAGCC 1064
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Db      241 T 241


RESULT 15
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; Sequence 62, Application PCT/US0239126
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  KARLE, Amy E.
;  APPLICANT:  CHIEN, David
;  APPLICANT:  WILSON, Amy D.
;  APPLICANT:  SWARNAKAR, Anita
;  APPLICANT:  GORVAD, Ann E.
;  APPLICANT:  HAFALIA, April J.A.
;  APPLICANT:  EMERLING, Brooke M.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  JIN, Pei
;  APPLICANT:  GRIFFIN, Jennifer A.
;  APPLICANT:  MARQUIS, Joseph P.
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  CHAWLA, Narinder K.
;  APPLICANT:  LEHR-MASON, Patricia M.
;  APPLICANT:  KHARE, Reena
;  APPLICANT:  LEE, Sally
;  APPLICANT:  HAWKINS, Phillip R.
;  APPLICANT:  BECHA, Shanya D.
;  APPLICANT:  LEE, Soo Yeun
;  APPLICANT:  SPRAGUE, William W.
;  APPLICANT:  ZEBARJADIAN, Yeganeh
;  TITLE OF INVENTION: KINASES AND PHOSPHATASES
;  FILE REFERENCE: PF-1315 PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/39126
;  CURRENT FILING DATE: 2002-12-06
;  PRIOR APPLICATION NUMBER: US 60/340,235
;  PRIOR FILING DATE: 2001-12-07
;  PRIOR APPLICATION NUMBER: US 60/343,007
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: US 60/343,546
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: US 60/354,398
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: US 60/357,675
;  PRIOR FILING DATE: 2002-02-15
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PERL Program
; SEQ ID NO 62
;   LENGTH: 1421
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 7507104CB1
PCT-US02-39126-62

  Query Match             14.0%;  Score 192.6;  DB 1;  Length 1421;
  Best Local Similarity   58.9%;  Pred. No. 3e-34;
  Matches  386;  Conservative    0;  Mismatches  264;  Indels   15;  Gaps    2;

Qy      710 GGGCCATCTTGGTGCGGAGAGATGAGATACGG[illegible] 769

Db      577 GGGCCATCATTGTCCGGAATGGTGAAA[illegible] 636

Qy      770 CTGAG[illegible] 829

Db      637 CTGAG[illegible] 696

Qy      830 TCAC[illegible] 889

Db      697 TCACCCACCTTGA[illegible]AGAGTTCTG[illegible]CAAGGAGCTGGGGCAGAGGA[illegible] 756

Qy      890 [illegible] 949

Db      757 [illegible] 816

Qy      950 [illegible]

Db      817 [illegible]

Qy     1010 [illegible]

Db      877 [illegible]

Qy     1070 [illegible]

Db      937 [illegible]

Qy     1130 [illegible]

Db      997 [illegible]

Qy     1190 [illegible] 1246

Db     1057 [illegible] 1116

Qy     1247 [illegible] 1294

Db     1117 [illegible] 1176

Qy     1295 [illegible] 1354

Db     1177 [illegible] 1236

Qy     1355 AGGGT 1359
             |||
Db     1237 CAGGT 1241
```

```
[illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

RESULT [illegible]
[illegible]
; Sequence [illegible], Application [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: Zhang, [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible] A
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: Ma, [illegible]
;  APPLICANT: Wang, [illegible]
;  APPLICANT: Wang, [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION: Polypeptides
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: 09/488,725
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: [illegible]
;   LOCATION: ([illegible])..([illegible])
[illegible]

  Query Match [illegible]
  Best Local Similarity [illegible]; Pred. No. [illegible]
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]
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```
Qy   680 [illegible]
Db   857 [illegible]

Qy   740 [illegible]
Db   917 [illegible]

Qy   800 [illegible]
Db   977 [illegible]

Qy   860 [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

RESULT 12
US-[illegible]
; Sequence [illegible], Application US/[illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible], Jeffrey J.; [illegible], Angelo M.
;  APPLICANT: Stuart, Susan G.; [illegible]
;  APPLICANT: Murphy, [illegible]; Naughton, Rebecca F.
;  TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIV
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: 08/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible],814
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible],864
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible],920
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
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Qy        955 [illegible] 1014
Db        866 CTTATATATGGAGAAGGCAAGAAC[illegible]GAGTAA[illegible]GGGA 925

Qy       1015 CTGGGAGACCATCAG[illegible]AAAA[illegible]GC 1074
Db        926 CTTGGGGA[illegible]TATGACTTGAAG[illegible]TCATGACTCAACATCTACATAAAACCATTCCTGTCT 985

Qy       1075 [illegible]GACTGTC[illegible]GGATGTGGA[illegible]ACAGGAGGATGATGTG 1134
Db        986 [illegible]AG[illegible]GAGA[illegible]CAGATA[illegible]AGATGAGGTG 1045

Qy       1135 GTTGTCATGGTAACTGATGGACT[illegible]GGGATGTACT[illegible]CAACGACGAGGTGGCATGGCTG 1194
Db       1046 CTGATCCTGGCTACTGATGGACTCTGGGATGTCTTATCCAACGAAGAAGTAGCGGAAGCA 1105

Qy       1195 GTGCGGAGCTTGCCTCCCT---GGGAACCAAGAGGACCCACACAGGTTCTCAAAGCTGGGC 1251
Db       1106 ATCACTCAGTTTCTTCCTAACTGTGATCCAGACGACCCTCACAGATACACACTGGCGGCT 1165

Qy       1252 CAGATGCTGAT 1262
Db       1166 CAGGACTTGCT 1176


RESULT 1[illegible]
PCT-US02-39126-63
; Sequence 63, Application [illegible]
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  KABLE, Amy E.
;  APPLICANT:  CHIEN, David
;  APPLICANT:  WILSON, Amy D.
;  APPLICANT:  SWARNAKAR, Anita
;  APPLICANT:  GORVAD, Ann E.
;  APPLICANT:  BAUGHN, April J.A.
;  APPLICANT:  EMERLING, Brooke M.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  JIN, Pei
;  APPLICANT:  GRIFFIN, Jennifer A.
;  APPLICANT:  MARQUIS, Joseph P.
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  CHAWLA, Narinder K.
;  APPLICANT:  LEHR-MASON, Patricia M.
;  APPLICANT:  KHARE, Reena
;  APPLICANT:  LEE, Sally
;  APPLICANT:  HAWKINS, Phillip R.
;  APPLICANT:  BECHA, Shanya D.
;  APPLICANT:  LEE, Soo Yeun
;  APPLICANT:  [illegible], William W.
;  APPLICANT:  ZEBARJADIAN, Yeganeh
;  TITLE OF INVENTION: KINASES AND PHOSPHATASES
;  FILE REFERENCE: PF-1315 PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/39126
;  CURRENT FILING DATE:  2002-12-06
;  PRIOR APPLICATION NUMBER: US 60/340,2[illegible]
;  PRIOR FILING DATE: 2001-12-07
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: US 60/354,[illegible]
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2002-02-15
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PERL Program
; SEQ ID NO 63
;   LENGTH: 1487
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: [illegible]
PCT-US02-39126-63

  Query Match             18.[illegible]%;  Score 2[illegible];  DB [illegible];  Length 1487;
  Best Local Similarity   54.[illegible]%;  Pred. No. [illegible]e-47;
  Matches  628;  Conservative    0;  Mismatches  485;  Indels  [illegible];  Gaps  [illegible];

Qy        223 GAGATTATCAAT[illegible] 282
Db        174 [illegible] 232

Qy        283 [illegible]GCACATG[illegible] 342
Db        233 [illegible] 289

Qy        343 TTCCTGACAGG[illegible]CAG[illegible]CA[illegible] 402
Db        290 [illegible]GACTCTGCTT[illegible]TACTACTGGGGCCTATTTGATGGCATGCAGGGGG[illegible]GAGCTCCTGAA 349

Qy        403 TTGGCTGCCAA[illegible] 462
Db        350 ATGGCCTCA[illegible] 40[illegible]

Qy        463 TTCCTCC[illegible] 522
Db        410 CTTCAGGA[illegible] 462

Qy        523 [illegible] 582
Db        463 AGATT[illegible] 508

Qy        583 [illegible] 642
Db        509 [illegible]

Qy        643 [illegible]
Db        5[illegible] [illegible] 628

Qy        703 GATAG[illegible] 762
Db        629 GATA[illegible]

Qy        763 [illegible] 822
Db        689 CCGGAGACTGAG[illegible] 74[illegible]

Qy        823 [illegible] 882
Db        7[illegible] [illegible]

Qy        883 [illegible] 942
Db        [illegible]

Qy        943 [illegible]
Db        [illegible] [illegible]

Qy       1003 [illegible]TAAG 10[illegible]
Db        [illegible] [illegible]

Qy       1063 [illegible] 1122
Db        989 [illegible] 1[illegible]

Qy       1123 GA[illegible] 1182
Db       1049 [illegible]

Qy       1183 [illegible] 12[illegible]
```

```
[illegible]

RESULT 8
[illegible]
; Sequence [illegible], Application [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: Stuart, Susan [illegible]
;  APPLICANT: [illegible], Sara J.; Naughton, Rebecca E.
;  TITLE OF INVENTION: [illegible] OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIVE S
;  FILE REFERENCE: PD 1028 2 [illegible]N
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: 2003-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible],868
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  [illegible] Application [illegible] File Wrapper [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: [illegible]
;   OTHER INFORMATION: [illegible]
;   FEATURE:
;   NAME/KEY: [illegible]
;   LOCATION: [illegible]
;   OTHER INFORMATION: [illegible]
[illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy       1051 [illegible]
Db          1 [illegible]

Qy       1111 [illegible]
Db         61 [illegible]

Qy       1171 [illegible]
Db        121 [illegible]

Qy       1231 [illegible]
Db        180 [illegible]

Qy       1291 [illegible]
Db        [illegible]


RESULT 9
US-10-144-771-6858
; Sequence 6858, Application US/10144771
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
;  FILE REFERENCE: CL001321
;  CURRENT APPLICATION NUMBER: US/10/144,771
;  CURRENT FILING DATE: 2002-05-15
;  NUMBER OF SEQ ID NOS: [illegible]
; SEQ ID NO 6858
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-144-771-6858

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches 28[illegible]; Indels [illegible]; Gaps [illegible];

Qy        535 [illegible]
Db        446 [illegible]

Qy        595 [illegible]
Db        [illegible]

Qy        655 [illegible]
Db        566 [illegible]

Qy        715 [illegible]
Db        626 [illegible]

Qy        775 [illegible]
Db        686 [illegible]

Qy        835 [illegible]
Db        746 [illegible]

Qy        [illegible]
Db        [illegible]
```

```
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PERL Program
; SEQ ID NO 65
;    LENGTH: 1480
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: misc_feature
;    OTHER INFORMATION: Incyte ID No: 7507[illegible]
PCT-US02-09126-65

  Query Match             19.1%;  Score 263.2;  DB 1;  Length 1480;
  Best Local Similarity   61.0%;  Pred. No. 2.[illegible];
  Matches  427;  Conservative    0;  Mismatches  27[illegible];  Indels    0;  Gaps    0;

Qy        [illegible]
Db        516 AGAAGGAAGTGAGCCACGAGAGCCTGGTAGTGGGGGCCATTGAGAATGCCTTCCAGCTCA 575

Qy        596 [illegible] 655
Db        576 [illegible]

Qy        656 TGGTGGCTGTGTGCCTGCAGGGAAAGCTGTACATGGCCAATGCTGGGGATAGGCAGGGCA 715
Db        [illegible]

Qy        716 [illegible]
Db        696 [illegible]

Qy        776 [illegible]
Db        756 [illegible]

Qy        836 [illegible]
Db        [illegible]

Qy        896 [illegible]
Db        876 [illegible]

Qy        956 [illegible]
Db        936 [illegible]

Qy       1016 [illegible]
Db        [illegible]

Qy       1076 [illegible]
Db       1056 [illegible]

Qy       1136 [illegible]
Db       1116 [illegible]

Qy       1196 [illegible]
Db       1176 [illegible]


RESULT 7
US-10-144-771-12171
; Sequence 12171, Application US/10144771
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: HUMAN GENOME [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/10/144,771
;  CURRENT FILING DATE: 2002-05-15
;  NUMBER OF SEQ ID NOS: [illegible]
; SEQ ID NO 12171
;    LENGTH: [illegible]
;    TYPE: DNA
;    ORGANISM: HUMAN
US-10-144-771-12171

  Query Match             [illegible];  Score 262.8;  DB 6;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  713;  Conservative    0;  Mismatches  517;  Indels  [illegible];  Gaps  [illegible];

Qy        127 [illegible]
Db        223 [illegible] 282

Qy        [illegible] AAA 24[illegible]
Db        283 [illegible] 342

Qy        244 [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        4[illegible]
Db        [illegible]

Qy        [illegible] 565
Db        [illegible]

Qy        [illegible] 625
Db        [illegible] 760

Qy        [illegible] 685
Db        [illegible] 820

Qy        [illegible] 745
Db        [illegible]

Qy        [illegible] 805
Db        [illegible]

Qy        [illegible] 865
Db        [illegible]

Qy        [illegible]
Db       1001 [illegible]

Qy        [illegible]
Db       1061 [illegible]

Qy        [illegible]
```

```
Db     [illegible]
Qy     [illegible] TTTCATAAATC [illegible]
Db     [illegible] TTTCATAAATC [illegible]

RESULT [illegible]
[illegible]
; Sequence [illegible], Application US/[illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible], Peter S.
;  APPLICANT: [illegible]
;  APPLICANT: [illegible], Christopher [illegible]
;  APPLICANT: Van [illegible] Veer, [illegible]
;  APPLICANT: Van de Vijver, [illegible]
;  APPLICANT: Bernards, Rene
;  TITLE OF INVENTION: [illegible] Prognosis [illegible] Breast Cancer Patients
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-0[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2002-0[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2002-0[illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
; SEQ ID NO [illegible]
;  LENGTH: [illegible]
;  TYPE: DNA
;  ORGANISM: Homo sapiens
[illegible]

  Query Match              [illegible]%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches [illegible];  Conservative    [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

RESULT 6
[illegible]
; Sequence 65, Application PCT/US02[illegible]126
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  KABLE, Amy E.
;  APPLICANT:  [illegible]IEN, David
;  APPLICANT:  WILSON, Amy D.
;  APPLICANT:  SWARNAKAR, Anita
;  APPLICANT:  [illegible]RVAL, Ann E.
;  APPLICANT:  BAFALIA, April J.A.
;  APPLICANT:  EMERLING, Brooke M.
;  APPLICANT:  RAMKUMAR, [illegible]
;  APPLICANT:  JIN, Pei
;  APPLICANT:  GRIFFIN, Jennifer A.
;  APPLICANT:  MARQUIS, Joseph P.
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  CHAWLA, Narinder K.
;  APPLICANT:  LEHR-MASON, Patricia M.
;  APPLICANT:  KHARE, [illegible]
;  APPLICANT:  LEE, Sally
;  APPLICANT:  HAWKINS, Phillip R.
;  APPLICANT:  BECHA, Shanya D.
;  APPLICANT:  LU, [illegible] Yuan
;  APPLICANT:  SPRAGUE, William W.
;  APPLICANT:  [illegible]RABJAL[illegible]AN, Yeganeh
;  TITLE OF INVENTION: KINASES AND PHOSPHATASES
;  FILE REFERENCE: PF[illegible]
;  CURRENT APPLICATION NUMBER: PCT/US02/[illegible]126
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: [illegible]-12-1[illegible]
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: [illegible]-12-[illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]-02-04
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2002-02-[illegible]
```

```
Qy        301 [illegible] 360

Db        301 [illegible] 342

Qy        361 [illegible] 420

Db        343 ------------------------------------------------------------ 342

Qy        421 [illegible] 480

Db        343 ------------------------------------------------------------ 342

Qy        481 CCCATGCACCTCAATGGCCGCTGCATCTGCCCCAGTGACCCTCAGTTTGTGGAGGAAAAG 540

Db        343                                                              342

Qy        541 [illegible] 600

Db        343 ---------------------------------------------------------GAT 345

Qy        601 [illegible] 660

Db        346 [illegible] 405

Qy        661 [illegible] 720

Db        406 [illegible] 465

Qy        721 [illegible] 780

Db        466 [illegible] 525

Qy        781 [illegible] 840

Db        526 CGGATCCAGCAGCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTG 585

Qy        841 GAGTTCCCTGGCGGCTGAAGGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCAC 900

Db        586 [illegible] 645

Qy        901 [illegible] 960

Db        646 [illegible] 705

Qy        961 [illegible] 1020

Db        706 [illegible] 765

Qy       1021 [illegible] 1080

Db        766 GACCATCAGCTCAGAGTCCTGGACACAAACATCCAGCTCAAGG[illegible] 825

Qy       1081 CCACAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTC 1140

Db        826 CCACAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTC 885

Qy       1141 ATGGCAACTGATGGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGG 1200

Db        886 ATGGCAACTGATGGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGG 945

Qy       1201 AGCTTCCTCCCTGGGAACCAAGAGGACCCA------------------------CACAGG 1236

Db        946 AGCTTCCTCCCTGGGAACCAAGAGGACCCACACAGCTATTTGCTAGATGGCTTTCACAGG 1005

Qy       1237 TTCTCAAAGCCGGGCCAGATGCGGATACACAGCACACACGGAAAGAAAGACAGTTCACA 1296

Db       1006 TTCTCAAAGCCGGGCCAGATGCGGATACACAGCACACACGGAAAGAAAGACAGTTCACA 1065

Qy       1297 GAGGAAGGGCAGGTGTCCTACGATGACGTCTCTGTGTTCGTGATTCCCTTGCACAGTCAG 1356

Db       1066 GAGGAAGGGCAGGTGTCCTACGATGACGTCTCTGTGTTCGTGATTCCCTTGCACAGTCAG 1125

Qy       1357 GGCCAAGAGAGGAGCAACTGA [illegible]

Db       1126 GGCCAAGAGAGGAGCAACTGA [illegible]


RESULT 4
US-10-349-781-54107
; Sequence 54107, Application US/10349781
; GENERAL INFORMATION:
;  APPLICANT: Sollhamer, Jeffrey [illegible]; Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.; Stuve, Laura L.
;  APPLICANT:  Mullahy, Sara J.; Naughton, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIV
;  FILE REFERENCE: PD-1028-2 CON
;  CURRENT APPLICATION NUMBER: US/10/349,781
;  CURRENT FILING DATE: 2003-01-21
;  PRIOR APPLICATION NUMBER: 09/549,764
;  PRIOR FILING DATE: 2000-04-[illegible]
;  PRIOR APPLICATION NUMBER: 08/[illegible]
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: 60/032,858
;  PRIOR FILING DATE: 1996-12-13
;  PRIOR APPLICATION NUMBER: 08/734,[illegible]
;  PRIOR FILING DATE: 1996-10-18
;  PRIOR APPLICATION NUMBER: 60/006,111
;  PRIOR FILING DATE: 1995-10-24
;  PRIOR APPLICATION NUMBER: 08/733,814
;  PRIOR FILING DATE: 1996-10-18
;  PRIOR APPLICATION NUMBER: 60/005,864
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: 08/763,920
;  PRIOR FILING DATE: 1996-12-11
;  PRIOR APPLICATION NUMBER: 60/008,794
;  PRIOR FILING DATE: 1995-12-14
;  PRIOR APPLICATION NUMBER: 08/772,[illegible]
;  PRIOR FILING DATE: 1996-12-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 61458
;  SOFTWARE: PERL Program
; SEQ ID NO 54107
;   LENGTH: 476
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: [illegible]
US-10-349-781-54107

  Query Match             26.6%;  Score 367.2;  DB 6;  Length 476;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  369;  Conservative    0;  Mismatches   [illegible];  Indels    0;  Gaps    0;

Qy        225 [illegible] 284

Db        165 [illegible] 224

Qy        285 [illegible] 344

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Qy        345 [illegible] 404

Db        225 [illegible] 284

Qy        405 [illegible] 464

Db        285 [illegible] 344

Qy        465 [illegible] 524

Db        345 [illegible] 404

Qy        525 [illegible] 584
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RESULT [illegible]
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; Sequence [illegible], Application US/[illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible], Kimberly
;  APPLICANT: [illegible], Bryan
;  APPLICANT: [illegible], Meera
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
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;  APPLICANT:  [illegible], Lisa
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  [illegible], Luca
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Taupier Jr, Raymond J.
;  APPLICANT:  Gusev, Vladimir Y.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  [illegible], Adam R.
;  APPLICANT:  Pena, Carol E. A
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Grosse, William M.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-258
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: 2002-01-31
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/266,[illegible]
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-02-0[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: 60/[illegible],459
;  PRIOR FILING DATE: [illegible]
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-[illegible]

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  Best Local Similarity   80.[illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative   [illegible];  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

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;  PRIOR APPLICATION NUMBER: 60/267,459
;  PRIOR FILING DATE: 2001-02-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1391
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 197
;   LENGTH: 2185
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-072-012-197

  Query Match             97.5%;  Score 1346;  DB 6;  Length 2185;
  Best Local Similarity   98.3%;  Pred. No. 6.5e-295;
  Matches 1380;  Conservative    0;  Mismatches    0;  Indels   24;  Gaps    1;

Qy          1 [illegible] 60
Db          1 [illegible] 60

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCCTGGGCGGCATGCCAGCCCCGTGCCCTACCGACGGCCCGGCTTCCTTCCGGCTCC 120

Qy        121 AGCTCCAGCCCCGGGGCGGCCGACGCCTCGGCGCCCCAGACTCCCGGCCCGTGCGCAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCTCCAGCCCCGGGGCGGCCGACGCCTCGGCGCCCCAGACTCCCGGCCCGTGCGCAGC 180

Qy        181 CCGGCACGAGGACGTACGTTACCCTGGAATGCAGGCTACGCTGAGATTATCAATGCAGAG 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGGCACGAGGACGTACGTTACCCTGGAATGCAGGCTACGCTGAGATTATCAATGCAGAG 240

Qy        241 AAATCTGAATTCAATGAGGATCAAGCCGCCTGTGGAAACTTGTGCATCGGAGATGTGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 [illegible] 300

Qy        301 TTTGGGGCTGAAGAAGAGTGGCTGACCCTGTGCCCAGAGGAGTTCCTGACAGGCCATTAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGCTGAAGAAGAGTGGCTGACCCTGTGCCCAGAGGAGTTCCTGACAGGCCATTAC 360

Qy        361 [illegible] 420
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Db        361 [illegible] 420

Qy        421 [illegible] 480
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Db        421 [illegible] 480

Qy        481 [illegible] 540
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Db        481 [illegible] 540

Qy        541 [illegible] 600
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Db        541 [illegible] 600

Qy        601 [illegible] 660
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Qy        661 [illegible] 720
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Db        661 [illegible] 720

Qy        721 [illegible] 780
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Db        721 [illegible] 780

Qy        781 [illegible] 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 [illegible] 840

Qy        841 [illegible] 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 [illegible] 900

Qy        901 [illegible] 960
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Db        901 [illegible] 960

Qy        961 [illegible] 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 [illegible] 1020

Qy       1021 [illegible] 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1081 [illegible] 1140
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Qy       1141 [illegible] 1200
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Qy       1201 AGCTTCCTCCCTGGGAACCAAGAGGACCCA------------------------CACAGG 1236
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Qy       1237 [illegible] 1296
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Db       1261 TTCTCAAAGCTGGCCCAGATGCTGATAGACAGCACACAGGGAAAGGAAGAGAGTTCAGA 1320

Qy       1297 GAGGAAGGGCAGGTGTCCTACGATGACGTCTCTGTGTTCGTGATTCCCTGGCACAGTCAG 1356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GAGGAAGGGCAGGTGTCCTACGATGACGTCTCTGTGTTCGTGATTCCCTGGCACAGTCAG 1380

Qy       1357 GGCCAAGAGAGAGATGACTATGA 1379
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Db       1381 GGCCAAGAGAGAGATGACTATGA 1403


RESULT 2
US-10-144-771-11494
; Sequence 11494, Application US/10144771
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
;  FILE REFERENCE: CL001321
;  CURRENT APPLICATION NUMBER: US/10/144,771
;  CURRENT FILING DATE: 2002-05-15
;  NUMBER OF SEQ ID NOS: 47245
; SEQ ID NO 11494
;   LENGTH: 1285
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-144-771-11494

  Query Match             63.1%;  Score 843.6;  DB 6;  Length 1285;
  Best Local Similarity   85.9%;  Pred. No. [illegible]e-182;
  Matches  962;  Conservative    0;  Mismatches  149;  Indels   [illegible];  Gaps    2;

Qy        [illegible]
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Qy        [illegible]
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Qy        [illegible] 398
Db        [illegible]

Qy        399 [illegible] 458
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[illegible]
[illegible]

[illegible]

Run on:        February [illegible], 2003, [illegible] ; Search time [illegible] Seconds
                                          (without alignments)
                                          [illegible] Million cell updates/sec

Title:         US-09-866-987-3
Perfect score: [illegible]
Sequence:      [illegible]

Scoring table: IDENTITY_NUC
               Gapop [illegible] , Gapext [illegible]

Searched:      [illegible] seqs, [illegible] residues

Total number of hits satisfying chosen parameters: [illegible]

Minimum DB seq length: [illegible]
Maximum DB seq length: [illegible]

Post-processing: Minimum Match [illegible]
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                 Listing first [illegible] summaries

Database :     Published Applications NA New:*
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               2:  [illegible] NEW_PUB.seq:*
               3:  [illegible] NEW_PUB.seq:*
               4:  [illegible] NEW_PUB.seq:*
               5:  [illegible] NEW_PUB.seq:*
               6:  [illegible] NEW_PUB.seq:*
               7:  [illegible] NEW_PUB.seq:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                                     SUMMARIES

Result           %
    No.   Score  Match Length DB ID                          Description

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     5   [illegible]                                         Sequence [illegible], App
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    10   [illegible]                                         Sequence [illegible], App
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    22   [illegible]                                         Sequence 10, Appl
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c   29    49.4   3.6   1485  5  US-09-724-676-19546            Sequence 19546, A
c   30    49.4   3.6   1485  5  US-09-724-676A-19546           Sequence 19546, A
c   31    49.4   3.6   1505  5  US-09-724-676-19539            Sequence 19539, A
c   32    49.4   3.6   1505  5  US-09-724-676A-19539           Sequence 19539, A
c   33    49.4   3.6   1511  5  US-09-724-676-19543            Sequence 19543, A
c   34    49.4   3.6   1511  5  US-09-724-676A-19543           Sequence 19543, A
c   35    49.4   3.6   1512  5  US-09-724-676-19521            Sequence 19521, A
c   36    49.4   3.6   1512  5  US-09-724-676A-19521           Sequence 19521, A
c   37    49.4   3.6   1518  5  US-09-724-676-19525            Sequence 19525, A
c   38    49.4   3.6   1518  5  US-09-724-676A-19525           Sequence 19525, A
c   39    49.4   3.6   1525  5  US-09-724-676-19531            Sequence 19531, A
c   40    49.4   3.6   1525  5  US-09-724-676A-19531           Sequence 19531, A
c   41    49.4   3.6   1531  5  US-09-724-676-19535            Sequence 19535, A
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c   43    49.4   3.6   1650  5  US-09-724-676-19538            Sequence 19538, A
c   44    49.4   3.6   1650  5  US-09-724-676A-19538           Sequence 19538, A
c   45    49.4   3.6   1656  5  US-09-724-676-19541            Sequence 19541, A

                                    ALIGNMENTS

RESULT 1
US-10-[illegible]
; Sequence [illegible], Application US/10[illegible]
; GENERAL INFORMATION:
;  APPLICANT: Tchernev, Velizar
;  APPLICANT: Spytek, Kimberly
;  APPLICANT: Zerhusen, Bryan
;  APPLICANT: Patturajan, Meera
;  APPLICANT: Shimkets, Richard
;  APPLICANT: Li, Li
;  APPLICANT: Gangolli, Esha
;  APPLICANT: Padigaru, Muralidhara
;  APPLICANT: Anderson, David W.
;  APPLICANT: Rastelli, Luca
;  APPLICANT: Miller, Charles E.
;  APPLICANT: Gerlach, Valerie
;  APPLICANT: Taupier Jr., Raymond J.
;  APPLICANT: Gusev, Vladimir Y.
;  APPLICANT: Colman, Steven D.
;  APPLICANT: Wolenc, Adam R.
;  APPLICANT: Pena, Carol E. A
;  APPLICANT: Furtak, Katarzyna
;  APPLICANT: Grosse, William M.
;  APPLICANT: Alsobrook II, John P.
;  APPLICANT: Lepley, Denise M.
;  APPLICANT: Rieger, Daniel K.
;  APPLICANT: Burgess, Catherine E.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 214[illegible]
;  CURRENT APPLICATION NUMBER: US/1[illegible]
;  CURRENT FILING DATE: 2002-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: 60/26[illegible],412
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/26[illegible],106
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: 60/26[illegible],975
;  PRIOR FILING DATE: [illegible]
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                    GenCore version 5.1.3
          Copyright (c) 1993 - 2003 Compugen Ltd.

 OM nucleic - nucleic search, using sw model

Run on:          February 23, 2003, 15:14:13 ; Search time 65 Seconds
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                                      6510.984 Million cell updates/sec

Title:           US-09-866-987-3
Perfect score:   1358
Sequence:        1 atgtcgccgagctggttccg..........aagaagcagtgaccactga 1358

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        441762 seqs, 15[illegible]8381 residues

Total number of hits satisfying chosen parameters:      882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Issued_Patents_NA:*
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                2: [illegible]:*
                3: [illegible]:*
                4: [illegible]P_COMB.seq:*
                5: [illegible]:*
                6: [illegible]:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                   %
Result           Query
   No.   Score   Match Length DB  ID                            Description
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 c   1    49.8    3.6   6714  4  US-09-299-141-6              Sequence 6, Appl
 c   2    49.8    3.6   6924  4  US-09-299-141-9              Sequence 9, Appl
 c   3    49.8    3.6   6924  4  US-09-299-141-10             Sequence 10, Appl
 c   4    49.8    3.6   6924  4  US-09-299-141-11             Sequence 11, Appl
 c   5    48.2    3.5   1491  4  US-09-082-092-9              Sequence 9, Appl
 c   6    48.2    3.5   1917  1  US-0[illegible]-288-292A-45  Sequence 45, Appl
     7    47      3.4    349  4  US-09-198-119C-34            Sequence 34, Appl
 c   8    46.4    3.4    774  3  US-08-415-655-11             Sequence 11, Appl
 c   9    45.2    3.3    645  4  US-09-535-0[illegible]       Sequence [illegible], Appl
    10    43.6    3.2 152371  3  US-09-128-155-16             Sequence 16, Appl
 c  11    43.4    3.2   1488  4  US-09-096-776B-3             Sequence 3, Appl
 c  12    43.4    3.2   2734  4  US-09-096-776B-1             Sequence 1, Appl
 c  13    43.2    3.2   3046  3  US-09-083-351-1              Sequence 1, Appl
 c  14    43.2    3.2   3040  4  US-09-083-352-1              Sequence 1, Appl
 c  15    43      3.2   1028  4  US-08-118-250-1              Sequence 1, Appl
 c  16    43      3.2   1028  4  US-08-478-747-1              Sequence 1, Appl
    17    42.8    3.2   8460  1  US-08-469-005A-3             Sequence 3, Appl
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 c  19    42.4    3.1    320  4  US-09-165-264-7              Sequence 7, Appl
 c  20    42.4    3.1    320  4  US-09-165-264-13             Sequence 13, Appl
 c  21    41.4    3.0    319  4  US-09-165-264-8              Sequence 8, Appl
    22    41.4    3.0   4252  2  US-08-475-844-4              Sequence 4, Appl
    23    41.4    3.0   4252  5  PCT-US95-08422-4             Sequence 4, Appl
    24    41.2    3.0   1413  4  US-08-984-709A-52            Sequence 52, Appl
    25    41.2    3.0   6453  1  US-08-306-691B-14            Sequence 14, Appl
    26    41.2    3.0   6453  3  US-09-209-668-14             Sequence 14, Appl
    27    41.2    3.0   6453  3  US-09-356-952-8              Sequence 8, Appl
    28    41      [illegible]    US-[illegible]A-11           Sequence 11, Appl
 c  29    40.8    3.0   3978  3  US-08-726-214-1              Sequence 1, Appl
 c  30    40.8    3.0   45[illegible] 4  US-0[illegible]-4[illegible]-1  Sequence 1, Appl
 c  31    40.4    2.9   3332  4  US-09-423-890-11             Sequence 11, Appl
 c  32    40.2    2.9   8158  1  US-0[illegible]-945-283-1    Sequence 1, Appl
 c  33    40      2.9   1413  4  US-08-984-709A-52            Sequence 52, Appl
 c  34    39.8    2.9    320  4  US-09-165-264-11             Sequence 11, Appl
 c  35    39.6    2.9   7218  1  US-08-232-463-14             Sequence 14, Appl
 c  36    39.4    2.9    700  4  US-09-236-097-7              Sequence 7, Appl
 c  37    39.4    2.9   2502  1  US-08-073-384C-7             Sequence 7, Appl
 c  38    39.4    2.9   2502  1  US-08-254-359A-7             Sequence 7, Appl
 c  39    39.4    2.9   2502  1  US-0[illegible]-185-045-7    Sequence 7, Appl
 c  40    39.4    2.9   2502  1  US-08-481-238-7              Sequence 7, Appl
 c  41    39.4    2.9   2502  2  US-08-471-66[illegible]B-7   Sequence 7, Appl
 c  42    39.4    2.9   2502  2  US-08-481-956-7              Sequence 7, Appl
 c  43    39.4    2.9   2502  2  US-08-757-653-7              Sequence 7, Appl
 c  44    39.4    2.9   2502  2  US-08-[illegible]-491-7      Sequence 7, Appl
 c  45    39.4    2.9   2502  2  US-08-756-386-7              Sequence 7, Appl

                              ALIGNMENTS

RESULT 1
US-09-299-141-6/c
; Sequence 6, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: [illegible], MICHAEL
;  TITLE OF INVENTION: [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: 1999-04-23
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 1[illegible]
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 6714
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:[illegible]
;   OTHER INFORMATION: p43CB A1
US-09-299-141-6

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  Best Local Similarity   54.7%;  Pred. No. [illegible];
  Matches   99;  Conservative    [illegible];  Mismatches   82;  Indels   [illegible];  Gaps   [illegible];

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Db       1[illegible]52 [illegible] 1[illegible]

Qy         79 [illegible] 138
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Qy        [illegible] [illegible] 1[illegible]
Db       1[illegible]52 [illegible] 1[illegible]

Qy        199 C 199
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Db       1472 C 1472


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; Sequence 9, Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p[illegible]
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Db [illegible]

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Db [illegible]


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; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
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US-[illegible]

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Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]

Db [illegible]


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; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
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;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
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US-[illegible]

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Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]

Db [illegible]


RESULT [illegible]
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; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;     APPLICANT: [illegible]
;     APPLICANT: [illegible], Anita
;     APPLICANT: [illegible]
;    APPLICANT:  Itoh, Susumu
;    APPLICANT:  Afrakhte, Mozhgan
;    APPLICANT:  Souchelnytskyi, Serhiy
;    APPLICANT:  Frodin, Greder
;    APPLICANT:  Landstrom, Marene
;    APPLICANT:  Heldin, Nils-Erik
;    APPLICANT:  Heldin, Carl-Henrik
;    APPLICANT:  ten Dijke, Peter
;    TITLE OF INVENTION:  SMAD7 AND USES THEREOF
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210 2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/082,992
;      FILING DATE:  20 MAY 1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/047,221
;      FILING DATE:  20 MAY-1997
;      APPLICATION NUMBER:  60/060,465
;      FILING DATE:  30 SEP-1997
;      APPLICATION NUMBER:  60/075,91[illegible]
;      FILING DATE:  25-FEB-1998
;      APPLICATION NUMBER:  60/077,[illegible]
;      FILING DATE:  06-MAR-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7032
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-082-992-9

  Query Match             3.5%;  Score 48.2;  DB 1;  Length 1491;
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Db        302 [illegible] 243

Qy         65 [illegible] 124

Db        242 [illegible] 183

Qy        125 [illegible] 184

Db        182 [illegible] 123

Qy        185 C 185
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Db        122 C 122
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US-09-288-292A-45/c
; Sequence 45, Application US/09288292A
; Patent No. 6359194
; GENERAL INFORMATION:
;  APPLICANT: Dean A. Falb
;  APPLICANT:  Katherine Galvin
;  APPLICANT:  Michael Donovan
;  APPLICANT:  Dennis Huszar
;  APPLICANT:  Michael A. Gimbrone Jr.
;  TITLE OF INVENTION: Compositions and Methods for the Treatment and Diagnosis of
;  TITLE OF INVENTION:  Cardiovascular Disease
;  FILE REFERENCE: 7853-140-999
;  CURRENT APPLICATION NUMBER: US/09/288,292A
;  CURRENT FILING DATE:  1999-04-08
;  PRIOR APPLICATION NUMBER: 08/87[illegible]
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: 08/799,910
;  PRIOR FILING DATE: 1997-02-14
;  PRIOR APPLICATION NUMBER: 60/011,[illegible]
;  PRIOR FILING DATE: 1996-02-[illegible]
;  PRIOR APPLICATION NUMBER: 08/48[illegible]
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/[illegible],844
;  PRIOR FILING DATE: 1995-02-[illegible]
;  NUMBER OF SEQ ID NOS: 4[illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
;   LENGTH: 1817
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-288-292A-45

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Qy          5 [illegible] 64

Db        456 [illegible] 397

Qy         65 [illegible] 124

Db        396 [illegible] 337

Qy        125 [illegible] 184

Db        336 [illegible] 277

Qy        185 [illegible] 185
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Db        276 [illegible] 276


RESULT 7
US-09-198-11[illegible]-94
; Sequence 94, Application US/09198[illegible]
; Patent No. 6417428
; GENERAL INFORMATION:
;  APPLICANT:  Thomashow, Michael
;  APPLICANT:  Stockinger, Eric
;  APPLICANT:  Jaglo-Ottosen, Kirsten
;  APPLICANT:  Gilmour, Sarah
;  APPLICANT:  Zarka, Daniel
;  APPLICANT:  Jiang, Cai-zhong
;  TITLE OF INVENTION:  Plant Having Altered Environmental Stress Tolerance
;  FILE REFERENCE:  [illegible] Seq List
;  CURRENT APPLICATION NUMBER: US/09/198,[illegible]
;  CURRENT FILING DATE:  1998-11-2[illegible]
;  PRIOR APPLICATION NUMBER:  US [illegible]
;  PRIOR FILING DATE:  [illegible]
;  PRIOR APPLICATION NUMBER:  US 09/018,2[illegible]
;  PRIOR FILING DATE:  1998-02-0[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 199[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 199[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1998-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 199[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1998-[illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
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;   FEATURE:
;   OTHER INFORMATION: [illegible]
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  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

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Db [illegible]

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]


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;    APPLICANT: [illegible]
;    APPLICANT: [illegible]
;    TITLE OF INVENTION: [illegible]
;    TITLE OF INVENTION: p[illegible], A CYCLIN DEPENDENT KINASE INHIBITOR AND [illegible]
;    TITLE OF INVENTION: SAME
;    NUMBER OF SEQUENCES: [illegible]
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: [illegible]
;      STREET: [illegible] Avenue of the Americas
;      CITY: New York
;      STATE: New York
;      COUNTRY: [illegible]
;      ZIP: [illegible]
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: [illegible]
;      COMPUTER: IBM P[illegible]
;      OPERATING SYSTEM: [illegible]
;      SOFTWARE: PatentIn Release #[illegible], Version #[illegible]
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/[illegible]
;      FILING DATE:
;      CLASSIFICATION: [illegible]
;    ATTORNEY/AGENT INFORMATION:
;      NAME: [illegible]
;      REGISTRATION NUMBER: [illegible]
;      REFERENCE/DOCKET NUMBER: [illegible]
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: [illegible]
;      TELEFAX: [illegible]
;  INFORMATION FOR SEQ ID NO: [illegible]
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: [illegible] base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;    MOLECULE TYPE: [illegible]
;    HYPOTHETICAL: N
;    ANTI-SENSE: N
US-08-[illegible]

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  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

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Db [illegible]

Qy [illegible]

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Db [illegible]


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; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible], Alexander [illegible]
;  APPLICANT: [illegible], Sean V.
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: [illegible] IS A TUMOR SUPPRESSOR THAT IS MUTATED IN [illegible]
;  TITLE OF INVENTION: AND OTHER CANCER TYPES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: 2[illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
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;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-[illegible]

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  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]


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; Sequence [illegible], Application US/[illegible]
; Patent No. 6117654
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;  TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 10454/052001
;  CURRENT APPLICATION NUMBER: US/09/128,155
;  CURRENT FILING DATE: 1998-08-[illegible]
;  EARLIER APPLICATION NUMBER: US 60/091,650
;  EARLIER FILING DATE: 1998-07-02
;  EARLIER APPLICATION NUMBER: US 60/054,646
;  EARLIER FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
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;   LENGTH: 152331
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(152331)
;   OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

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Qy         63 [illegible] 122

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Qy        123 [illegible] 182

Db      22117 [illegible] 22176

Qy        183 [illegible] 204

Db      22177 [illegible] 22198


RESULT 11
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; Sequence 3, Application US/09096776B
; Patent No. 6270994
; GENERAL INFORMATION:
;  APPLICANT:  Miyazono, Kohei
;  APPLICANT:  Kawabata, Masahiro
;  TITLE OF INVENTION:   SMAD6 AND USES THEREOF
;  FILE REFERENCE:   L0461/7038
;  CURRENT APPLICATION NUMBER: US/09/096,776B
;  CURRENT FILING DATE:  1998-06-12
;  PRIOR APPLICATION NUMBER:   US 60/049,[illegible]
;  PRIOR FILING DATE:   1997-06-13
;  PRIOR APPLICATION NUMBER:   US 60/05[illegible],[illegible]4
;  PRIOR FILING DATE:   1997-07-18
;  PRIOR APPLICATION NUMBER:   US 60/066,17[illegible]
;  PRIOR FILING DATE:   1997-11-18
;  NUMBER OF SEQ ID NOS:   1[illegible]
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1488
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-096-776B-3

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Db        2[illegible] [illegible]

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Db        2[illegible] [illegible]

Qy        125 [illegible]

Db        1[illegible] [illegible]

Qy        185 [illegible] 185

Db        1[illegible] [illegible] 1[illegible]


RESULT 12
US-09-096-776B-1/c
; Sequence 1, Application US/09096776B
; Patent No. 6270994
; GENERAL INFORMATION:
;  APPLICANT:  Miyazono, Kohei
;  APPLICANT:  Kawabata, Masahiro
;  TITLE OF INVENTION:   SMAD6 AND USES THEREOF
;  FILE REFERENCE:   L0461/7038
;  CURRENT APPLICATION NUMBER: US/09/096,776B
;  CURRENT FILING DATE:  1998-06-12
;  PRIOR APPLICATION NUMBER:   US 60/049,[illegible]
;  PRIOR FILING DATE:   1997-06-13
;  PRIOR APPLICATION NUMBER:   US 60/05[illegible],[illegible]4
;  PRIOR FILING DATE:   1997-07-18
;  PRIOR APPLICATION NUMBER:   US 60/066,17[illegible]
;  PRIOR FILING DATE:   1997-11-18
;  NUMBER OF SEQ ID NOS:   1[illegible]
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 2[illegible]3[illegible]
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: ([illegible])..([illegible])
US-09-096-776B-1

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  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
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Db        [illegible]

Qy         65 [illegible] 124

Db        [illegible]

Qy        125 [illegible] 184

Db        [illegible]

Qy        185 C 185

Db        869 C 869


RESULT 13
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; Sequence 1, Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;    APPLICANT:  [illegible]
;    APPLICANT:  Alward, Wallace L.M.
;    APPLICANT:  Stone, Edwin M.
;    APPLICANT:  Nishimura, Darryl
;    APPLICANT:  Patil, Shiva
;    TITLE OF INVENTION:  THERAPEUTICS AND DIAGNOSTICS [illegible]
;    TITLE OF INVENTION:  CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
;    TITLE OF INVENTION:  TRANSCRIPTION FACTOR
;    NUMBER OF SEQUENCES:  [illegible]
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  [illegible]
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/[illegible]
;      FILING DATE:  [illegible] MAY 1999
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold, Beth E.
;      REGISTRATION NUMBER:  [illegible]
;      REFERENCE/DOCKET NUMBER:  UIA-[illegible]
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-[illegible]
;      TELEFAX:  617-832-[illegible]
;  INFORMATION FOR SEQ ID NO:  [illegible]
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3946 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  477..[illegible]
US-09-[illegible]

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; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;    APPLICANT:  Sheffield, Val C.
;    APPLICANT:  Alward, Wallace L.M.
;    APPLICANT:  Stone, Edwin M.
;    APPLICANT:  Nishimura, Darryl
;    APPLICANT:  Patil, Shiva
;    TITLE OF INVENTION:  GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
;    TITLE OF INVENTION:  BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
;    NUMBER OF SEQUENCES:  [illegible]
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  [illegible]
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/[illegible]
;      FILING DATE:  [illegible] MAY 1999
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold, Beth E.
;      REGISTRATION NUMBER:  [illegible]
;      REFERENCE/DOCKET NUMBER:  UIA-[illegible]
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3946 base pairs
;      TYPE:  nucleic acid
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;      NAME/KEY:  CDS
;      LOCATION:  477..2[illegible]
US-09-083-352-1

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Db  [illegible]


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; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;    APPLICANT:  SUTHERLAND, Grant R
;    APPLICANT:  RICHARDS, Robert I
;    APPLICANT:  SCHLESSINGER, David
;    APPLICANT:  NAGARAJA, Ramaiah
;    APPLICANT:  KREMER, Eric J
;    APPLICANT:  YU, Sui
;    APPLICANT:  BAKER, Elizabeth
;    APPLICANT:  MULLEY, John C
;    APPLICANT:  MANDEL, Jean Louis
;    APPLICANT:  PRITCHARD, Melanie April
;    APPLICANT:  LYNCH, Michael
;    TITLE OF INVENTION:  DNA SEQUENCES RELATED TO IS[illegible]
;    TITLE OF INVENTION:  FRAGILE X SYNDROME
;    NUMBER OF SEQUENCES:  [illegible]
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;        STREET:  P.O. Box 1404
;        CITY:  Alexandria
;        STATE:  Virginia
;        COUNTRY:  United States
;        ZIP:  22313-1404
;     COMPUTER READABLE FORM:
;        MEDIUM TYPE:  Floppy disk
;        COMPUTER:  IBM PC compatible
;        OPERATING SYSTEM:  PC-DOS/MS-DOS
;        SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;        APPLICATION NUMBER:  US/08/118,26[illegible]
;        FILING DATE:  09-SEP-1993
;        CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  US 07/802,65[illegible]
;        FILING DATE:  05-DEC-1991
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  US 07/672,232
;        FILING DATE:  20-MAR-1991
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  US 07/638,518
;        FILING DATE:  04-JAN-1991
;     PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  US 07/966,517
;        FILING DATE:  2[illegible]-[illegible]-1992
;     ATTORNEY/AGENT INFORMATION:
;        NAME:  Crane Feury, Sharon E
;        REGISTRATION NUMBER:  3[illegible]
;        REFERENCE/DOCKET NUMBER:  020160-164
;     TELECOMMUNICATION INFORMATION:
;        TELEPHONE:  (703) 836-6620
;        TELEFAX:  (703) 836-2021
;  INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;        LENGTH:  [illegible] base pairs
;        TYPE:  nucleic acid
;        STRANDEDNESS:  single
;        TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-118-[illegible]

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  Best Local Similarity   57.4%;  Pred. No. [illegible];
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Db        421 [illegible]

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Job time : 24[illegible] secs
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              Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 23, 2003, 16:11:38 ; Search time 91 Seconds
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Title:           US-09-866-987-3
Perfect score:   1380
Sequence:        1 atgtccgaccgctgattccg..........aaaaccaatgaccactga 1380

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        442118 seqs, 28[illegible] residues

Total number of hits satisfying chosen parameters:       88[illegible]

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_NA:*
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                 14: [illegible]_PUBCOMB.seq:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES
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    2      536     38.8    547 10  US-09-867-701-2968         Sequence 2968, Ap
    3    243.4     17.6   5791 10  US-09-920-306A-1714        Sequence 1714, Ap
    4    243.1     17.6   5791 12  US-10-033-528-1714         Sequence 1714, Ap
    5       98      7.1    551 10  US-09-867-701-5460         Sequence 5460, Ap
c   6     48.2      3.5   1817 10  US-09-924-417-64           Sequence 64, Appl
    7       47      3.4    349  9  US-09-996-140-94           Sequence 94, Appl
c   8     46.8      3.4  43058 10  US-09-954-456-292          Sequence 292, App
c   9     46.8      3.4  43058 10  US-09-954-456-529          Sequence 529, App
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   23       43      3.1   1614 12  US-10-023-529-45           Sequence 45, Appl
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   25       43      3.1  12425  9  US-09-976-740-50           Sequence 50, Appl
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   28     42.2      3.1  42[illegible]  9  US-09-799-462A-17    Sequence 17, Appl
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c  33     41.2      3.0    485  9  US-10-004-717-59           Sequence 59, Appl
c  34       41      3.0 155[illegible]  9  US-10-026-188-6      Sequence 6, Appl
c  35     40.8      3.0   4[illegible]  9  US-10-[illegible]-1  Sequence 1, Appl
c  36     40.4      2.9    477 10  US-09-864-761-14662        Sequence 14662, A
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   38     40.4      2.9   1155 10  US-09-814-777A-21          Sequence 21, Appl
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                              ALIGNMENTS


RESULT 1
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; Sequence 3, Application US/09866987
; Patent No. US20020[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible]MAN, GEOFFREY [illegible]
;  APPLICANT:  MARTINEZ, RICARDO
;  APPLICANT:  WHITE, DAVID
;  APPLICANT:  [illegible]
;  APPLICANT:  [illegible]
;  APPLICANT:  [illegible], SEAN
;  APPLICANT:  [illegible]
;  APPLICANT:  [illegible]AN, PETER
;  TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
;  FILE REFERENCE: 0[illegible]/7180
;  CURRENT APPLICATION NUMBER: US/09/866,987
;  CURRENT FILING DATE: 2001-05-[illegible]
;  PRIOR APPLICATION NUMBER: 6[illegible]/2[illegible],29[illegible]
;  PRIOR FILING DATE: 20[illegible]-05-[illegible]
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.[illegible]
; SEQ ID NO 3
;   LENGTH: 1380
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
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;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: phosphatase nucleotide
US-09-866-987-3

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; Patent No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Algate, Paul A.
;  APPLICANT: Jones, Robert
;  APPLICANT: Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: 210121.497
;  CURRENT APPLICATION NUMBER: US/09/867,701
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2968
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US-09-867-701-2968

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; Sequence 1714, Application US/09920[illegible]A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE:  2001-07-31
;  NUMBER OF SEQ ID NOS: 17[illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
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;    ORGANISM: Homo sapiens
US-09-920-[illegible]A-1714

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; Sequence 1714, Application US/10033528
; Patent No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547C[illegible]
;  CURRENT APPLICATION NUMBER: US/10/033,528
;  CURRENT FILING DATE:  2001-12-26
;  NUMBER OF SEQ ID NOS: 1896
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1714
;    LENGTH: 5791
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-10-033-528-1714

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; Patent No. [illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible], [illegible] A.
;  APPLICANT: [illegible], Robert
;  APPLICANT: [illegible], Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/[illegible]
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
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;   LOCATION: (1)...([illegible])
;   OTHER INFORMATION: n = A,T,C or G
US-[illegible]

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  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

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Db  [illegible]

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; Sequence 64, Application US/09924417
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible], Dean
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;                      THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR
;                      DISEASE
;  NUMBER OF SEQUENCES: [illegible]
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: PENNIE & EDMONDS LLP
;   STREET: 1155 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: [illegible]
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ Version [illegible]
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/924,417
;   FILING DATE: [illegible] Aug [illegible]
;   CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/[illegible]
;   FILING DATE: 01-MAR-[illegible]
;   APPLICATION NUMBER: [illegible]
;   FILING DATE: [illegible]-JUN-[illegible]
;   APPLICATION NUMBER: [illegible]
;   FILING DATE: [illegible]-FEB-[illegible]
;   APPLICATION NUMBER: [illegible]
;   FILING DATE: [illegible]-FEB-[illegible]
;   APPLICATION NUMBER: [illegible]
;   FILING DATE: [illegible]-FEB-[illegible]
;   APPLICATION NUMBER: [illegible]
;   FILING DATE: [illegible]-JUN-[illegible]
;   APPLICATION NUMBER: [illegible]
;   FILING DATE: [illegible]-FEB-[illegible]
;  ATTORNEY/AGENT INFORMATION:
;   NAME: [illegible], [illegible] A
;   REGISTRATION NUMBER: [illegible]
;   REFERENCE/DOCKET NUMBER: [illegible]
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212) [illegible]
;   TELEFAX: (212)[illegible]
;   TELEX: [illegible] PENNIE
; INFORMATION FOR SEQ ID NO: 64:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: [illegible] base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: both
;   TOPOLOGY: unknown
;  MOLECULE TYPE: cDNA
;  SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-09-924-417-64

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy  [illegible]

Db  [illegible]

Qy  [illegible]

Db  [illegible]
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Qy        125 [illegible] 184
              [illegible]
Db        336 [illegible] 277

Qy        185 C 185
              |
Db        276 C 276


RESULT 7
US-09-996-140-94
; Sequence 94, Application US/09996140
; Patent No. US20020157136A1
; GENERAL INFORMATION:
;  APPLICANT: Thomashow, Michael
;  APPLICANT:  Stockinger, Eric
;  APPLICANT:  [illegible], [illegible]
;  APPLICANT:  Gilmour, Sarah
;  APPLICANT:  [illegible], [illegible]
;  APPLICANT:  Jiang, Cai-Zhong
;  TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL
;  TITLE OF INVENTION:  STRESS TOLERANCE
;  FILE REFERENCE: MBI[illegible]
;  CURRENT APPLICATION NUMBER: US/09/996,140
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: 09/706,270
;  PRIOR FILING DATE: 1996-09-04
;  PRIOR APPLICATION NUMBER: 09/[illegible]
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/017,816
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,2[illegible]
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/017,575
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,227
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/198,119
;  PRIOR FILING DATE: 1998-11-2[illegible]
;  PRIOR APPLICATION NUMBER: PCT/US99/01895
;  PRIOR FILING DATE: 1999-01-2[illegible]
;  NUMBER OF SEQ ID NOS: 25[illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94
;   LENGTH: 349
;   TYPE: DNA
;   ORGANISM: Zea maize
US-09-996-140-94

  Query Match             [illegible].4%;  Score 47;  DB [illegible];  Length 349;
  Best Local Similarity   5[illegible].1%;  Pred. No. [illegible];
  Matches   [illegible]2;  Conservative    0;  Mismatches   7[illegible];  Indels    0;  Gaps    0;

Qy         [illegible] [illegible]
              [illegible]
Db        102 [illegible]GGCTGGGTGTGCGGAG 161

Qy         79 [illegible] 138
              [illegible]
Db        162 [illegible]CAACAAGAA[illegible] 22[illegible]

Qy        1[illegible] [illegible] 18[illegible]
              [illegible]
Db        22[illegible] [illegible] 26[illegible]


RESULT 8
US-09-954-456-292/c
; Sequence 292, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Y[illegible], [illegible]
;  TITLE OF INVENTION: Process for Identifying Anti Cancer Therapeutic Agents Using
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-7[illegible]
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/23[illegible],617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,[illegible]
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US/60/23[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US/60/23[illegible]
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/23[illegible]
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/23[illegible]
;  PRIOR FILING DATE: 2000-09-2[illegible]
;  PRIOR APPLICATION NUMBER: US/60/23[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US/60/23[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US/60/23[illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 22[illegible]
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 292
;   LENGTH: 4[illegible]58
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-292

  Query Match             [illegible];  Score [illegible];  DB 1[illegible];  Length [illegible];
  Best Local Similarity   5[illegible];  Pred. No. [illegible];
  Matches   [illegible];  Conservative    [illegible];  Mismatches   77;  Indels    0;  Gaps    [illegible];

Qy         18 [illegible]
              [illegible]
Db      25721 [illegible]

Qy         78 [illegible]
              [illegible]
Db      25661 [illegible]

Qy        138 [illegible] 18[illegible]
              [illegible]
Db      2[illegible] [illegible]


RESULT 9
US-09-954-456-529/c
; Sequence 529, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti Cancer Therapeutic Agents Using
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-7[illegible]
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/23[illegible],617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,[illegible]
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,[illegible]
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/23[illegible]
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/23[illegible]
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/23[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn version [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-[illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]


RESULT [illegible]
US-[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: [illegible] Expression [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. [illegible]
US-[illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]
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Qy [illegible]

Db [illegible]


RESULT [illegible]
US-[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]/121,[illegible]
;  PRIOR FILING DATE: [illegible]-12
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.[illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ([illegible])
;   OTHER INFORMATION: [illegible]
US-[illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]


RESULT [illegible]
US-[illegible]
; Sequence [illegible], Application US/[illegible]
; Publication No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible] M.
;  APPLICANT: [illegible]
;  APPLICANT: [illegible] W.
;  APPLICANT: [illegible] A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-[illegible]-48

  Query Match             [illegible].2%;  Score 44.4;  DB 9;  Length 2561;
  Best Local Similarity   55.9%;  Pred. No. 0.13;
  Matches  1[illegible]4;  Conservative    0;  Mismatches   81;  Indels    1;  Gaps    1;

Qy         11 [illegible] 70
Db        620 [illegible] 679

Qy         71 [illegible] 129
Db        680 [illegible] 739

Qy        130 [illegible] 189
Db        740 [illegible] 799

Qy        190 GGACGC 195
Db        800 [illegible] 805


RESULT [illegible]
US-10-023-529-48
; Sequence 48, Application US/10023529
; Patent No. US20020123888A1
; GENERAL INFORMATION:
;  APPLICANT: Leeb, Ann M.
;  APPLICANT: Leeb, Robert S.
;  APPLICANT: Law, Simon W.
;  APPLICANT: Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-040-1
;  CURRENT APPLICATION NUMBER: US/10/023,529
;  CURRENT FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: 09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-10-023-529-48

  Query Match             [illegible];  Score 44.4;  DB 12;  Length 2561;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
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Qy         11 [illegible] 70
Db        620 [illegible] 679

Qy         71 [illegible] 129
Db        680 [illegible] 739

Qy        130 [illegible] 189
Db        740 [illegible] 799

Qy        190 GGACGC 195
Db        800 [illegible] 805


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US-10-023-523-48
; Sequence 48, Application US/10023523
; Patent No. US20020152485A1
; GENERAL INFORMATION:
;  APPLICANT: Leeb, Ann M.
;  APPLICANT: Leeb, Robert S.
;  APPLICANT: Law, Simon W.
;  APPLICANT: Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-040-1
;  CURRENT APPLICATION NUMBER: US/10/023,523
;  CURRENT FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: US/09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-10-023-523-48

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  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  104;  Conservative    0;  Mismatches   81;  Indels    1;  Gaps    1;

Qy         11 [illegible] 70
Db        620 [illegible] 679

Qy         71 [illegible] 129
Db        680 [illegible] 739

Qy        130 [illegible] 189
Db        740 [illegible] 799
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[illegible]

[illegible]
  [illegible] Application [illegible]
  Patent No. [illegible]
  GENERAL INFORMATION:
  APPLICANT: [illegible] Andreas [illegible]
  TITLE OF INVENTION: [illegible]
  FILE REFERENCE: [illegible]
  CURRENT APPLICATION NUMBER: [illegible]
  CURRENT FILING DATE: [illegible]
  NUMBER OF SEQ ID NOS: [illegible]
  SOFTWARE: PatentIn version [illegible]
  SEQ ID NO [illegible]
   LENGTH: [illegible]
   TYPE: DNA
   ORGANISM: [illegible]
   FEATURE:
   NAME/KEY: [illegible]
   LOCATION: [illegible]
  [illegible]

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  [illegible] Pred. No. [illegible]
  Matches [illegible] Mismatches [illegible]

[illegible]

[illegible]
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                         GenCore version 5.1.[illegible]
               Copyright (c) 1993 - 2003 Compugen Ltd.

 OM nucleic - nucleic search, using sw model

Run on:          February 23, 2003, 15:06:38 ; Search time 3779 Seconds
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Perfect score:   1380
Sequence:        1 atgtccgcggctgatttcg.........atgaagcagtgacgactga 1380

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2954643 seqs, 14551412878 residues

Total number of hits satisfying chosen parameters:       41[illegible]

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 4:  gb_om:*
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                 7:  gb_ph:*
                 8:  gb_pl:*
                 9:  gb_pr:*
                 10:  gb_ro:*
                 11:  gb_sts:*
                 12:  gb_sy:*
                 13:  gb_un:*
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                 15:  em_ba:*
                 16:  em_fun:*
                 17:  em_hum:*
                 18:  em_in:*
                 19:  em_mu:*
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                 36:  em_htg_mam:*
                 37:  em_htg_vrt:*
                 38:  em_sy:*
                 39:  em_htgo_hum:*
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                 41:  em_htgo_other:*

    Pred. No. is the number of results predicted by chance to have a
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        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                   SUMMARIES
                     %
Result               Query
  No.     Score    Match Length DB  ID                           Description
-----     -----    ----- ------ --  ----------                   -----------
    1      1380    100.0   1380  6  AX352514                     AX352514 Sequence
    2      1369     99.2   1847  6  AX[illegible]                AX[illegible] Sequence
    3    1076.4     78.0   2[illegible]  9  AK096681             AK096681 Homo sapi
    4      1049     76.0   2[illegible]  9  HSM8[illegible]      AL[illegible] Homo sapi
    5    1014.4     73.5   2429  9  AK056894                     AK056894 Homo sapi
    6       783     56.7   182[illegible]  9  BC[illegible]14    BC[illegible]14 Homo sapi
    7     281.8     20.4   1[illegible]  9  AK09[illegible]      AK09[illegible] Homo sapi
    8     281.8     20.4   [illegible]  9  BC[illegible]         BC[illegible] Homo sapi
    9     264.8     19.2   2518  6  AX419[illegible]             AX419[illegible] Sequence
   10     264.8     19.2   2518  9  HSM8[illegible]              AL[illegible]44 Homo sapi
   11     264.4     19.2   [illegible]  6  AX419116              AX419116 Sequence
   12     262.6     19.0   [illegible]  6  AX1[illegible]        AX[illegible] Sequence
c  13     260.2     18.9   [illegible]  9  A[illegible]2        A[illegible]2 Homo sapi
c  14     260.2     18.9   [illegible]  9  A[illegible]15       A[illegible] Homo sapi
   15     260.2     18.9   214[illegible]  9  A[illegible]      A[illegible] Homo sapi
c  16     260.2     18.9   2[illegible]1  2  AC044892           AC044892 Homo sapi
   17     243.4     17.6   [illegible]1  6  AX[illegible]        AX[illegible] Sequence
   18     243.4     17.6   57[illegible]1  9  AB[illegible]     AB[illegible] Homo sapi
   19     242.4     17.6   [illegible]  9  AK[illegible]15       AK[illegible] Homo sapi
   20     167.4     12.1    652  9  HSA[illegible]               A[illegible] Homo sapi
   21     162.6     11.8    [illegible]  9  HSA[illegible]       A[illegible] Homo sapi
   22     159.4     11.6    852  9  HSA336051                    AJ336051 Homo sapi
   23       157     11.4    [illegible]  9  HSN[illegible]48     X8[illegible] H.sapiens
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   25     129.2      9.4    [illegible]  9  HSA[illegible]       A[illegible] Homo sapi
   26     101.2      7.3   2[illegible]  3  AY076531             AY076531 Drosophil
   27     101.2      7.3   [illegible]  2  A[illegible]1794[illegible]   A[illegible] Drosophil
c  28     101.2      7.3 144746  3  AC130649                     AC130649 Drosophil
   29     101.2      7.3 17[illegible]  3  AC104515              AC104515 Drosophil
c  30     101.2      7.3 206849  2  AC011760                     AC011760 Drosophil
c  31     101.2      7.3 274[illegible]  3  AE00[illegible]74   AE00[illegible]74 Drosophil
c  32      68.6      5.0 12502[illegible]  9  AF429315         AF429315 Homo sapi
   33      66.2      4.8 12[illegible]  9  AF429[illegible]15     AF429[illegible]15 Homo sapi
c  34      64.8      4.7 157[illegible]47  2  AC115403          AC115403 Rattus no
c  35      62.6      4.5  44[illegible]  3  AL[illegible]        AL[illegible] Drosophil
c  36      61.2      4.4 135733  2  AC128114                     AC128114 Rattus no
   37      58.6      4.2 [illegible]  2  AC129[illegible]4       AC129[illegible] Rattus no
c  38      58.2      4.2 120000  2  AC127088                     AC127088 Rattus no
   39      58.2      4.2  [illegible]  2  AC121[illegible]       AC121[illegible] Rattus no
c  40      58.2      4.2 208428  2  AC094216                     AC094216 Rattus no
   41      58.2      4.2 27[illegible]  2  AC[illegible]4[illegible]   AC[illegible] Rattus no
c  42        58      4.2 161287  2  AC106114                     AC106114 Rattus no
c  43        58      4.2 [illegible]  2  AC[illegible]         AC[illegible] Rattus no
c  44      57.8      4.2  5[illegible]  2  AC0[illegible]4     AC0[illegible] Rattus no
   45      57.8      4.2 2[illegible]  2  AC[illegible]         AC[illegible] Rattus no


                                  ALIGNMENTS


RESULT 1
AX352514
LOCUS       AX352514            1380 bp    DNA     linear   PAT [illegible]
DEFINITION  Sequence 3 from Patent WO0192490.
ACCESSION   AX352514
VERSION     AX352514.1  GI:[illegible]
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Plowman,G.D., Whyte,D., Sudarsanam,S., Manning,G., [illegible]
            Martinez,R., Ellis,R.J. and Flanagan,P.
  TITLE     Mammalian protein phosphatases
  JOURNAL   Patent: WO 0192490-A 3 06-DEC-2001;
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                    (US)
FEATURES             Location/Qualifiers
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                     /organism="synthetic construct"
                     /db_xref="[illegible]"
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BASE COUNT   [illegible]
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Db   1141 [illegible]

Qy   1201 [illegible]
Db   1201 [illegible]

Qy   1261 [illegible]
Db   1261 [illegible]

Qy   1321 [illegible]
Db   1321 [illegible]


RESULT 3
AX202284
LOCUS       AX[illegible]          [illegible] bp    DNA     linear   PAT [illegible]
DEFINITION  Sequence 13 from Patent WO[illegible].
ACCESSION   AX[illegible]
VERSION     AX202284.1  GI:[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1837)
  AUTHORS   Bandman,O., Tang,Y.T., Azimzai,Y., Yue,H., Baughn,M.R.,
            Hillman,J.L., Lal,P., Wang,D., Gandhi,A.R., Policky,J.L. and
            Mathur,P.
  TITLE     Phosphatases
  JOURNAL   Patent: WO [illegible]-A [illegible]
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1837
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /note="[illegible] ID NO: [illegible]"
BASE COUNT   [illegible] a   [illegible] c   [illegible] g   [illegible] t
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  Matches [illegible]  Conservative  [illegible]  Mismatches  [illegible]  Indels  [illegible]  Gaps  [illegible]

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Db        181 [illegible] 240

Qy        241 [illegible] 300
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Db        241 [illegible] 300

Qy        301 [illegible] 360
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Db        301 [illegible] 360

Qy        361 [illegible] 420
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Db        361 [illegible] 420

Qy        421 [illegible] 480
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Db        421 [illegible] 480

Qy        481 [illegible] 540
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Db        481 [illegible] 540

Qy        541 [illegible] 600
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Db        541 [illegible] 600

Qy        601 [illegible] 660
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Qy        661 [illegible] 720
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Db        661 [illegible] 720

Qy        721 [illegible] 780
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Db        721 [illegible] 780

Qy        781 [illegible] 840
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Db        781 [illegible] 840

Qy        841 [illegible] 900
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Db        841 [illegible] 900

Qy        901 [illegible] 960
              [illegible]
Db        901 [illegible] 960

Qy        961 [illegible] 1020
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Db        961 [illegible] 1020

Qy       1021 [illegible] 1080
              [illegible]
Db       1021 [illegible] 1080

Qy       1081 [illegible] 1140
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Db       1081 [illegible] 1140

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              [illegible]
Db       1141 [illegible] 1200

Qy       1201 [illegible] 1260
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Db       1201 [illegible] 1260

Qy       1261 [illegible] 1320
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Db       1261 [illegible] 1320

Qy       1321 [illegible] 1380
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Db       1321 [illegible] 1380

Qy       1381 A 1381
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Db       1381 A 1381


RESULT [illegible]
AK096681
LOCUS       AK096681               [illegible] bp    mRNA    linear   [illegible]
DEFINITION  Homo sapiens cDNA [illegible] fis, clone PEBLM2005282, [illegible]
            [illegible] (EC [illegible]).
ACCESSION   AK096681
VERSION     AK096681.1  GI:[illegible]
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens peripheral blood mononuclear cells (HPBMC[illegible]) cDNA to
            mRNA, clone_lib:PEBLM2 clone:PEBLM2005282.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   [illegible], Takahashi-Fujii,A., Tanase,T., [illegible], Takeuchi,K.,
            Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
            Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
            Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
            Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
            Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B.,
            Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and
            Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2121)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) Takao Isogai, [illegible] (HRI [illegible]);
            Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-[illegible], Fax:[illegible],
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
FEATURES             Location/Qualifiers
     source          1..2121
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="PEBLM2005282"
                     /cell_type="peripheral blood mononuclear cells
                     (HPBMC[illegible])"
                     /clone_lib="PEBLM2"
                     /note="cloning vector: pME18SFL3; primary culture
                     peripheral blood mononuclear cells"
     CDS             [illegible]
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="[illegible]"
                     /db_xref="GI:[illegible]"
                     /translation="[illegible]
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BASE COUNT      457 a   [illegible] c   [illegible] g   [illegible] t
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Qy     [illegible]
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Qy     [illegible]
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Qy     [illegible]
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Qy     [illegible]
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Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
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Qy     [illegible]
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Qy     [illegible]
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Qy     [illegible]

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Qy     1119 [illegible] 1178
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Qy     1179 [illegible] 1238
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Qy     1239 [illegible] 1298
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Qy     1299 [illegible] 1358
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Qy     1359 [illegible] 1380
Db     1319 [illegible] 1340


RESULT 4
[illegible]
LOCUS       [illegible]  2184 bp    mRNA    linear   [illegible]
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686N[illegible] (from clone DKFZp686N[illegible])
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2184)
  AUTHORS   [illegible] Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) [illegible] Heidelberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by DKFZ (German Cancer Research Center
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp686N[illegible]) is available at the [illegible]
            Please contact the RZPD: Ressourcenzentrum, [illegible]
            [illegible] GERMANY; Email: [illegible] Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="[illegible]"
                     /clone="DKFZp686N[illegible]"
                     /clone_lib="[illegible]"
                     /clone_lib="[illegible] (synonym: [illegible]). Vector [illegible]
                     [illegible]"
                     /dev_stage="adult"
     polyA_signal    [illegible]
     polyA_site      [illegible]
BASE COUNT    [illegible]
ORIGIN

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  Best Local Similarity   [illegible]  Pred. No. [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
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Qy        345 CCTGACAGGCCATTACTGGGCACTGTTCGATGGGCAGGGCGTCCTGCAGCAGCCATCTT 404
              [illegible]
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Qy        405 [illegible] 464

Db        248 [illegible] 307

Qy        465 [illegible] 524

Db        308 [illegible] 367

Qy        525 GTTTGTGGAGGAAAAGGGCATCAGGGCAGAAGACTTGGTGATTGGGGATTTGACAGTGC 584

Db        368 [illegible] 427

Qy        585 [illegible] 644

Db        428 CTTTCAGGAATGTGATGAGGTGATGGGCGGAGCTGGAGGCTCAGGCAGATGCCCC 487

Qy        645 [illegible] 704

Db        488 [illegible] 547

Qy        705 [illegible] 764

Db        548 [illegible] 607

Qy        765 AGAGACTGAGGGGCAGCGGATCCAGCAGCT------------------------------ 794

Db        608 [illegible] 667

Qy        795 ------------------------------------------------------------ 794

Db        668 [illegible] 727

Qy        795 -------GGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCC 847

Db        728 CAGCCCAGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCC 787

Qy        848 [illegible] 907

Db        788 [illegible] 847

Qy        908 [illegible] 967

Db        848 [illegible] 907

Qy        968 [illegible] 1027

Db        908 [illegible] 967

Qy       1028 [illegible] 1087

Db        968 [illegible] 1027

Qy       1088 [illegible] 1147

Db       1028 [illegible] 1087

Qy       1148 [illegible] 1207

Db       1088 [illegible] 1147

Qy       1208 [illegible] 1267

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Qy       1268 [illegible] 1327

Db       1208 [illegible] 1267

Qy       1328 [illegible]

Db       1268 [illegible]


RESULT 5
AK056804
LOCUS       AK056804                2412 bp    mRNA    linear   [illegible]
DEFINITION  Homo sapiens cDNA FLJ32242 fis, clone PROST2005121, weakly similar
            to PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16).
ACCESSION   AK056804
VERSION     AK056804.1  GI:16552415
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens prostate cDNA to mRNA, clone_lib:PROST2
            clone:PROST2005121.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ishibashi,T., Kanehori,K., Yoshida,M., Watanabe,S., Ishihara,S.,
            Ono,Y., Hotta,I., Hiraoka,S., Murakawa,K., Takiguchi,S.,
            Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
            Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
            Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
            Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y.,
            Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A.,
            Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2412)
  AUTHORS   Isogai,T., Otsuki,T. and Sugiyama,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: RAB and
            HRI.
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                     /db_xref="taxon:9606"
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                     /tissue_type="prostate"
                     /clone_lib="PROST2"
                     /note="cloning vector: pME18SFL3"
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  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy        22[illegible] [illegible]

Db        14[illegible] [illegible]
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[illegible]

LOCUS       [illegible]                    mRNA    [illegible]
DEFINITION  [illegible] MGC:[illegible] IMAGE:[illegible], mRNA, [illegible]
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    MGC.
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SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible] JUN 2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD [illegible],
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium ([illegible])
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA [illegible]
            Web site: http://[illegible].stanford.edu
            Contact: (Dickson, Mark) [illegible]
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://[illegible]
            Series: IRAK Plate: 11 Row: [illegible] Column: [illegible].
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="MGC:[illegible] IMAGE:[illegible]"
                     /tissue_type="Uterus, leiomyosarcoma"
                     /clone_lib="NIH_MGC_[illegible]"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
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                     /product="Unknown (protein for MGC:17869)"
                     /protein_id="[illegible]"
                     /db_xref="GI:[illegible]"
                     /translation="[illegible]
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                     [illegible]
                     [illegible]VVVMA[illegible]
                     [illegible]VSYDBVSVFVIPLHSQGQFSSDR"
BASE COUNT   [illegible]
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

[illegible]
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Db       [illegible] 584

Qy    958 [illegible] 1017
Db    585 [illegible] 644

Qy   1018 [illegible]
Db    645 GGAGACCATCAGCTCAGA[illegible]

Qy   1078 [illegible] 1137
Db    705 [illegible] 764

Qy   1138 [illegible] 1197
Db    765 [illegible]

Qy   1198 [illegible] 1257
Db    825 [illegible]

Qy   1258 [illegible]
Db    885 [illegible]

Qy   1318 [illegible]
Db    945 [illegible]

Qy   1378 TGA 1380
Db   1005 TGA 1007

RESULT 7
AK[illegible]
LOCUS       AK[illegible]          1687 bp    mRNA    linear   PRI 15-JUL-2002
DEFINITION  Homo sapiens cDNA FLJ[illegible] fis, clone TESTI2012104, weakly similar
            to PROBABLE PROTEIN PHOSPHATASE 2C [illegible] (EC 3.1.[illegible]).
ACCESSION   AK[illegible]
VERSION     AK093270.1  GI:21752092
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens testis cDNA to mRNA, clone_lib:TESTI2
            clone:TESTI2012104.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.,
            [illegible]
            Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
            Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
            Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
            Saito,K. [illegible]
            Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A.,
            Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1687)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
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  Best Local Similarity   54.[illegible]%;  Pred. No. [illegible];
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Db    [illegible]

Qy    494 [illegible]
Db    611 [illegible]

Qy    535 [illegible]
Db    [illegible]

Qy    [illegible]
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Qy    772 [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]
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[illegible]

RESULT [illegible]
[illegible]
LOCUS       [illegible]     [illegible] bp    mRNA    linear   PRI [illegible]
DEFINITION  Homo sapiens, Similar to RIKEN cDNA [illegible], clone
            MGC:[illegible] IMAGE:[illegible], mRNA, complete cds.
ACCESSION   [illegible]
VERSION     [illegible]  GI:[illegible]
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD [illegible]
            USA
  REMARK    NIH-MGC Project URL: http://mgc.[illegible]
COMMENT     Contact: MGC help desk
            Email: [illegible]
            Tissue Procurement: [illegible]
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://[illegible]/
            Contact: [illegible]
            [illegible], Wetherby,K.D., [illegible]
            [illegible], Blakesley,R.W., Bouffard,G.G., Brinkley,[illegible]
            [illegible]
            [illegible], Maduro,[illegible], Maskeri,[illegible], Mullikin,[illegible]
            [illegible]
            [illegible], Touchman,J.W., [illegible], Vogt,[illegible], Walker,M.A.,
            Zhang,[illegible] and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://[illegible]
            Series: IRAL Plate: 2[illegible] Row: [illegible] Column: [illegible]
            This clone was selected for full length sequencing because it
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                     [illegible]
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  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

[illegible]
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Db      924 [illegible] 983
Qy      892 [illegible]
Db      984 [illegible]
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Db     1104 [illegible]
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Qy     1132 [illegible]
Db     1224 [illegible]
Qy     1192 [illegible]
Db     1284 [illegible]
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Qy     1357 [illegible]
Db     1464 [illegible]

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LOCUS       AX419118                2518 bp    DNA     linear   PAT [illegible]
DEFINITION  Sequence 3 from Patent WO0218565.
ACCESSION   AX419118
VERSION     AX419118.1  [illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human protein phosphatase [illegible]-like enzyme
  JOURNAL   Patent: WO 0218565-A 3 07-MAR-2002;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
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                     /protein_id="CAD[illegible].1"
                     /db_xref="[illegible]"
                     /translation="MASEL[illegible]LKDLKEVSLESLVVGATENA[illegible]MAKE
                     [illegible]
                     [illegible]
                     [illegible]
                     [illegible]
                     NK[illegible]PVEVIP[illegible]SYS"
BASE COUNT      597 a    768 c    75[illegible] g    484 t
ORIGIN

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Qy      447 [illegible]
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Db [illegible]

RESULT [illegible]
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DEFINITION  Homo sapiens mRNA; cDNA DKFZp[illegible] (from clone DKFZp[illegible]);
            partial cds.
ACCESSION   AL[illegible]
VERSION     AL[illegible]  GI:[illegible]
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) MIPS, Am Klopferspitz [illegible],
            Martinsried, GERMANY
COMMENT     [illegible] Wiemann, Molecular [illegible] Analysis, German Cancer
            Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
            sequenced by BMFZ (biomedical Research Center at the Charite,
            Berlin/Germany) within the cDNA sequencing consortium of the German
            Genome Project.
            This clone (DKFZp[illegible]) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, [illegible]
            Berlin, Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://[illegible]/cDNA/.
FEATURES             Location/Qualifiers
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                     and [illegible] NotI [illegible]"
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     gene            [illegible]
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ORIGIN

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[illegible]
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DEFINITION  Sequence [illegible] from Patent WO[illegible].
ACCESSION   AX[illegible]
VERSION     AX[illegible]  GI:[illegible]
KEYWORDS    .
SOURCE      human.
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human protein phosphatase [illegible] like enzyme
  JOURNAL   Patent: WO [illegible] A 1 07-MAR-2002;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
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Qy        883 [illegible]
Db        [illegible]

Qy        943 [illegible]
Db        [illegible]

Qy       1003 [illegible]
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Qy       [illegible]
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Qy       1240 [illegible]
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Qy       [illegible]

Db        817 [illegible]

Qy       1348 CACAGCAGG[illegible]
Db        877 [illegible]


RESULT 12
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LOCUS       AX400071          [illegible] bp    DNA     linear   PAT [illegible]
DEFINITION  Sequence 24 from Patent WO [illegible]
ACCESSION   AX400071
VERSION     AX400071.1  GI:[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   [illegible]
  TITLE     Nucleic acids and polypeptides
  JOURNAL   Patent: WO [illegible]-A 24 07-MAR-2002;
            HYSEQ, INC. (US)
FEATURES             Location/Qualifiers
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                     /db_xref "taxon:9606"
     CDS             182..[illegible]
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                     /db_xref "GI:[illegible]"
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ORIGIN

  Query Match             [illegible];  Score [illegible];  DB 6;  Length [illegible];
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  Matches  [illegible];  Conservative    [illegible];  Mismatches  [illegible];  Indels   [illegible];  Gaps    [illegible];

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
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Qy        [illegible]
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[illegible]

[illegible]
[illegible]
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DEFINITION  Homo sapiens [illegible] BAC [illegible] (Baylor [illegible]
            [illegible] BAC Library) complete sequence.
ACCESSION   A[illegible]
VERSION     A[illegible]
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   M[illegible], Adenuga,A.[illegible], Bouck,J., [illegible], Chen,[illegible], Chen,Z.,
            Culpepper,P., [illegible], [illegible], [illegible], [illegible],
            [illegible], [illegible], Garcia,D.K., Gorrell,H., Gorrell,J.H.,
            He,X., Hernandez,[illegible], [illegible], Kowalewski,N., [illegible],
            Lichtarge,[illegible], Liu,W., [illegible], Lu,[illegible], Martinez,[illegible], Moore,S.,
            Morris,[illegible], Nguyen,N., [illegible], Pampel,[illegible], Parish,[illegible],
            Perez,[illegible]M., Rashid,N.[illegible], Rives,[illegible]M., Scherer,S.E., Shen,H.,
            Simon,M.[illegible], V[illegible], Wei,Y., Williamson,A.[illegible], Worley,K., Zhou,X.,
            Muzny,D.[illegible] and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to [illegible])
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) [illegible], Molecular and Human Genetics, Baylor
            College of Medicine, [illegible] Houston, TX [illegible], USA
REFERENCE   3  (bases 1 to [illegible])
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, [illegible]
            [illegible] Houston, TX [illegible], USA
COMMENT     [illegible] sequence [illegible] replaced [illegible]
            INFORMATION: http://[illegible]/ [illegible] email
            [illegible]

            [illegible] SEQUENCE [illegible] does not necessarily represent the
            entire [illegible] overlapping [illegible] are
            [illegible] and submitted [illegible] the sequence for the remainder of
            the [illegible] in the record for the [illegible]
            [illegible] clones are noted at the beginning and end of the
            features listing.

            ANNOTATION [illegible]:
              STSs are identified using e-PCR (Genome Res. [illegible]) against
            [illegible] database that includes entries from dbSTS, [illegible], and
            local mapping efforts.
              Repeats are identified using RepeatMasker (A. Smit and P. Green,
            unpublished) for Human and Mouse sequences.
              Genes and Region of sequence similarity are identified by BLAST
            (Nuc. Acids Res. [illegible]) similarity (expect [illegible]) to the
            EST and cDNA sequences. [illegible] at least [illegible]
            flanked by consensus splice sites that maintained sequence
            continuity across the splice junctions. Sequences that are [illegible]
            identical matches are annotated as similar.

            SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
            standard [illegible] double strand coverage with a minimum of [illegible] and 2
            reads with no ambiguities or 2 chemistries with a minimum of 2
            clones and [illegible] reads with no ambiguities. If the sequence quality for
            a region does not meet this standard, it will be indicated in the
            [illegible] low coverage.

            QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
            standards [illegible] estimated error rate less than 1 per [illegible] bases.
            Reports of lowest quality individual bases and measures of base
            quality are listed below. Description of the metrics can be found
            at URL: http://[illegible]/quality.[illegible]/genbank.[illegible]
            html.

            [illegible]

                          Summary Statistics
            Contig length:                                   [illegible]
            Phrap [illegible]:                               [illegible]
            Average error rate (RMS Phrap estimate):         [illegible]
            Fraction of Phrap values less than 10:           [illegible]
            Number of consensus changing edits:              [illegible]
            Number of N's in consensus:                      [illegible]

                          Consensus changing edits
            Position      Original context           Edited context
            [illegible]   [illegible]agtage(n)tgcattccag  tccagcgtage(c)tgcattc[illegible]
            [illegible]   [illegible]tatttaa(n)aaaaatata  [illegible]tttatttaa(a)[illegible]
            [illegible]148  attaaaaaaa(n)atacatttttt  attaaaaaaa(a)atacattttt
            4[illegible]  atacatatat aa(n)aaaatatata  atacatataa(a)[illegible]
            47[illegible]  ttttatattt(n)atataaatata  ttttatattt(a)at[illegible]
            [illegible]   [illegible]gg(n)[illegible]  [illegible]gg(t)[illegible]

                  Distribution of quality [illegible] Bases

             [illegible]                                     *
             [illegible]                                     *
             [illegible]                                     *
             #  [illegible]                                  *
             Bases                                       *   *
                                                         *   *
                                                         *   *
                                                         *   *
                                                     *   *   *
                                         *   *   *   *   *   *
                         *   *   *   *   *   *   *   *   *   *
                    [illegible]
                              Phrap Value Range

            Version: [illegible]
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                     /note="Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
                     Eutheria; Primates; Catarrhini; Hominidae; Homo."
     repeat_region   1..[illegible]
                     /rpt_family="Alu"
     repeat_region   78..[illegible]
                     /rpt_family="AluSx"
     gene            complement(join(588..1542,[illegible],2124..[illegible],
                     2487..2550,2734..2853))
                     /note="Unigene cluster containing AI378477, [illegible],
                     AA22[illegible], [illegible], AA72888[illegible], [illegible], and AA292266."
     STS             647..785
                     /standard_name="[illegible]"
                     /db_xref="GDB:[illegible]6425"
     STS             [illegible]5..86[illegible]
                     /standard_name="[illegible]"
                     /db_xref="dbSTS:[illegible]27[illegible]"
     misc_feature    5021..[illegible]289
                     /note="Region: Similar to H.sapiens genomic DNA, X8[illegible]."
     repeat_region   5178..[illegible]
                     /rpt_family="GC_rich"
     repeat_region   529[illegible]..55[illegible]
                     /rpt_family="GC_rich"
     misc_feature    [illegible]..[illegible]
                     /note="Region: Similar to H.sapiens genomic DNA, X87528."
     repeat_region   [illegible]19..6602
                     /rpt_family="AluSx"
     repeat_region   complement(7672..7745)
                     /rpt_family="L1M4"
     repeat_region   complement(7747..7[illegible]2[illegible])
                     /rpt_family="AluSp"
     repeat_region   8106..817[illegible]
                     /rpt_family="MER4A2"
     repeat_region   complement(8207..849[illegible])
                     /rpt_family="AluSx"
     repeat_region   complement(8542..859[illegible])
                     /rpt_family="AluSp"
     repeat_region   9144..9289
                     /rpt_family="MER4[illegible]"
     repeat_region   complement(942[illegible]..9582)
                     /rpt_family="FRAM"
     repeat_region   complement(9586..9631)
                     /rpt_family="(TAGA)n"
     repeat_region   complement(96[illegible]..9894)
                     /rpt_family="AluJo"
     repeat_region   [illegible]935..10052
                     /rpt_family="MIR"
     repeat_region   complement(1[illegible]124..[illegible]026[illegible])
                     /rpt_family="L2"
     repeat_region   11050..11126
                     /rpt_family="L2"
     repeat_region   11143..11426
                     /rpt_family="AluSp"
     repeat_region   11960..1205[illegible]
                     /rpt_family="GC_rich"
     gene            join(12104..12195,1608[illegible]..[illegible],[illegible]..[illegible],[illegible]..[illegible],
                     [illegible]92..[illegible]17,21117..212[illegible]7,21405..21[illegible]2[illegible],21986..22[illegible]75)
                     /note="Unigene cluster containing AI[illegible], AA[illegible],
                     W[illegible]722, T[illegible]4[illegible]1, AA[illegible]08[illegible], R[illegible], and AA[illegible]812[illegible]."
     repeat_region   complement(14187..14295)
                     /rpt_family="MIR"
     repeat_region   complement(14866..15168)
                     /rpt_family="AluSq"
     repeat_region   complement(15624..15725)
                     /rpt_family="(CA)n"
     repeat_region   complement(1725[illegible]..1754[illegible])
                     /rpt_family="AluY"
     repeat_region   complement(1816[illegible]..1845[illegible])
                     /rpt_family="AluSp"
     STS             [illegible]
                     /standard_name="G[illegible]2122"
                     /db_xref="[illegible]"
     STS             22320..2249[illegible]
                     /standard_name="[illegible]"
                     /db_xref="GDB:[illegible]"
     repeat_region   complement(228[illegible]..2[illegible]2[illegible])
                     /rpt_family="M[illegible]"
     repeat_region   complement(24[illegible]..24822)
                     /rpt_family="L2"
     repeat_region   complement(25824..26124)
                     /rpt_family="AluSp"
     repeat_region   complement(30769..30824)
                     /rpt_family="([illegible])n"

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible]41;
  Matches  2[illegible];  Conservative    [illegible];  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy        [illegible]4 [illegible]
              [illegible]
Db       4212 [illegible]

Qy        [illegible]4 [illegible]
              [illegible]
Db       41[illegible]2 [illegible]

Qy        4[illegible]4 GTGGAA[illegible]
              [illegible]
Db       4102 GTGGAA[illegible]

Qy        5[illegible]4 AG[illegible]
              [illegible]
Db       4[illegible]12 A[illegible]

Qy        5[illegible]4 TTGGAGA[illegible] 5[illegible]
              ||||||||||||||||||||||||
Db       [illegible]932 TTGGAGA[illegible]


RESULT 14
AC092045/c
LOCUS       AC[illegible]      [illegible] bp    DNA     linear   [illegible]
DEFINITION  Homo sapiens chromosome [illegible] clone RP11-168J18, complete sequence.
ACCESSION   AC[illegible]
VERSION     AC092045.2  GI:1[illegible]281[illegible]
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171343)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C. and
            Hansen,E.D.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 171343)
  AUTHORS   Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,[illegible] and
            Hansen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]-JUN-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 171343)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C. and
            Hansen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (2[illegible]-[illegible]-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
COMMENT     On Aug [illegible], 2001 this sequence version replaced gi:[illegible].
              [illegible] Genome Center
                Center: University of Washington Genome Center
                Center code: UWGC
                Web site: http://www.genome.washington.edu
```

```
Contact: [illegible]
[illegible] Center [illegible]
                Project Information
Center project name: [illegible]
Center clone name: RP11-[illegible] ([illegible])
                Summary Statistics
Sequencing vector: M13; [illegible] reads
Sequencing vector: plasmid; [illegible] reads
Chemistry: Dye-terminator [illegible] reads
Chemistry: Dye-primer Bodipy; [illegible] reads
Chemistry: Dye-terminator Big Dye; [illegible] reads
Assembly program: Phrap; version [illegible]
Consensus quality: [illegible] bases at least Q[illegible]
Consensus quality: [illegible] bases at least Q[illegible]
Consensus quality: [illegible] bases at least Q[illegible]
Insert size: [illegible]
Insert size: [illegible]
Quality coverage: [illegible]
Quality coverage: [illegible]

[illegible]
[illegible] RP11-[illegible] (HWS[illegible]) A[illegible]
[illegible] RP11-[illegible] (HWS[illegible]) A[illegible]

Sequence Quality Assessment:
 This entry has been manually edited with sequence quality
 estimates adapted to the Phrap assembly program.
 All manually edited bases have been reset to quality [illegible]
 [illegible] are expected to have less than
 [illegible]
 Base by base quality values are not generally available from the
 Genbank [illegible] but are available as part
 of this entry's ASN.1 file.

This sequence was finished [illegible]
[illegible] were either double stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., phred
quality [illegible]); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13
subclone; and the assembly was confirmed by [illegible]

Sequence Validation:
 This sequence has been validated by Multiple Complete Digest
 [illegible] of the experimentally derived [illegible]
 fragments with sequence predicted fragments is given below.
 [illegible] and
 vector, in order to accurately represent the entire circular BAC.
 Small fragments [illegible] (approximately [illegible]),
 are not resolved in the fingerprint and hence do not appear
 in the table. [illegible]
 between the experimental and predicted values. [illegible]
 fragments are separated by [illegible]
        BamHI                EcoRI               HindIII

SeqMap  Fragment      SeqMap  Fragment      SeqMap  Fragment

[illegible]
```

```
[illegible]

FEATURES             Location/Qualifiers
```

```
  source          1..171343
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /chromosome="3"
                  /clone="RP11-168J18"
                  /clone_lib="RPCI human BAC library 11"
BASE COUNT     39241 a  46165 c  45178 g  40769 t
ORIGIN

  Query Match            16.9%;  Score [illegible];  DB [illegible];  Length 171343;
  Best Local Similarity   98.9%;  Pred. No. 1.2e-41;
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy        334 [illegible] 393
              [illegible]
Db     165894 [illegible] 165835

Qy        394 [illegible] 453
              [illegible]
Db     165834 [illegible] 165775

Qy        454 [illegible] 513
              [illegible]
Db     165774 [illegible] 165715

Qy        514 [illegible] 573
              [illegible]
Db     165714 [illegible] 165655

Qy        574 TTGGATAGTGCTTTTCAGGAATGTG 598
              |||||||||||||||||||||||||
Db     165654 TTGGATAGTGCTTTTCAGGAATGTG 165630


RESULT 15
AC094021
LOCUS       AC094021               214160 bp    DNA     linear   HTG 27-MAR-2002
DEFINITION  Homo sapiens chromosome 3 clone RP11-80I18, complete sequence.
ACCESSION   AC094021 AC069253
VERSION     AC094021.2  GI:19745081
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Raymond,C., Saenphimmachak,C. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-2002) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
COMMENT     On Mar 27, 2002 this sequence version replaced gi:[illegible].
            ------------ Genome Center
                Center: University of Washington Genome Center
                Center Code: UWGC
                Web site: http://www.genome.washington.edu
                Contact: [illegible]@u.washington.edu
                Drafting Center: BCM
            ------------ Project Information
                Center project name: chr3
                Center clone name: RP11-80I18 (tc[illegible])
            ------------ Summary Statistics
                Sequencing vector: M13; L08752; 49% of reads
                Sequencing vector: plasmid; 51% of reads
                Chemistry: Dye-terminator [illegible]; [illegible]% of reads
                Chemistry: Dye-primer Bodipy; 11% of reads
                Chemistry: Dye-terminator Big Dye; [illegible]% of reads
                Assembly program: Phrap; version [illegible]
                Consensus quality: [illegible] bases at least Q[illegible]
                Consensus quality: [illegible] bases at least Q[illegible]
                Consensus quality: [illegible] bases at least Q[illegible]
                Insert size: 214160; sum of contigs
                Quality coverage: [illegible]x in Q[illegible] bases; sum of contigs
            ------------
            Overlapping Sequences:
                5': Mapping in progress
                3': RP11-[illegible] ([illegible]) AC0[illegible]
            ------------
            Sequence Quality Assessment:
             This entry has been annotated with sequence quality
             estimates computed by the Phrap assembly program.
             All manually edited bases have been reduced to quality zero.
             Quality levels above 40 are expected to have less than
             1 error in 10,000 bp.
             Base-by-base quality values are not generally visible in the
             GenBank flat file format but are available as part
             of this entry's ASN.1 file.

            This sequence was finished as follows unless otherwise noted:
            all regions were either double stranded or sequenced with an
            alternate chemistry or covered by high quality data (i.e., Phred
            quality >  30); an attempt was made to resolve all sequencing
            problems, such as compressions and repeats; all regions were
            covered by at least one plasmid subclone or more than one M13
            subclone; and the assembly was confirmed by restriction digest.
            ------------
            Sequence Validation:
             This sequence has been validated by Multiple Complete Digest
             Fingerprinting. Comparison of the experimentally derived digest
             fragments with sequence-predicted fragments is given below.
             The electronically digested sequence consists of both insert and
             vector, in order to accurately represent the entire original BAC.
             Small fragments below a variable cutoff (approximately [illegible])
             are not resolved in the fingerprint and hence don't appear
             in the table. There are no significant remaining discrepancies
             between the experimental and predicted values. Closely spaced
             fragments are separated by dashed lines.
                  BglII                   EcoRI                   HindIII
            ------------------------------------------------------------------------
            SeqDetMap  FingPrint    SeqDetMap  FingPrint    SeqDetMap  FingPrint
            ------------------------------------------------------------------------

                 [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ------
                 [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ------
                 [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ------
                 [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ------
                 [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ------
                 [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ------
                 [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ------
                 [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ------
                 [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ------
                 [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ------
                 [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ------
                 [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
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[illegible] "[illegible] human [illegible] library [illegible]"
BASE COUNT [illegible]
ORIGIN

  Query Match [illegible]  Length [illegible]
  Best Local Similarity [illegible]  Pred. No. [illegible]
  Matches [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    451 [illegible]
Db    [illegible]

Qy    514 [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Search completed: [illegible]
Job time : [illegible]
```

```
                     GenCore version 5.1.x
            Copyright (c) 1993 - 2003 Compugen Ltd.

 OM nucleic - nucleic search, using sw model

Run on:          February 2x, 2003, 11:39:22 ; Search time xx Seconds
                                              (without alignments)
                                              9742.187 Million cell updates/sec

Title:           US-09-866-987-3
Perfect score:   1380
Sequence:        1 atatcccgccaactgattcca..........aaaaaaaatgaccactaa 1380

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2185xx5 seqs, 112x9x159 residues

Total number of hits satisfying chosen parameters:      43x478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :        N_Geneseq_101002:*
                 1:  [illegible]*
                 2:  [illegible]*
                 3:  [illegible]*
                 4:  [illegible]*
                 5:  [illegible]*
                 6:  [illegible]*
                 7:  [illegible]*
                 8:  [illegible]*
                 9:  [illegible]*
                 10:  [illegible]*
                 11:  [illegible]*
                 12:  [illegible]*
                 13:  [illegible]*
                 14:  [illegible]*
                 15:  [illegible]*
                 16:  [illegible]*
                 17:  [illegible]*
                 18:  [illegible]*
                 19:  [illegible]*
                 20:  [illegible]*
                 21:  [illegible]*
                 22:  [illegible]*
                 23:  [illegible]*
                 24:  [illegible]*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES

                     %
Result               Query
  No.    Score    Match Length DB  ID                          Description
------------------------------------------------------------------------------
   1     1369     99.2    1837  22  AAH22961                   Human phosphatase
   2      917     66.4     917  24  ABA94426                   Human protein phos
   3      546     38.8     547  24  ABL79990                   Human ovarian can
   4      264.8   19.2    2518  24  ABK47452                   DNA encoding huma
   5      262.4   19.0    4262  17  AAI38484                   Rat petrin cDNA cl
   6      262.4   19.0    4515  17  AAI38486                   Rat petrin cDNA.
   7      243.4   17.6    1617  23  AAS93649                   DNA encoding a no
   8      243.4   17.6    1887  22  AAI58166                   Human polynucleoti
   9      243.4   17.6    5791  24  ABK46163                   cDNA encoding No.
  10      242.4   17.6    1xxx  22  AAH1xxxx                   Human cDNA sequenc
  11      x78     1x.x    x7x   17  AAIxx4x2                   Rat petrin cDNA cl
  12      105.2    7.9    72x   21  AAA02311                   Human colon cancer
  13      103      7.5    x0x   2x  AAZ12811                   Human gene express
  14      102.8    7.4    xxx   2x  AAXxxx54                   Human validated ex
  15      101.2    7.3    2087  23  ABL25549                   Drosophila melanog
  16      101.2    7.3    x2x7  2x  ABL25548                   Drosophila melanog
  17       98      7.1    55x   21  ABL82492                   Human ovarian canc
  18       9x      x.x    xxx   2x  AAX9x4x2                   Human tumour x.x
  19       87.x    x.x    xx4   21  AAAx18xx                   Human colon cancer
  20       8x.x    x.1    xx4   21  AAA00279                   Human colon cancer
  21       81.2    x.x    x2xx  2x  ABV22xxx                   Human prostate exp
  22       81.2    x.x    12xx  2x  ABV2x1xx                   Human prostate exp
  23       81.2    x.x    225x  2x  ABV27918                   Human prostate exp
  24       81.2    x.x    12xx  2x  ABV2xxxx                   Human prostate exp
  25       81.2    x.x    12xx  23  ABV28039                   Human prostate exp
c 26       76.8    5.6    xx2   22  AAHxxxxx                   Human cDNA xxxxx (
  27       6x      4.x    xxx   17  AAIxx48x                   Rat petrin cDNA cl
  28       50.4    3.7    164x  22  AAS0x0xx                   Angiotensin conver
c 29       49.8    3.6    x7xx  21  AAZ45xxx                   Nucleotide sequenc
c 30       49.8    3.6    x92x  21  AAZ45931                   Nucleotide sequenc
c 31       49.8    3.6    x924  21  AAZ45935                   Nucleotide sequenc
c 32       49.4    3.6    2xxx  2x  AAK7x4xx                   Human immune/haema
  33       49.2    3.6    7x0   22  AAI59952                   Human polynucleoti
c 34       49      3.6    xxx   24  ABK4745x                   Protein phosphatas
c 35       48.8    3.5    xxx7  24  ABQ6845x                   Listeria mono prot
c 36       48.2    3.5    14x1  20  AAX15147                   Nucleotide sequenc
c 37       48.2    3.5    28x7  24  AADxxxxx                   Human Sxxxx cDNA.
c 38       48      3.5    95x   24  ABQ37014                   Oligonucleotide to
  39       48      3.5    95x   24  ABQ37015                   Oligonucleotide to
  40       47.x    3.x    x7x7  22  AAxx12xx                   HSV 2 E xxxx, 1xx
  41       47.x    3.x    2xxx  22  AAK7x41x                   Human immune/haema
  42       47      3.x    xxx   2x  AAAx2x04                   A. baya xxx xxxx
  43       4x.x    3.x    1xxx  21  ABNx74xx                   Seq #xxx used to
c 44       46.8    3.4    1xx43 24  ABL61982                   Lung cancer relate
  45       4x.x    3.x    xxxx  2x  ABLx5215                   Lung cancer relate

                              ALIGNMENTS

RESULT 1
AAH22961
ID   AAH22961 standard; cDNA; 1837 BP.
XX
AC   AAH22961;
XX
DT   17-SEP-2001  (first entry)
XX
DE   Human phosphatase (PP) encoding cDNA (clone ID 1724117CB1).
XX
KW   Phosphatase; PP; Alzheimer's disease; Huntington's disease; human
KW   immune disorder; cancer; [illegible]; anti-inflammatory; cytostatic;
KW   neuroprotective; anticonvulsant; ss.
XX
OS   Homo sapiens.
XX
FH   Key                 Location/Qualifiers
FT   CDS                 1..1xxx
FT                       /*tag=  a
FT                       /product= "phosphatase"
XX
PN   WO200153xx6-A2.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US01x88.
XX
PR   21-JAN-2000; 2000US-0177x19.
PR   28-JAN-2000; 2000US-178xxx.
PR   25-FEB-2000; 2000US-184956.
PR   17-MAR-2000; 2000US-190142.
XX
```

```
PA   [illegible] INCYTE GENOMICS INC.
XX
PI   [illegible] Hillman JL;
PI   [illegible]
XX
DR   WPI; [illegible]/[illegible].
DR   P-PSDB; AAB[illegible].
XX
PT   Novel phosphatases useful for treating diseases associated with
PT   decreased expression of functional phosphatases, e.g., Alzheimer's
PT   disease, Huntington's disease, immune disorders, and cancers -
XX
PS   Claim [illegible]; Page [illegible]; [illegible]pp; English.
XX
CC   The invention provides human phosphatases (PP) and polynucleotides
CC   encoding the phosphatases. The polypeptides can be expressed by standard
CC   recombinant methodology. The PP are useful for treating a disease or
CC   condition associated with decreased expression of functional
CC   phosphatases. Compositions containing an antagonist of PP may
CC   be used to treat a disease associated with decreased expression or
CC   overexpression of PP respectively. Such diseases may include
CC   Alzheimer's disease, Huntington's disease, immune disorders and
CC   cancers. The present sequence represents a human phosphatase encoding
CC   cDNA.
XX
SQ   [illegible]

  Query Match              [illegible]
  Best Local Similarity    [illegible]
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy          1 [illegible]
Db          1 [illegible]

Qy         61 [illegible]
Db         61 [illegible]

Qy        121 [illegible]
Db        121 [illegible]

Qy        181 [illegible]
Db        181 [illegible]

Qy        241 [illegible]
Db        241 [illegible]

Qy        301 [illegible]
Db        301 [illegible]

Qy        361 [illegible]
Db        361 [illegible]

Qy        421 [illegible]
Db        421 [illegible]

Qy        481 [illegible]
Db        481 [illegible]

Qy        541 [illegible]
Db        541 [illegible]

Qy        601 [illegible]
Db        601 [illegible]

Qy        661 [illegible]
Db        661 [illegible]

Qy        721 [illegible]
Db        721 [illegible]

Qy        781 [illegible]
Db        781 [illegible]

Qy        841 [illegible]
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Qy        901 [illegible]
Db        901 [illegible]

Qy        961 [illegible]
Db        961 [illegible]

Qy       1021 [illegible]
Db       1021 [illegible]

Qy       1081 [illegible]
Db       1081 [illegible]

Qy       1141 [illegible]
Db       1141 [illegible]

Qy       1201 [illegible]
Db       1201 [illegible]

Qy       1261 [illegible]
Db       1261 [illegible]

Qy       1321 [illegible]
Db       1321 [illegible]

Qy       1381 A 1381
              |
Db       1381 A 1381


RESULT [illegible]
ABA944[illegible]
ID   ABA944[illegible] standard; cDNA; [illegible] BP.
XX
AC   ABA944[illegible];
XX
DT   2[illegible]-MAR-2002 (first entry)
XX
DE   Human protein phosphatase (SH) [illegible] encoding cDNA.
XX
KW   Protein phosphatase; serine threonine phosphatase; PP; SH; SHP[illegible];
KW   cytostatic; immunosuppressive; vasotropic; analgesic; hypertensive;
KW   hypotensive; nootropic; neuroprotective; virucide; antibacterial; human;
KW   fungicide; [illegible]; antiinflammatory; [illegible];
KW   antiarthritic; [illegible]; antiasthmatic; osteopathic; antipsoriatic;
KW   [illegible]; antiallergic; antidiabetic; tranquilizer; [illegible];
KW   neuroleptic; antiparkinsonian; anesthetic; gene therapy; ss.
XX
```

```
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..917
FT                   /*tag=  a
FT                   /product= "[illegible]"
FT                   /note= "Sequence coding for approximately another 174
FT                          amino acid residues in the corresponding protein
FT                          is not printed in the specification."
XX
PN   WO200192491 A2.
XX
PD   06-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US17365.
XX
PR   30-MAY-2000; 2000US-208261P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman GD,  Whyte D,  Sudarsanam S,  Manning G,  Caenepeel S;
PI   Martinez R,  Hunter RJ,  Flanagan P;
XX
DR   WPI; 2002-114346/15.
DR   P-PSDB; ABB67[illegible]4.
XX
PT   New phosphatase polypeptides for treating e.g., cancers, immune related
PT   diseases and disorders, cardiovascular [illegible] brain or
PT   neuronal associated diseases
XX
PS   Claim 28; Fig 1A; 161pp; English.
XX
CC   The invention relates to human protein phosphatase polypeptides and
CC   polynucleotides. The phosphatase polypeptides are useful for diagnosing
CC   and treating various phosphatase-related diseases and conditions, such as
CC   cancers, immune related diseases and disorders, cardiovascular diseases
CC   (e.g., reperfusion restenosis), brain or neuronal-associated diseases,
CC   metabolic disorders (e.g., diabetes or obesity), central or peripheral
CC   nervous system diseases and conditions (e.g., pain, migraine, mood
CC   disorders, hypotension, or hypertension), psychotic and neurological
CC   disorders (e.g., anxiety, schizophrenia), neurodegenerative diseases
CC   (e.g., Alzheimer's or Parkinson's disease), infections caused by viral
CC   (e.g., human immunodeficiency virus (HIV)), bacterial, fungal or prion-
CC   agents, ocular diseases, macular degeneration, and inflammatory disorders
CC   (e.g., rheumatoid arthritis, multiple sclerosis, osteoarthritis). The
CC   polypeptides may also be used for screening for small molecule compounds
CC   that inhibit the catalytic activity of the encoded protein phosphatase
CC   with potential use for treating the above mentioned diseases, for
CC   generating antibodies or hybridomas, and as a diagnostic tool for
CC   detecting a disease or disorder. Genetic sequences of phosphatases are
CC   useful in gene therapy. The present sequence represents a cDNA encoding
CC   a novel human serine threonine phosphatase (STP)-like phosphatase
CC   polypeptide SGP[illegible].
XX
SQ   Sequence 917 BP; 161 A; 276 C; 310 G; 170 T;   other;

  Query Match             66.4%;  Score 917;  DB 24;  Length 917;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-[illegible];
  Matches  917;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 [illegible] 60
                [illegible]
Db          1 [illegible] 60

Qy         61 [illegible] 120
                [illegible]
Db         61 [illegible] 120

Qy        121 [illegible] 180
                [illegible]
Db        121 [illegible] 180

Qy        181 [illegible] 240
                [illegible]
Db        181 [illegible] 240

Qy        241 [illegible] 300
                [illegible]
Db        241 [illegible] 300

Qy        301 [illegible] 360
                [illegible]
Db        301 [illegible] 360

Qy        361 [illegible] 420
                [illegible]
Db        361 [illegible] 420

Qy        421 [illegible] 480
                [illegible]
Db        421 [illegible] 480

Qy        481 [illegible] 540
                [illegible]
Db        481 [illegible] 540

Qy        541 [illegible] 600
                [illegible]
Db        541 [illegible] 600

Qy        601 [illegible] 660
                [illegible]
Db        601 [illegible] 660

Qy        661 [illegible] 720
                [illegible]
Db        661 [illegible] 720

Qy        721 [illegible] 780
                [illegible]
Db        721 [illegible] 780

Qy        781 [illegible] 840
                [illegible]
Db        781 [illegible] 840

Qy        841 [illegible] 900
                [illegible]
Db        841 [illegible] 900

Qy        901 CACATGATGGCTGGAC 917
                ||||||||||||||||
Db        901 [illegible] 917


RESULT 3
ABL79990
ID   ABL79990 standard; cDNA; [illegible] BP.
XX
AC   ABL79990;
XX
DT   17-MAY-2002  (first entry)
XX
DE   Human ovarian cancer related cDNA clone SEQ ID NO:[illegible].
XX
KW   Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200195801-A2.
XX
PD   06-DEC-2001.
XX
PF   29-MAY-2001; 2001WO-US17256.
XX
PR   26-MAY-2000; 2000US-207484P.
```

```
XX
PA    [illegible]
XX
PI    [illegible]
XX
DR    W[illegible]
XX
PT    [illegible] therapy and diagnosis of ovarian cancer comprising
PT    polypeptides [illegible] polypeptide [illegible]
PT    polypeptides, antibody specific to polypeptide [illegible] expressing
PT    polypeptide
XX
PS    [illegible]
XX
CC    The present invention describes a composition (I) comprising carriers
CC    and immunostimulants and a polypeptide (II) [illegible]
CC    polypeptide encoded by a polynucleotide (III) having a DNA sequence
CC    [illegible] sequences as given in [illegible]
CC    [illegible] (III) encoding (II) having a sequence (S), [illegible]
CC    population of (II), or antigen presenting cells that express (II).
CC    (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC    (III) can be used for detecting ovarian cancer in a patient's biological
CC    sample preferably serum or ovarian tissue. The method comprises
CC    contacting a biological sample from a patient with (IV), detecting the
CC    amount of polynucleotide hybridising to (IV) and comparing the amount to
CC    a predetermined cut off value and thereby detecting ovarian cancer in the
CC    patient, where the amount of polynucleotide hybridising to (IV) is
CC    detected preferably by polymerase chain reaction (PCR). (I) comprising
CC    (III) and/or (II) is useful for stimulating and/or expanding T cells
CC    specific for an ovarian tumour protein comprising contacting T cells
CC    with (II) or (III). (III) [illegible]
CC    [illegible] for inhibiting expression of the tumour polypeptides
CC    [illegible]
CC    [illegible] cDNA library, which are well known
CC    techniques.
XX
SQ    Sequence [illegible]

  Query Match              [illegible]
  Best Local Similarity    [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible] AATAAA[illegible]
Db    [illegible] AATAAA[illegible]

Qy    [illegible]
Db    [illegible]


RESULT 4
ABK4[illegible]
ID    ABK4[illegible] standard; DNA; [illegible] BP.
XX
AC    ABK4[illegible];
XX
DT    [illegible] JUN 2002  (first entry)
XX
DE    DNA encoding human protein phosphatase II[illegible] like (PPIIC) enzyme.
XX
KW    Protein phosphatase II[illegible] like; agonist; antagonist; apoptosis; AIDS;
KW    Acquired immunodeficiency virus; genetic immunodeficiency; PPIIC;
KW    neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW    retinitis pigmentosa; amyotropic lateral sclerosis; myelodysplasia;
KW    aplastic anaemia; ischaemic injury; myocardial infarction; stroke;
KW    reperfusion injury; toxin induced disease; cirrhosis; wasting disease;
KW    cachexia; viral infection; hepatitis; osteoporosis; cancer; diabetes;
KW    central nervous system disorder; CNS disorder; cardiovascular disorder;
KW    inflammatory disorder; chronic obstructive pulmonary disease; [illegible]
KW    gene; ds; human.
XX
OS    Homo sapiens.
XX
FH    Key             Location/Qualifiers
FT    CDS             [illegible]
FT                    /*tag= [illegible]
FT                    /product= "PPIIC"
FT                    /note= "Protein phosphatase II[illegible] like enzyme.
FT                           Specifically claimed in claim [illegible]"
FT    misc_binding    [illegible]
FT                    /*tag= [illegible]
FT                    /note= "Bound by the antisense oligonucleotide shown
FT                           in ABK[illegible]"
XX
PN    W[illegible] A[illegible]
XX
PD    [illegible] MAR [illegible]
XX
PF    [illegible]
XX
PR    [illegible] 2000; [illegible] US[illegible]
PR    [illegible]
XX
PA    (FARB ) BAYER AG.
XX
PI    Xiao Y;
XX
DR    WPI; 2002-[illegible]/[illegible].
DR    P-PSDB; AAU[illegible].
XX
PT    New protein phosphatase II[illegible] like enzyme and polynucleotides, useful for
PT    treating a disease associated with an increase or decrease in
PT    apoptosis, e.g. neurodegenerative diseases, viral infections,
PT    myelodysplasia, cancer, diabetes
XX
PS    [illegible] [illegible]pp; English.
XX
CC    The invention describes an isolated polynucleotide (I) which encodes a
CC    protein phosphatase II[illegible] (PPIIC) like enzyme (II). (I) and (II) can be
CC    used in diagnostic assays for detecting diseases and abnormalities or
CC    susceptibility to diseases and abnormalities related to the presence of
CC    mutations in the nucleic acid sequences encoding the enzyme. (I) and (II)
CC    or its antagonists, agonists, or modulators are useful for treating a
CC   disease or disorder associated with an increase in apoptosis such as AIDS
CC   or other infections or genetic immunodeficiencies, neurodegenerative
CC   diseases (e.g. Alzheimer's disease or Parkinson's disease, retinitis
CC   pigmentosa, or amyotrophic lateral sclerosis), myelodysplasia (e.g.
CC   aplastic anaemia), ischaemic injuries (e.g. myocardial infarction, stroke
CC   or reperfusion injury), toxin induced diseases (e.g. alcohol induced
CC   liver damage or cirrhosis), wasting diseases (e.g. cachexia), viral
CC   infections (e.g. hepatitis B or C), and osteoporosis, or a decrease in
CC   apoptosis such as cancer, diabetes, CNS disorders, cardiovascular
CC   disorders, chronic obstructive pulmonary disease (COPD), and inflammatory
CC   disorders. Regulation of human PP2C-like enzyme can be used to treat
CC   disorders such as diabetes, CNS disorders, cardiovascular disorders,
CC   COPD, and cancers (e.g. leukaemia, lymphoma, or cancers of the organs).
CC   This sequence encodes the novel human protein phosphatase 2C-like enzyme
CC   described in the invention.
XX
SQ   Sequence 2518 BP; 507 A; 768 C; 759 G; 484 T; [illegible] other;

  Query Match             19.2%;  Score 264.8;  DB 21;  Length 2518;
  Best Local Similarity   57.7%;  Pred. No. 7.8e-52;
  Matches [illegible];  Conservative    0;  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy        445 [illegible] 504
Db       1369 [illegible] 1428

Qy        505 [illegible] 564
Db       1429 [illegible] 1487

Qy        565 [illegible] 624
Db       1488 [illegible] 1547

Qy        625 [illegible] 684
Db       1548 [illegible] 1607

Qy        685 [illegible] 744
Db       1608 [illegible] 1667

Qy        745 [illegible] 804
Db       1668 [illegible] 1727

Qy        805 [illegible] 864
Db       1728 [illegible] 1787

Qy        865 GATGACTTCGGACAGAAGGTTTTGTTCAGGGATCACCACATGAGTGGCTGGAGCTACAAA 924
Db       1788 [illegible] 1847

Qy        925 [illegible] 984
Db       1848 [illegible] 1907

Qy        985 [illegible] 1044
Db       1908 [illegible] 1967

Qy       1045 [illegible] 1104
Db       1968 [illegible] 2027

Qy       1105 [illegible] 1164
Db       2028 [illegible] 2087

Qy       1165 [illegible] 1224
Db       2088 [illegible] 2147

Qy       1225 [illegible]
Db       2148 [illegible] 2207

Qy       1265 [illegible]
Db       2208 [illegible] 2267

Qy       [illegible]
Db       [illegible]


RESULT [illegible]
AAT38484
ID   AAT38484 standard; cDNA; 4262 BP.
XX
AC   AAT38484;
XX
DT   16-JAN-1997  (first entry)
XX
DE   Rat petrin cDNA clone [illegible].
XX
KW   Petrin; neurite outgrowth associated protein; CNS;
KW   central nervous system; myelin; protein phosphatase 2C; stroke;
KW   neurodegeneration; gene therapy; ss.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   misc_difference [illegible]
FT                   /*tag=  a
FT                   /note= "base [illegible] is given as [illegible] the
FT                           specification"
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PN   WO9632476-A1.
XX
PD   17-OCT-1996.
XX
PF   12-APR-1996;   96WO-US05214.
XX
PR   12-APR-1995;   95US-0421771.
XX
PA   (MOUN ) MOUNT SINAI HOSPITAL CORP.
XX
PI   Labes M,  Lozano A,  Roach A,  Roder J;
XX
DR   WPI; 1996-477127/47.
DR   P-PSDB; AAW04327.
XX
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, Petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 2; Page 50-52; 119pp; English.
XX
CC   A cDNA sequence (AAT38484) coding for petrin (AAW04327) [illegible]
CC   involved in neuronal [illegible] growth inhibition. It was [illegible]
CC   from fragments [illegible] (see also AAT38479-83) isolated from an
CC   adult rat brain cDNA library in lambda [illegible] by screening with
CC   a monoclonal antibody [illegible] the effect [illegible]
CC   of CNS myelin inhibitors. The petrin gene is expressed in neurons
CC   in brain tissue, particularly in cerebellar Purkinje cells. [illegible]
CC   used to produce petrin protein and to prepare probes. Antisense
CC   sequences (see also AAT38485) can be used in gene therapy [illegible]
CC   axonal regeneration.
XX
SQ   Sequence 4262 BP; 921 A; 1104 C; 1150 G; 1087 T; [illegible] other;

  Query Match             [illegible];  Score 262.4;  DB 17;  Length 4262;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy    [illegible]
Db    [illegible]
Qy    [illegible]
Db    [illegible]
Qy    [illegible]
Db    [illegible]
Qy    [illegible]
Db    [illegible]
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Qy    [illegible]
Db    [illegible]
Qy    [illegible]
Db    [illegible]
Qy    [illegible]
Db    [illegible]
Qy    [illegible]
Db    [illegible]

[illegible]
AAI[illegible]
ID   AAI[illegible] standard; cDNA; [illegible]
XX
AC   AAI[illegible]
XX
DT   [illegible] (first entry)
XX
DE   Rat petrin cDNA.
XX
KW   [illegible]
KW   [illegible]
KW   [illegible] gene therapy; ss.
XX
OS   [illegible]
XX
FH   Key             Location/Qualifiers
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FT                   /*tag= a
FT                   /product= "petrin"
FT   misc_difference [illegible]
FT                   /*tag= b
FT                   /note= "base [illegible] is given as b in the
FT                          specification"
XX
PN   W[illegible]-A1.
XX
PD   [illegible]
XX
PF   [illegible]
XX
PR   [illegible]
XX
PA   (M[illegible]) M[illegible] SINAI H[illegible]
XX
PI   [illegible]
XX
DR   WPI; [illegible]
DR   P-PSDB; AAW[illegible]
XX
PT   Assay for substances that modulate response of neuronal cells [illegible]
PT   neurite growth [illegible] protein, [illegible] useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke [illegible]
PT   CNS degenerative diseases
XX
PS   Claim [illegible]; [illegible]
XX
CC   A nucleotide sequence (AAI[illegible]) codes for petrin (AAW[illegible]), a protein
CC   involved in modulating neurite growth inhibition. It was isolated
CC   from an adult rat brain cDNA library in lambda gt11 by screening
CC   with probes based on partial petrin clones (see also AAI[illegible]).
CC   The human petrin locus was localised to chromosome 12. The gene
CC   is expressed in neurons in brain tissue, partic. in cerebellum
CC   Purkinje cells. It can be used to produce petrin protein and to
CC   prepare probes. Antisense sequences (see also AAI38485) can be used
CC   in gene therapy to enhance axonal regeneration.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy    [illegible]
Db    [illegible]
Qy    [illegible]
Db    [illegible]
Qy    [illegible]
Db    [illegible]
Qy    [illegible]
Db    [illegible]
Qy    [illegible]
Db    [illegible]
Qy    [illegible]
Db    [illegible]
Qy    [illegible]
Db    [illegible]
```

```
Qy        918 [illegible]
Db       1511 ATACAAAACTATTGAGGATGATGACTTGAAG[illegible] 157[illegible]

Qy        978 [illegible] 1037
Db       1571 [illegible] 1630

Qy       1038 [illegible] 1097
Db       1631 [illegible]

Qy       1098 [illegible] 1157
Db       1691 [illegible] 175[illegible]

Qy       1158 [illegible] 1214
Db       1751 [illegible]

Qy       1215 [illegible] 1262
Db       1811 [illegible] 1858


RESULT 7
AAS[illegible]
ID   AAS[illegible]40 standard; cDNA; 1[illegible]17 BP.
XX
AC   AAS[illegible]640;
XX
DT   1[illegible]-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #29444.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   W[illegible] A2.
XX
PD   11-[illegible]-2001.
XX
PF   [illegible]
XX
PR   [illegible]-MAR-[illegible]
PR   2[illegible]-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   [illegible] Y1;
XX
DR   WPI; 2[illegible]/7[illegible].
DR   P-PSDB; AB[illegible]453.
XX
PT   [illegible]
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 1; SEQ ID No 29444; 1[illegible]pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1[illegible]17 BP; [illegible] A; 442 C; 4[illegible]7 G; [illegible] T; 0 other;

  Query Match             [illegible]%;  Score [illegible];  DB 2[illegible];  Length 1[illegible];
  Best Local Similarity   57.9%;  Pred. No. 6.5e-17;
  Matches  45[illegible];  Conservative    [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy        500 [illegible]
Db        741 [illegible]

Qy        560 [illegible]
Db        7[illegible]1 [illegible]

Qy        620 [illegible]
Db        8[illegible]1 [illegible]

Qy        680 [illegible]
Db        911 [illegible]

Qy        740 [illegible]
Db        971 [illegible]

Qy        800 [illegible]
Db       1031 [illegible]

Qy        860 [illegible] 919
Db       1[illegible] [illegible]

Qy        920 [illegible]
Db       1151 [illegible]

Qy        980 [illegible]
Db       1211 [illegible]

Qy       1040 [illegible]
Db       1271 [illegible]

Qy       1100 [illegible]
Db       1331 [illegible]

Qy       1160 [illegible]
Db       1391 [illegible]

Qy       1217 [illegible]
Db       1451 [illegible]

Qy       1277 G 1277
              |
Db       1511 G 1511
```

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RESULT [illegible]
AA[illegible]
ID   AA[illegible] standard; cDNA; [illegible] BP.
XX
AC   AA[illegible];
XX
DT   [illegible] (first entry)
XX
DE   Human polynucleotide SEQ ID NO [illegible].
XX
KW   Human; [illegible]; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; [illegible];
KW   amyotrophic lateral sclerosis; Shy Drager Syndrome; chemotactic;
KW   [illegible]; [illegible]; [illegible] sclerosis; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   W[illegible]-A1.
XX
PD   [illegible]
XX
PF   [illegible] W[illegible]
XX
PR   [illegible] CN[illegible]
PR   [illegible] APR 2000; 2000CN-[illegible].
PR   [illegible]
PR   [illegible] FEB 2000; 2000CN-[illegible].
PR   [illegible] APR [illegible]
PR   [illegible] FEB 2000; [illegible]
PR   [illegible]
PR   [illegible] NOV [illegible]
XX
PA   (BIOW-) BIOWL INC.
XX
PI   [illegible] Y, [illegible], Anand V, [illegible], Ma Y, [illegible], Wang [illegible]
PI   Wang [illegible], Wang [illegible], Wilson [illegible], Xu [illegible], Xue AJ, Yang Y, Zhang [illegible]
PI   [illegible] JA, [illegible], Friedman R, [illegible] R;
XX
DR   WPI; [illegible].
DR   P-PSDB; AAM[illegible].
XX
PT   Novel nucleic acids and polypeptides useful for treating disorders
PT   such as central nervous system injuries
XX
PS   Claim [illegible]; SEQ ID NO [illegible]; [illegible]pp; English.
XX
CC   The invention relates to human nucleic acids (AA[illegible] AA[illegible]) and
CC   the encoded polypeptides (AAM[illegible] AAM[illegible]) with neutrophic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are used
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   [illegible] and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis and Shy Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: immune system suppression,
CC   [illegible] activity, chemotactic/chemokinetic activity, [illegible]
CC   and thrombolytic activity, cancer diagnosis and therapy, [illegible]
CC   [illegible] activity, arthritis and inflammation, leukaemia and
CC   CNS disorders.
CC   Note: the sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy        500 [illegible]
Db        [illegible]

Qy        560 [illegible]
Db        [illegible]

Qy        620 [illegible]
Db        [illegible]

Qy        680 [illegible]
Db        [illegible]

Qy        740 [illegible]
Db        [illegible]

Qy        800 [illegible]
Db        [illegible]

Qy        860 [illegible]
Db        [illegible]

Qy        920 [illegible]
Db        [illegible]

Qy        980 [illegible]
Db        [illegible]

Qy       1040 [illegible]
Db       1217 [illegible] 1276

Qy       1100 [illegible]
Db       1277 [illegible]

Qy       1160 [illegible]
Db       1337 [illegible]

Qy       1217 [illegible]
Db       [illegible]

Qy       1277 [illegible] 12[illegible]
                 |
Db       1457 [illegible] 14[illegible]


RESULT [illegible]
ABK4[illegible]
ID   ABK4[illegible] standard; cDNA; [illegible] BP.
XX
AC   ABK4[illegible];
XX
DT   [illegible] JUN [illegible] (first entry)
XX
DE   cDNA encoding [illegible] protein SEQ ID NO [illegible].
XX
KW   Human; [illegible]; [illegible]; [illegible]; immunogenic;
KW   gene therapy; [illegible].
XX
OS   Homo sapiens.
XX
PN   W[illegible]-A1.
```

```
XX
PD   14-FEB-2002.
XX
PF   31-JUL-2001; 2001WO-US24218.
XX
PR   03-AUG-2000; 2000US-222836P.
PR   28-MAR-2001; 2001US-279763P.
PR   29-JUN-2001; 2001US-302051P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   King GE, Meagher MJ, Xu J, Secrist H;
XX
DR   WPI; 2002-241709/29.
XX
PT   New colon cancer polypeptides and polynucleotides, useful as vaccines,
PT   for diagnosing, preventing, and treating colon cancer, and as markers
PT   for the progression of cancer
XX
PS   Claim 1; SEQ ID No 1714; 147pp; English.
XX
CC   The invention relates to polynucleotides encoding colon tumour proteins.
CC   The polynucleotides and encoded polypeptides are useful in pharmaceutical
CC   compositions, such as vaccines, for the diagnosis, prevention, and
CC   treatment of colon cancer. Polynucleotide sequences may be used as
CC   hybridisation probes or primers, and in the design and preparation of
CC   ribozyme molecules for inhibiting expression of tumour polypeptides and
CC   proteins in tumour cells. The compositions are useful for stimulating an
CC   immune response against cancer, particularly for the immunotherapy of
CC   colon cancer, and as markers for the progression of cancer.
CC   ABK14457-ABK16237 represent coding sequences of human colon tumour
CC   proteins of the invention.
CC   Note: With the exception of SEQ ID No 1 and 2, the sequence data
CC   for this patent did not form part of the printed specification but was
CC   supplied by the European Patent Office.
XX
SQ   Sequence 5791 BP; 1436 A; 1312 C; 1395 G; 1648 T; 0 other;

  Query Match             17.6%;  Score 213.4;  DB 24;  Length 5791;
  Best Local Similarity   57.9%;  Pred. No. 9.2e-47;
  Matches  452;  Conservative    0;  Mismatches  326;  Indels    3;  Gaps    1;

Qy        500 [illegible] 559

Db        401 GCTCCCCAGCACGGCCCCCACACGCTTCTTTACCGAGAAGAAGATTCCCCATGAGTGCC 460

Qy        560 [illegible] 619

Db        461 [illegible] 520

Qy        620 [illegible] 679

Db        521 [illegible] 580

Qy        680 [illegible] 739

Db        581 [illegible] 640

Qy        740 [illegible] 799

Db        641 [illegible] 700

Qy        800 [illegible] 859

Db        701 [illegible] 760

Qy        860 [illegible] 919

Db        761 [illegible] 820

Qy        920 [illegible] 979

Db        821 [illegible] 880

Qy        980 [illegible] 1039

Db        881 [illegible] 940

Qy       1040 [illegible] 1099

Db        941 [illegible] 1000

Qy       1100 [illegible] 1156

Db       1001 [illegible] 1060

Qy       1157 [illegible] 1216

Db       1061 [illegible] 1120

Qy       1217 [illegible] 1276

Db       1121 [illegible] 1180

Qy       1277 G 1277
              |
Db       1181 G 1181


RESULT 10
AAH17958
ID   AAH17958 standard; cDNA; 1963 BP.
XX
AC   AAH17958;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:17757.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116128.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J,
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full length cDNAs
XX
PS   Claim 8; SEQ ID 17757; 2537pp; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   [illegible] represents a fragment of a polynucleotide which comprises a 5' end
CC   sequence and an [illegible] complementary to a
CC   polynucleotide which comprises a 3' end sequence, where the
CC   [illegible] comprises at least [illegible] nucleotides and the [illegible]
CC   the 5' end sequence/3' end sequence is selected from those defined in
CC   the specification. The primers can be used in antisense therapy and
CC   in gene therapy. The primers are used for synthesising polynucleotides,
CC   particularly full length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the protein encoded by
CC   the full length cDNAs. The primers allow obtaining of the full length
CC   cDNAs easily without any specialised method. AAH[illegible] to AAH[illegible] and
CC   AAH[illegible] to AAH[illegible] represent human cDNA sequences; AAB[illegible] to
CC   AAB[illegible] represent human amino acid sequences and AAH[illegible] to AAH[illegible]
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy   [illegible]
Db   [illegible]
Qy   [illegible]
Db   [illegible]
Qy   [illegible]
Db   [illegible]
Qy   [illegible]
Db   [illegible]
Qy   [illegible]
Db   [illegible]
Qy   [illegible]
Db   [illegible]
Qy   [illegible]
Db   [illegible]
Qy   [illegible]
Db   [illegible]
Qy   [illegible]
Db   [illegible]
Qy   [illegible]
Db   [illegible]
Qy   [illegible]
Db   [illegible]
Qy   [illegible]
Db   [illegible]
Qy   [illegible]
Db   [illegible]
Qy   [illegible]
Db   [illegible]

RESULT 11
AAI[illegible]
ID   AAI[illegible] standard; cDNA; [illegible] BP.
XX
AC   AAI[illegible];
XX
DT   [illegible]-JAN-[illegible]  (first entry)
XX
DE   Rat petrin cDNA clone DI 41s.
XX
KW   Petrin; neurite outgrowth associated protein; CNS;
KW   central nervous system; myelin; protein phosphatase [illegible]; stroke;
KW   neurodegeneration; gene therapy; ss.
XX
OS   Rattus sp.
XX
PN   WO[illegible]-A1.
XX
PD   [illegible].
XX
PF   [illegible]-APR-[illegible];   [illegible]WO-CA[illegible].
XX
PR   [illegible]-APR-[illegible];   [illegible]US-[illegible].
XX
PA   (MOUN-) MOUNT SINAI HOSPITAL CORP.
XX
PI   Gates M, [illegible] A, Roach A, Roder J;
XX
DR   WPI; [illegible].
XX
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, Petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 2; Page [illegible]; [illegible]pp; English.
XX
CC   A cDNA clone (AAI[illegible]), designated DI 41s, is a fragment of clone
CC   DI (see also AAI[illegible] and AAI[illegible]) that codes for petrin (AAW[illegible]),
CC   a protein [illegible] in mediating neurite growth inhibition. [illegible]
CC   was isolated from an adult rat brain cDNA library by screening with
CC   a monoclonal antibody capable of neutralising the inhibition of
CC   neurite growth [illegible] several neuronal types on CNS myelin substrates.
CC   The gene is expressed in neurons in brain tissue, partic. in
CC   cerebellar Purkinje cells. [illegible] can be used to produce petrin
CC   protein and to prepare probes. Antisense sequences (see also
CC   AAI[illegible]) can be used in gene therapy to enhance axonal regeneration.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy   [illegible]
Db   [illegible]
Qy   [illegible]
Db   [illegible]
Qy   [illegible]
Db   [illegible]
Qy   [illegible]
Db   [illegible]
Qy   [illegible]
```

```
Db        267 [illegible] 326

Qy       1054 [illegible] 1113

Db        327 [illegible] 386

Qy       1114 [illegible] 1173

Db        387 [illegible] 446

Qy       1174 [illegible] 1187

Db        447 AATGAAGAAGTAGT 460


RESULT 12
AAA[illegible]
ID   AAA[illegible] standard; cDNA; 729 BP.
XX
AC   AAA[illegible];
XX
DT   15-MAY-2000  (first entry)
XX
DE   Human colon cancer cell line polynucleotide sequence SEQ ID NO:2[illegible].
XX
KW   Human; colon cancer; tumour; diagnosis; gene expression product;
KW   probe; detecting cancerous state; metastasis; identification;
KW   breast cancer; oestrogen receptor-positive breast cancer; therapy;
KW   oestrogen receptor negative breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO[illegible]-A2.
XX
PD   18-NOV-1999.
XX
PF   13-MAY-1999;   99WO-US10602.
XX
PR   14-MAY-1998;   98US-0085426.
PR   15-MAY-1998;   98US-0085537.
PR   15-MAY-1998;   98US-0085696.
PR   21-OCT-1998;   98US-0105234.
PR   27-OCT-1998;   98US-0105877.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE ) HYSEQ INC.
XX
PI   Williams LT,  Escobedo J,  Innis MA,  Garcia PD,  Sudduth-Klinger J;
PI   Reinhard C,  Giese K,  Randazzo F,  Kennedy GC,  Pot D,  Kassam A;
PI   Lamson G,  Drmanac R,  Crkvenjakov R,  Dickson M,  Drmanac S,  Labat I;
PI   Leshkowitz D,  Kita D,  Garcia V,  Jones LW,  Stache-Crain B;
XX
DR   WPI; 2000-[illegible]/[illegible].
XX
PT   Polynucleotide library used to determine cancerous states of mammalian
PT   cells -
XX
PS   Claim 1; Page 904; 1097pp; English.
XX
CC   AAA[illegible] to AAA[illegible] represent polynucleotides isolated from cDNA
CC   libraries constructed from human colon cancer cell lines. The present
CC   invention also describes a method of detecting differentially expressed
CC   genes correlated with a cancerous state of a mammalian cell, comprising
CC   detecting at least one differentially expressed gene product in a test
CC   sample derived from a cell suspected of being cancerous, where detection
CC   of the differentially expressed gene product is correlated with a
CC   cancerous state of the cell from which the test sample was derived.
CC   The polynucleotides sequences can be used in a method for detecting
CC   differentially expressed genes correlated with a cancerous state of a
CC   mammalian cell. The polynucleotides can also be used as probes for
CC   detecting and mapping related genes. They can be used in diagnosis and
CC   prognosis of diseases and disorders (e.g. identification of
CC   pre-metastatic or metastatic cancerous states, stages of cancer or
CC   responsiveness of cancer to therapy). This is particularly for breast
CC   cancer, oestrogen receptor positive breast cancer, oestrogen receptor
CC   negative breast cancer, lung cancer, and colon cancer.
XX
SQ   Sequence 729 BP; [illegible] A; [illegible] C; 185 G; 161 T; 5 other;

  Query Match             [illegible]%;  Score [illegible];  DB 21;  Length 729;
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  266;  Conservative    [illegible];  Mismatches  2[illegible];  Indels   [illegible];  Gaps   [illegible];

Qy        [illegible]

Db         25 [illegible] 84

Qy        951 [illegible]

Db         85 [illegible] 144

Qy       10[illegible] [illegible]

Db        145 [illegible] 204

Qy       1071 [illegible]

Db        205 [illegible] 264

Qy       1131 [illegible]

Db        265 [illegible] 324

Qy       1191 [illegible] 1247

Db        325 [illegible] 384

Qy       1248 [illegible]

Db        385 [illegible] 444

Qy       1296 [illegible]

Db        445 [illegible]

Qy       1356 [illegible]

Db        505 AGGC 508


RESULT 13
AAZ12841
ID   AAZ12841 standard; cDNA; [illegible] BP.
XX
AC   AAZ12841;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Human gene expression product cDNA sequence SEQ ID NO:[illegible].
XX
KW   Human; gene; gene expression product; diagnosis; therapy; probe;
KW   detection; mapping; tissue typing; profiling; forensic; cancer;
KW   genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9938972-A2.
XX
PD   05-AUG-1999.
XX
PF   28-JAN-1999;   99WO-US[illegible].
XX
PR   03-APR-1998;   98US-0080666.
PR   28-JAN-1998;   98US-[illegible].
PR   24-FEB-1998;   98US-[illegible].
PR   [illegible] MAR [illegible]
PR   [illegible] APR [illegible]
XX
PA   ([illegible] ) [illegible] N [illegible]
PA   (HYSE ) HYSEQ INC.
XX
PI   [illegible] M, [illegible]
PI   Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
PI   [illegible] W, Kassam A, Kennedy [illegible], Kita D, Labat I;
PI   Lamson G, Leshkowitz [illegible], [illegible], Randazzo F, Reinhard C;
PI   Stache-Crain B, Sudduth-Klinger J, Williams LT;
XX
DR   WPI; [illegible]/[illegible].
XX
PT   New human genes and their expression products which are
PT   differentially expressed in different cell types
XX
PS   [illegible]; English.
XX
CC   The present invention describes a library of human polynucleotides
CC   comprising the sequences given in AA[illegible] to AA[illegible]. Also described is
CC   a method of detecting differentially expressed genes correlated with the
CC   cancerous state of a mammalian cell, comprising detecting at least one
CC   differentially expressed gene product in a test sample from a cell
CC   suspected of being cancerous, where the gene product is encoded by one
CC   of the polynucleotide sequences given in AA[illegible] to AA[illegible]. The
CC   polynucleotides can be used as a source of primers and probes, which can
CC   be used for a variety of purposes, e.g. detection of expression levels,
CC   support tissue typing or [illegible], forensic genetic analysis and
CC   detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC   can be used for raising antibodies for experimental, diagnostic and
CC   therapeutic purposes. The polynucleotides may also be used to construct
CC   arrays for diagnostics (which may be used to detect or identify known
CC   encoded proteins), and to detect differences in expression levels between
CC   two tissues (e.g. to identify abnormal or diseased tissue in a human), to
CC   identify a genetic predisposition or susceptibility to a disease (such as
CC   cancer). The polynucleotides of the invention are especially used in the
CC   diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC   and lung cancer. The polynucleotides can also be used to screen for
CC   peptide [illegible] and antagonists.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match              [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity    [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

[illegible]

RESULT [illegible]
AAX[illegible]
ID   AAX[illegible] standard; cDNA; [illegible] BP.
XX
AC   AAX[illegible];
```

```
XX
DT   [illegible] SEP [illegible] (first entry)
XX
DE   Human validated cancer cell derived cDNA #2[illegible].
XX
KW   Cancer; human; colon; breast; lung; transmembrane receptor; ATPase;
KW   integral membrane protein; aspartyl protease; GATA family; wnt family;
KW   transcription factor; G-protein alpha subunit; protein phosphatase;
KW   phorbolester binding protein; diacylglycerol binding protein; trypsin;
KW   protein kinase; tyrosine phosphatase; developmental signalling protein;
KW   WW/rsp5/WWP domain; therapy; forensic; genetic mapping; diagnostic;
KW   detection; treatment; cervical; melanoma; colorectal adenocarcinoma;
KW   Wilm's tumour; retinoblastoma; sarcoma; myosarcoma; lung carcinoma;
KW   leukemia; lymphoma; dysplasia; hyperplasia; endometrial; adrenal;
KW   prostate; ss.
XX
OS   Homo sapiens.
XX
PN   W[illegible]-A1.
XX
PD   [illegible]-JUL-1999.
XX
PF   [illegible]-DEC-1998; [illegible]WO-US[illegible].
XX
PR   21-DEC-1997; [illegible].
PR   23-DEC-1997; [illegible].
PR   [illegible] APR 1998; [illegible].
PR   21-OCT-1998; [illegible].
PR   27-OCT-1998; [illegible].
XX
PA   (CHIR ) CHIR N [illegible].
PA   (HYSE ) HYSEQ INC.
XX
PI   Crkvenjakov R, [illegible] M, [illegible] E, [illegible] S;
PI   Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
PI   Jones LW, Kassam A, Kennedy GC, Kita D, Labat I;
PI   Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
PI   Stache-Crain B, Sudduth-Klinger J, Williams LT;
XX
DR   WPI; [illegible]/[illegible].
XX
PT   New isolated human polynucleotides
XX
PS   Claim 1; Page [illegible]; [illegible]pp; English.
XX
CC   This invention describes novel isolated human polynucleotides [illegible]
CC   by screening for differential expression in colon cancer, breast cancer
CC   and lung cancer cell lines. The polynucleotides of the invention are
CC   represented in AAX[illegible]-X[illegible] and encode polypeptides of protein
CC   families selected from 4 transmembrane segments integral membrane
CC   proteins, 7 transmembrane receptors, ATPases associated with various
CC   cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of
CC   transcription factors, G protein alpha subunit, phorbolesters or
CC   diacylglycerol binding proteins, protein kinase, protein phosphatase 2C,
CC   protein tyrosine phosphatase, trypsin, wnt family of developmental
CC   signalling proteins and WW/rsp5/WWP domain containing proteins. The
CC   encoded polypeptides also have a functional domain selected from Ank
CC   repeat, basic region plus leucine zipper transcription factors,
CC   bromodomain, EF hand, SH3 domain, WD domain/G beta repeats, zinc finger
CC   (C2H2 type), zinc finger (C3HC4 class), and zinc binding metalloprotease
CC   domain. The polynucleotides encode polypeptides with similarity to known
CC   protein families and are predicted to have similar properties. The novel
CC   polynucleotides can be used to develop products for use as therapeutic
CC   agents and in forensics, genetic analysis, mapping and diagnostic
CC   applications. In particular, the product can be used for the detection
CC   and management of cancers. They can be used for treating e.g. cervical
CC   cancers, melanomas, colorectal adenocarcinomas, Wilm's tumour, sarcomas,
CC   retinoblastomas, osteosarcomas, lung carcinomas, leukemias, such as chronic
CC   myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and
CC   myeloid leukemia, and lymphomas such as histiocytic lymphoma, and/or
CC   hereditary conditions, dysplasia [illegible] congenital [illegible] dysplasia,
CC   epithelial dysplasia of the cervix, fibrous dysplasia of bones, and
CC   mammary dysplasia, hyperplasias, e.g. endometrial, adrenal, breast,
CC   prostate or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of
CC   the skin.
XX
SQ   Sequence 750 BP; 170 A; 203 C; 182 G; 180 T; 15 other;

  Query Match             7.4%;  Score 102.8;  DB 20;  Length 750;
  Best Local Similarity   54.4%;  Pred. No. 2.5e-14;
  Matches  257;  Conservative    0;  Mismatches  199;  Indels   16;  Gaps    2;

Qy        904 ATCAGTGGCTGGAGCTACAAACGTGTGGAGAAATGGGATCTCAAGTACCCACTGATCCAT 963
Db         58 [illegible] 117

Qy        964 [illegible] 1023
Db        118 [illegible] 177

Qy       1024 [illegible]
Db        178 [illegible]

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DT   25-MAR-2002  (first entry)
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DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 28126.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions
XX
PS   Claim 1; SEQ ID NO 28126; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01846-ABL16175) and the encoded proteins
CC   (ABP87747-ABP[illegible]).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2087 BP; [illegible]

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  Best Local Similarity   [illegible];  Pred. No. 7.9e-14;
  Matches  287;  Conservative    [illegible];  Mismatches  25[illegible];  Indels   [illegible];  Gaps    [illegible];

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Qy        [illegible]
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Qy        981 [illegible] 1040
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Qy       1257 [illegible]
Db       1652 [illegible]


Search completed: February 23, 2003, 15:06:28
Job time : 343 secs
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                    GenCore version 5.1.3
           Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 23, 2003, 12:47:47 ; Search time 66 Seconds
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Title:           US-09-866-987-3
Perfect score:   1380
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        441372 seqs, 153348381 residues

Total number of hits satisfying chosen parameters:       882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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     Pred. No. is the number of results predicted by chance to have a
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     and is derived by analysis of the total score distribution.

                              SUMMARIES
                   %
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c  2    49.8     3.6    6924  4  US-09-299-141-9                Sequence 9, Appl
c  3    49.8     3.6    6924  4  US-09-299-141-10               Sequence 10, Appl
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c  5    48.2     3.5    1491  4  US-09-082-092-9                Sequence 9, Appl
c  6    48.2     3.5    1517  3  US-08-280-252A-45              Sequence 45, Appl
   7      47     3.4     349  4  US-09-198-119[illegible]-44    Sequence 44, Appl
c  8    47.1     3.4     774  3  US-08-415-655-11               Sequence 11, Appl
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c 11    43.4     3.1    1488  4  US-09-096-776B-3               Sequence 3, Appl
c 12    43.1     3.1    2533  4  US-09-096-776B-1               Sequence 1, Appl
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c 15      43     3.1    1328  4  US-08-118-203-1                Sequence 1, Appl
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c 19    42.4     3.1     32[illegible]  4  US-09-165-264-7      Sequence 7, Appl
c 20    42.4     3.1     32[illegible]  4  US-09-165-264-13     Sequence 13, Appl
c 21    41.4     3.0     319  4  US-09-165-264-8                Sequence 8, Appl
  22    41.4     3.0    4252  2  US-08-475-844-4                Sequence 4, Appl
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  24    41.2     3.0    1413  4  US-08-984-7[illegible]9A-52    Sequence 52, Appl
  25    41.2     3.0    6453  [illegible]  US-08-306-651B-14    Sequence 14, Appl
  26    41.2     3.0    6453  3  US-09-209-668-1[illegible]     Sequence 1[illegible], Appl
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  28    41.2     3.0    12[illegible]  [illegible]  US-[illegible]A-1[illegible]  Sequence [illegible], Appl
c 29    40.8     3.0    4678  3  US-08-726-214-1                Sequence 1, Appl
c 30    40.8     3.0    4523  4  US-09-473-7[illegible]-1       Sequence 1, Appl
c 31    40.4     2.9    [illegible]  4  US-09-42[illegible]-89[illegible]-11  Sequence 11, Appl
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c 33      40     2.9    141[illegible]  1  US-0[illegible]-984-7[illegible]A-52  Sequence 5[illegible], Appl
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c 38    39.4     2.9    2502  1  US-08-254-359A-7               Sequence 7, Appl
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c 42    39.4     2.9    2502  2  US-08-484-956-7                Sequence 7, Appl
c 43    39.4     2.9    2502  2  US-08-[illegible]-7            Sequence 7, Appl
c 44    39.4     2.9    2502  2  US-08-599-491-7                Sequence 7, Appl
c 45    39.4     2.9    2502  2  US-08-[illegible]-7            Sequence 7, Appl


                              ALIGNMENTS


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; Sequence 6, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: 1999-04-2[illegible]
;  EARLIER APPLICATION NUMBER: 60/08[illegible],[illegible]25
;  EARLIER FILING DATE: 199[illegible]-[illegible]-24
;  NUMBER OF SEQ ID NOS: 1[illegible]
;  SOFTWARE: PatentIn Ver. 2.[illegible]
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;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p43[illegible]b-AT
US-09-299-141-6

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Db     1652 [illegible] [illegible]

Qy       [illegible] [illegible] [illegible]
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Qy      199 C 199

Db     1472 C 1472


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; Sequence 9, Application US/09299141
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p[illegible]AT
[illegible]

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  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

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Db [illegible]

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Qy [illegible]

Db [illegible]


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; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
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;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p[illegible]AT
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Db [illegible]


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; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p4[illegible]AT
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Db [illegible]

Qy [illegible]
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Db [illegible]

Qy [illegible]

Db [illegible]


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; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;    APPLICANT: [illegible]
;    APPLICANT: [illegible], Anita
;    APPLICANT: [illegible]
;     APPLICANT:  Itoh, Susumu
;     APPLICANT:  Afrakhte, [illegible]
;     APPLICANT:  Souchelnytskyi, Serhiy
;     APPLICANT:  Brodin, Gregor
;     APPLICANT:  Landstrom, Marene
;     APPLICANT:  Heldin, Nils Erik
;     APPLICANT:  Heldin, Carl-Henrik
;     APPLICANT:  ten Dijke, Peter
;     TITLE OF INVENTION:  SMAD7 AND USES THEREOF
;     NUMBER OF SEQUENCES:  1[illegible]
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;       STREET:  600 Atlantic Avenue
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  U.S.A.
;       ZIP:  02210-2211
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  [illegible]
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/082,992
;       FILING DATE:  20-MAY-1998
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/047,221
;       FILING DATE:  20-MAY 1997
;       APPLICATION NUMBER:  60/[illegible],485
;       FILING DATE:  30-SEP 1997
;       APPLICATION NUMBER:  60/[illegible]
;       FILING DATE:  25-FEB 1998
;       APPLICATION NUMBER:  60/077,[illegible]
;       FILING DATE:  06-MAR-1998
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Van Amsterdam, John R.
;       REGISTRATION NUMBER.  4[illegible],212
;       REFERENCE/DOCKET NUMBER.  [illegible]/7[illegible]32
;     TELECOMMUNICATION INFORMATION.
;       TELEPHONE:  617-720-3500
;       TELEFAX.  617 720 2441
;       TELEX:
;   INFORMATION FOR SEQ ID NO:  9.
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  [illegible] base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-09-082-992-9

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Db        [illegible] [illegible]

Qy        185 [illegible] 185

Db        122 [illegible] 122
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; Patent No. 6359194
; GENERAL INFORMATION:
;  APPLICANT: Dean A. [illegible]
;  APPLICANT:  [illegible]
;  APPLICANT:  Michael [illegible]
;  APPLICANT:  Dennis [illegible]
;  APPLICANT:  Michael A. [illegible]
;  TITLE OF INVENTION: Compositions and Methods for the [illegible]
;  TITLE OF INVENTION:  [illegible]
;  FILE REFERENCE: 7853-14[illegible]
;  CURRENT APPLICATION NUMBER: US/09/288,232A
;  CURRENT FILING DATE:  1999-04-08
;  PRIOR APPLICATION NUMBER:  08/[illegible]
;  PRIOR FILING DATE: 1997-[illegible]-06
;  PRIOR APPLICATION NUMBER:  08/[illegible]
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;  PRIOR APPLICATION NUMBER: [illegible]/306,844
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version [illegible]
; SEQ ID NO 45
;   LENGTH: 1817
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-288-232A-45

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  Matches   [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

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Db        45[illegible] [illegible]

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Db        [illegible]


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;  APPLICANT:  [illegible]
;  APPLICANT:  [illegible]
;  APPLICANT:  [illegible], Kirsten
;  APPLICANT:  [illegible]
;  APPLICANT:  Zarka, Daniel
;  APPLICANT:  [illegible]
;  TITLE OF INVENTION:  Plant Having Altered Environmental Stress [illegible]
;  FILE REFERENCE:  [illegible]
;  CURRENT APPLICATION NUMBER: US/09/[illegible]
;  CURRENT FILING DATE:  [illegible]
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;  PRIOR FILING DATE:  [illegible]
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;  PRIOR FILING DATE:  [illegible]
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;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 60/018,[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 60/017,[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 60/019,[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 60/019,[illegible]
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;   LENGTH: [illegible]
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;   OTHER INFORMATION: [illegible]
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  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

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;    APPLICANT: [illegible]
;    TITLE OF INVENTION: [illegible]
;    TITLE OF INVENTION: p[illegible] A CYCLIN DEPENDENT KINASE INHIBITOR AND [illegible] OF
;    TITLE OF INVENTION: SAME
;   NUMBER OF SEQUENCES: [illegible]
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: [illegible]
;     STREET: [illegible] Avenue of the Americas
;     CITY: New York
;     STATE: New York
;     COUNTRY: United States of America
;     ZIP: [illegible]
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: [illegible]
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.[illegible]
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/[illegible]
;     FILING DATE:
;     CLASSIFICATION: [illegible]
;   ATTORNEY/AGENT INFORMATION:
;     NAME: [illegible]
;     REGISTRATION NUMBER: [illegible]
;     REFERENCE/DOCKET NUMBER: [illegible]
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (212) [illegible]
;     TELEFAX: (212) [illegible]
;  INFORMATION FOR SEQ ID NO: [illegible]
;    SEQUENCE CHARACTERISTICS:
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;       LENGTH: [illegible] base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
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  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

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Qy  [illegible]

Db  [illegible]


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; Sequence 30, Application US/[illegible]008
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: Wong, Alexander K.C.
;  APPLICANT: Tavtigian, Sean V.
;  APPLICANT: Teng, David H.-F.
;  TITLE OF INVENTION: PRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
;  TITLE OF INVENTION: AND OTHER CANCER TYPES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/[illegible],008
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: U.S. 60/1[illegible],806
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO 30
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-[illegible]-008-30

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  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

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Qy  [illegible]

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RESULT 10
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; Sequence [illegible], Application US/[illegible]
; Patent No. 6117654
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;  TITLE OF INVENTION: NOVEL MOLECULES [illegible]
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 09404/052001
;  CURRENT APPLICATION NUMBER: US/09/128,155
;  CURRENT FILING DATE: 1998-08-[illegible]
;  EARLIER APPLICATION NUMBER: US 60/091,659
;  EARLIER FILING DATE: 1998-07-02
;  EARLIER APPLICATION NUMBER: US 60/054,646
;  EARLIER FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 152831
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(152831)
;   OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

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Qy         63 [illegible] 122
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Qy        123 [illegible] 182
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Qy        183 [illegible] 204
Db      22177 [illegible] 22198


RESULT 11
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; Sequence 3, Application US/09096776B
; Patent No. 6270994
; GENERAL INFORMATION:
;  APPLICANT:  Miyazono, Kohei
;  APPLICANT:  Kawabata, Masahiro
;  TITLE OF INVENTION:   SMADS AND USES THEREOF
;  FILE REFERENCE:   L0461/7038
;  CURRENT APPLICATION NUMBER: US/09/096,776B
;  CURRENT FILING DATE:  1998-06-12
;  PRIOR APPLICATION NUMBER:   US 60/049,990
;  PRIOR FILING DATE:   1997-06-13
;  PRIOR APPLICATION NUMBER:   US 60/053,040
;  PRIOR FILING DATE:   1997-07-18
;  PRIOR APPLICATION NUMBER:   US 60/066,173
;  PRIOR FILING DATE:   1997-11-18
;  NUMBER OF SEQ ID NOS:   10
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1488
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-096-776B-3

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  Best Local Similarity   52.5%;  Pred. No. 0.2;
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Qy         65 [illegible] 124
Db        2[illegible] [illegible] [illegible]

Qy        125 [illegible] 184
Db        179 [illegible] 12[illegible]

Qy        185 C 185
Db        119 C 119


RESULT 12
US-09-096-776B-1/c
; Sequence 1, Application US/09096776B
; Patent No. 6270994
; GENERAL INFORMATION:
;  APPLICANT:  Miyazono, Kohei
;  APPLICANT:  Kawabata, Masahiro
;  TITLE OF INVENTION:   SMADS AND USES THEREOF
;  FILE REFERENCE:   L0461/7038
;  CURRENT APPLICATION NUMBER: US/09/096,776B
;  CURRENT FILING DATE:  1998-06-12
;  PRIOR APPLICATION NUMBER:   US 60/049,990
;  PRIOR FILING DATE:   1997-06-13
;  PRIOR APPLICATION NUMBER:   US 60/053,040
;  PRIOR FILING DATE:   1997-07-18
;  PRIOR APPLICATION NUMBER:   US 60/066,173
;  PRIOR FILING DATE:   1997-11-18
;  NUMBER OF SEQ ID NOS:   10
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 2534
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (751)..(2235)
US-09-096-776B-1

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  Matches   95;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

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Db       1049 [illegible] [illegible]

Qy         65 [illegible] 124
Db        989 [illegible] [illegible]

Qy        125 [illegible] 184
Db        929 [illegible] [illegible]

Qy        185 C 185
Db        869 C 869


RESULT 13
US-09-083-351-1/c
; Sequence 1, Application US/09083351
; Patent No. 6087[illegible]
; GENERAL INFORMATION:
;    APPLICANT:  Sheffield, Val C.
;    APPLICANT:  Alward, Wallace L.M.
;    APPLICANT:  Stone, Edwin M.
;    APPLICANT:  Nishimura, Darryl
;    APPLICANT:  Patil, Shiva
;    TITLE OF INVENTION:  THERAPEUTICS AND DIAGNOSTICS FOR
;    TITLE OF INVENTION:  CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
;    TITLE OF INVENTION:  TRANSCRIPTION FACTOR
;    NUMBER OF SEQUENCES:  [illegible]
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  [illegible]
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.[illegible], Version #1.[illegible]
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/[illegible]
;      FILING DATE:  [illegible] MAY [illegible]
;      CLASSIFICATION:  [illegible]
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold, Beth E.
;      REGISTRATION NUMBER:  [illegible]
;      REFERENCE/DOCKET NUMBER:  [illegible]
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-[illegible]
;      TELEFAX:  617-[illegible]
;  INFORMATION FOR SEQ ID NO:  [illegible]:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  [illegible] base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  [illegible]
US-09-[illegible]

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; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;    APPLICANT:  Sheffield, Val C.
;    APPLICANT:  Alward, Wallace L.M.
;    APPLICANT:  Stone, Edwin M.
;    APPLICANT:  Nishimura, Darryl
;    APPLICANT:  Patil, Shiva
;    TITLE OF INVENTION:  GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
;    TITLE OF INVENTION:  BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
;    NUMBER OF SEQUENCES:  [illegible]
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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  [illegible]
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/[illegible]
;      FILING DATE:  12 MAY [illegible]
;      CLASSIFICATION:  [illegible]
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold, Beth E.
;      REGISTRATION NUMBER:  [illegible]
;      REFERENCE/DOCKET NUMBER:  [illegible]
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-[illegible]
;      TELEFAX:  617-[illegible]
;  INFORMATION FOR SEQ ID NO:  [illegible]:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  [illegible] base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  [illegible]
US-09-[illegible]

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  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches   [illegible];  Conservative    [illegible];  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

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Qy     148 [illegible]
Db     [illegible]

Qy     208 AA[illegible]
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; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;    APPLICANT:  SUTHERLAND, Grant R.
;    APPLICANT:  RICHARDS, Robert I.
;    APPLICANT:  SCHLESSINGER, David
;    APPLICANT:  NAGARAJA, Ramaiah
;    APPLICANT:  KREMER, Eric J.
;    APPLICANT:  YU, [illegible]
;    APPLICANT:  BAKER, Elizabeth
;    APPLICANT:  MULLEY, [illegible]
;    APPLICANT:  MANDEL, [illegible]
;    APPLICANT:  PRITCHARD, Melanie April
;    APPLICANT:  LYNCH, Michael
;    TITLE OF INVENTION:  DNA SEQUENCES RELATED TO ISOLATE
;    TITLE OF INVENTION:  FRAGILE X SYNDROME
;    NUMBER OF SEQUENCES:  [illegible]
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;       STREET:  P.O. Box 1404
;       CITY:  Alexandria
;       STATE:  Virginia
;       COUNTRY:  United States
;       ZIP:  22313-1404
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/118,200
;       FILING DATE:  09-SEP-1993
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/802,658
;       FILING DATE:  05-DEC-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/672,242
;       FILING DATE:  20-MAR-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/638,518
;       FILING DATE:  04-JAN-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/994,517
;       FILING DATE:  23-DEC-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  [illegible], Sharon E
;       REGISTRATION NUMBER:  36,113
;       REFERENCE/DOCKET NUMBER:  02016-164
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703) 836-6620
;       TELEFAX:  (703) 836-2021
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1028 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-118-200-1

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  Best Local Similarity   57.4%;  Pred. No. 0.25;
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Qy        155 [illegible]
              [illegible]
Db        361 [illegible]


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                    GenCore version 5.1.3
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 23, 2003, 13:50:53 ; Search time 92 Seconds
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Title:           US-09-866-987-3
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Scoring table:   IDENTITY_NUC
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Searched:        442118 seqs, 280819700 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 2: [illegible]NEW_PUB.seq:*
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                 13: [illegible]NEW_PUB[illegible]:*
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      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

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Result              Query
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    2      536    38.8    547 10  US-09-867-701-[illegible]   [illegible]
    3    243.4    17.6   5791 10  US-09-920-30[illegible]A-1714  Sequence 1714, Ap
    4    243.4    17.6   5791 12  US-10-03[illegible]-[illegible]23-1714  Sequence 1714, Ap
    5       98     7.1    551 10  US-09-867-701-5466          Sequence 5466, Ap
c   6     48.2     3.5   1817 10  US-09-924-417-64            Sequence 64, Appl
    7       47     3.4    349  9  US-09-996-140-94            Sequence 94, Appl
c   8     46.8     3.4  43058 10  US-09-954-456-252           Sequence 252, App
c   9     46.8     3.4  43058 10  US-09-954-456-52[illegible]  Sequence [illegible], App
c  10     46.8     3.4  43058 10  US-09-880-107-3950          Sequence 3950, Ap
   11     46.4     3.4   3209 10  US-09-925-301-474           Sequence 474, App
   12     44.4     3.2   2561  9  US-09-976-740-48            Sequence 48, Appl
   13     44.4     3.2   2561 12  US-10-023-529-48            Sequence 48, Appl
   14     44.4     3.2   2561 12  US-10-023-529-48            Sequence 48, Appl
c  15     44.2     3.2   4286 10  US-09-899-[illegible]34A-1  Sequence 1, Appl
c  16     44.2     3.2   5100  9  US-09-954-483A-14           Sequence 14, Appl
c  17     44.2     3.2   6148  9  US-09-954-483A-1[illegible]  Sequence 1[illegible], Appl
   18     [illegible]  3.2  152[illegible]  [illegible]  US-10-05[illegible]-4[illegible]7-1[illegible]  Sequence 1[illegible], Appl
c  19     43.4     3.1   1488 10  US-09-923-922-3             Sequence 3, Appl
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   22       43     3.1   1613  9  US-09-976-740-45            Sequence 45, Appl
   23       43     3.1   1614 12  US-10-023-529-45            Sequence 45, Appl
   24       43     3.1   1614 12  US-10-023-529-45            Sequence 45, Appl
   25       43     3.1   2425  9  US-09-976-740-50            Sequence 50, Appl
   26       43     3.1   2425 12  US-10-023-529-50            Sequence 50, Appl
   27       43     3.1   2425 12  US-10-023-529-50            Sequence 50, Appl
   28     42.2     3.1   [illegible]  9  US-09-7[illegible]-4[illegible]2A-17  Sequence 17, Appl
   29     42.2     3.1  42999  9  US-10-125-767-17            Sequence 17, Appl
   30     42.2     3.1  42999  9  US-[illegible]-[illegible]12A-17  Sequence 17, Appl
c  31     41.4     3.0   127[illegible]  9  US-10-032-393-47  Sequence 47, Appl
c  32     41.4     3.0   1273[illegible]  9  US-10-032-393-8  Sequence 8, Appl
c  33     41.2     3.0    485  9  US-10-[illegible]-[illegible]  Sequence 5[illegible], Appl
c  34       41     3.0 155071  9  US-10-026-188-6             Sequence 6, Appl
c  35     40.8     3.0   4523  9  US-10-175-158-1             Sequence 1, Appl
c  36     40.4     2.9   1[illegible]  10  US-09-864-761-14662  Sequence 14662, A
   37     40.4     2.9   1038 10  US-09-917-800A-1479         Sequence 1479, Ap
   38     40.4     2.9   [illegible]  10  US-09-814-777A-21  Sequence 21, Appl
   39     40.4     2.9   1759 10  US-09-814-777A-19           Sequence 19, Appl
   40     40.4     2.9   1919 10  US-09-814-777A-17           Sequence 17, Appl
c  41     40.4     2.9   3332 12  US-10-[illegible]-864-11    Sequence 11, Appl
c  42     40.2     2.9   1167 10  US-09-778-844-166           Sequence 166, Appl
c  43     40.2     2.9   1183 10  US-09-778-844-167           Sequence 167, Appl
   44       40     2.9   14[illegible]  1[illegible]  US-09-96[illegible]-708-152  Sequence 152, Appl
   45     [illegible]  2.9  [illegible]  1[illegible]  US-09-764-878-884  Sequence 884, Appl

                               ALIGNMENTS

RESULT 1
US-09-866-987-3
; Sequence 3, Application US/09866987
; Patent No. US200200[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: WHYTE, DAVI
;  APPLICANT: MANNING, GERARD
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: FLANAGAN, PETER
;  TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
;  FILE REFERENCE: [illegible]/2180
;  CURRENT APPLICATION NUMBER: US/09/866,987
;  CURRENT FILING DATE: 2001-[illegible]
;  PRIOR APPLICATION NUMBER: 60/208,291
;  PRIOR FILING DATE: 2000-05-30
;  NUMBER OF SEQ ID NOS: 1[illegible]
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1380
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: phosphatase nucleotide
US-09-866-987-3

  Query Match             [illegible]
  Best Local Similarity   [illegible]; Pred. No. [illegible];
  Matches 1380; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

Qy          1 A[illegible]
              [illegible]
Db          1 A[illegible]

Qy         61 [illegible]
              [illegible]
Db         61 [illegible]
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[illegible]

RESULT 2
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; Sequence 2068, Application US/09867701
; Patent No. US[illegible]
; GENERAL INFORMATION:
;  APPLICANT: Algate, Paul A.
;  APPLICANT: [illegible]
;  APPLICANT: Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: 210121.4[illegible]7
;  CURRENT APPLICATION NUMBER: US/09/867,701
;  CURRENT FILING DATE: 2001-05-29
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2068
;   LENGTH: 547
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-867-701-2068

  Query Match [illegible]%;  Score [illegible];  DB [illegible];  Length 547;
  Best Local Similarity [illegible]%;  Pred. No. [illegible];
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Qy       1212 [illegible]
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Qy       1272 [illegible]
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Qy       1332 [illegible]GA 133[illegible]
Db        540 [illegible]GA 547


RESULT 3
US-09-920-309A-1714
; Sequence 1714, Application US/09920309A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon F.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547
;  CURRENT APPLICATION NUMBER: US/09/920,309A
;  CURRENT FILING DATE:  2001-07-31
;  NUMBER OF SEQ ID NOS: 1789
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1714
;   LENGTH: 5791
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-920-309A-1714

  Query Match             17.6%;  Score 214.1;  DB [illegible];  Length 5791;
  Best Local Similarity   57.9%;  Pred. No. 5.9e-51;
  Matches  452;  Conservative    0;  Mismatches  326;  Indels    3;  Gaps    1;

Qy        500 [illegible] 559
Db        401 [illegible] 460

Qy        560 TGGTGATCGGGCATTGGAGAGTGCCTTTCAGGAATGTGATGAGTGAT[illegible] 619
Db        461 TGGTCATC[illegible]GAAA[illegible]ATTCAAGGAAA[illegible] 520

Qy        620 TGGAGG[illegible]CAGGCCAGATGGGCGGCTGCACAGCC[illegible]GCAGGCAA 679
Db        521 [illegible] 580

Qy        680 [illegible]
Db        581 [illegible]

Qy        740 [illegible]
Db        641 [illegible] 700

Qy        800 [illegible]
Db        701 [illegible]

Qy        860 [illegible]
Db        761 [illegible]

Qy        920 [illegible]
Db        821 [illegible]

Qy        980 [illegible]
Db        881 [illegible]

Qy       1040 TGGACACAAACATGCAG[illegible]
Db        941 [illegible]

Qy       1[illegible] [illegible]

Db       1001 [illegible]

Qy       1160 [illegible]
Db       1061 [illegible]

Qy       1217 [illegible] 12[illegible]
Db       1121 [illegible]

Qy       1277 G 1277
Db       1181 [illegible] 1181


RESULT 4
US-10-033-528-1714
; Sequence 1714, Application US/10033528
; Patent No. US2002[illegible]1A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon F.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.[illegible]
;  CURRENT APPLICATION NUMBER: US/10/033,528
;  CURRENT FILING DATE:  2001-12-26
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1714
;   LENGTH: 5791
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-528-1714

  Query Match             17.6%;  Score 214.1;  DB 12;  Length 5791;
  Best Local Similarity   57.9%;  Pred. No. 5.9e-51;
  Matches  452;  Conservative    0;  Mismatches  326;  Indels    3;  Gaps    1;

Qy        500 [illegible] 559
Db        401 [illegible] 460

Qy        560 [illegible]
Db        461 [illegible] 520

Qy        620 [illegible]
Db        521 [illegible]

Qy        680 [illegible]
Db        581 [illegible]

Qy        740 [illegible]
Db        641 [illegible]

Qy        800 [illegible]
Db        701 [illegible]

Qy        860 [illegible]
Db        761 [illegible]

Qy        920 [illegible]
Db        821 [illegible]
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Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]

RESULT [illegible]
[illegible]
; Sequence [illegible], Application [illegible]
; Patent No. [illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible], Robert
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: [illegible]
;   OTHER INFORMATION: [illegible]
[illegible]

  Query Match          [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]
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RESULT 6
US [illegible]
; Sequence 64, Application US/[illegible]
; Patent No. US[illegible]A1
;  GENERAL INFORMATION:
;        APPLICANT: Falb, Dean
;        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;                            THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR
;                            DISEASE
;        NUMBER OF SEQUENCES: [illegible]
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: PENNIE & EDMONDS LLP
;             STREET: [illegible] Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: [illegible]
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version [illegible]
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/[illegible]
;             FILING DATE: [illegible]
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/[illegible]
;             FILING DATE: 04 MAR 1998
;             APPLICATION NUMBER: 08/[illegible]
;             FILING DATE: [illegible] JUN 1997
;             APPLICATION NUMBER: 08/[illegible],910
;             FILING DATE: [illegible] FEB 1997
;             APPLICATION NUMBER: 60/011,787
;             FILING DATE: 16 FEB 1996
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: [illegible] FEB 1996
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: [illegible]
;             APPLICATION NUMBER: 08/[illegible],844
;             FILING DATE: [illegible] FEB [illegible]
;        ATTORNEY/AGENT INFORMATION:
;             NAME: [illegible], Laura A
;             REGISTRATION NUMBER: [illegible]
;             REFERENCE/DOCKET NUMBER: [illegible]
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: [illegible]
;             TELEFAX: (212)[illegible]
;             TELEX: [illegible] PENNIE
;   INFORMATION FOR SEQ ID NO: [illegible]:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: [illegible] base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: both
;             TOPOLOGY: unknown
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: [illegible]:
US [illegible]

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length 1817;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]
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Qy        125 [illegible] 184
              [illegible]
Db        [illegible] [illegible] 277

Qy        185 [illegible] 185
              |
Db        276 [illegible] 276


RESULT 7
US-[illegible]-140-94
; Sequence 94, Application US/09996140
; Patent No. US2002[illegible]157136A1
; GENERAL INFORMATION:
;  APPLICANT: Thomashow, Michael
;  APPLICANT:  [illegible]kinger, Eric
;  APPLICANT:  Jaglo-Ottosen, Kirsten
;  APPLICANT:  Gilmour, Sarah
;  APPLICANT:  [illegible]
;  APPLICANT:  Jiang, Cai Zhong
;  TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL
;  TITLE OF INVENTION:  STRESS TOLERANCE
;  FILE REFERENCE: MBI0040US
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: 09/[illegible],27[illegible]
;  PRIOR FILING DATE: 199[illegible]-09-04
;  PRIOR APPLICATION NUMBER: 09/[illegible]
;  PRIOR FILING DATE: 1998-02-0[illegible]
;  PRIOR APPLICATION NUMBER: 09/017,816
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/[illegible],275
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/017,575
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/[illegible],227
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,234
;  PRIOR FILING DATE: 1998-02-0[illegible]
;  PRIOR APPLICATION NUMBER: 09/198,119
;  PRIOR FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: PCT/US99/01895
;  PRIOR FILING DATE: 1999-01-28
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Zea maize
US-[illegible]-94

  Query Match            [illegible].4%;  Score 47;  DB [illegible];  Length [illegible];
  Best Local Similarity   55.1%;  Pred. No. [illegible];
  Matches   92;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy         1[illegible] [illegible] 78
              [illegible]
Db         [illegible] [illegible] 161

Qy        79 [illegible] 1[illegible]
              [illegible]
Db       162 GTCCCCGAG[illegible]CAACAAGAAG[illegible] 221

Qy       159 [illegible] 185
              [illegible]
Db       222 [illegible] 248


RESULT 8
US-09-954-456-292/c
; Sequence 292, Application US/[illegible]
; Patent No. US2002[illegible]115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using [illegible]
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 68[illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]/954,456
;  CURRENT FILING DATE:  2001-[illegible]-18
;  PRIOR APPLICATION NUMBER: US/[illegible]
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,[illegible]
;  PRIOR FILING DATE: 2[illegible]
;  PRIOR APPLICATION NUMBER: US/[illegible]/234,92[illegible]
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/[illegible]/2[illegible],134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/[illegible]
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/[illegible]
;  PRIOR FILING DATE: 2[illegible]
;  PRIOR APPLICATION NUMBER: US/[illegible],711
;  PRIOR FILING DATE: 2[illegible]-27
;  PRIOR APPLICATION NUMBER: US/[illegible]
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/[illegible]
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/[illegible]
;  PRIOR FILING DATE: 2[illegible]-27
;  NUMBER OF SEQ ID NOS: 2[illegible]7[illegible]
;  SOFTWARE: PatentIn version [illegible]
; SEQ ID NO 292
;   LENGTH: 4[illegible]058
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-292

  Query Match            [illegible].4%;  Score 46.8;  DB 10;  Length 4[illegible];
  Best Local Similarity   [illegible]%;  Pred. No. 0.091;
  Matches   93;  Conservative    0;  Mismatches   77;  Indels    0;  Gaps    0;

Qy        18 [illegible] 77
              [illegible]
Db     25721 [illegible] 25[illegible]

Qy        78 CAG[illegible] 1[illegible]
              [illegible]
Db     25[illegible] [illegible]

Qy       138 [illegible] 187
              [illegible]
Db     25[illegible] [illegible]


RESULT 9
US-09-954-456-529/c
; Sequence 529, Application US/[illegible]
; Patent No. US2002[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using [illegible]
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 68[illegible]
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-[illegible]
;  PRIOR APPLICATION NUMBER: US/[illegible]/2[illegible],[illegible]17
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/[illegible]
;  PRIOR FILING DATE: 2000-09-2[illegible]
;  PRIOR APPLICATION NUMBER: US/[illegible]/234,[illegible]
;  PRIOR FILING DATE: 2[illegible]
;  PRIOR APPLICATION NUMBER: US/[illegible]/2[illegible],134
;  PRIOR FILING DATE: 2[illegible]
;  PRIOR APPLICATION NUMBER: US/[illegible]
;  PRIOR FILING DATE: 200[illegible]-26
;  PRIOR APPLICATION NUMBER: US/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn version [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
[illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible]

RESULT [illegible]
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; Sequence [illegible], Application US/[illegible]
; Patent No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-10-[illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.[illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: [illegible]
[illegible]

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  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible]

RESULT [illegible]
US-[illegible]-474
; Sequence 474, Application US/[illegible]
; Patent No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]-12
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: [illegible]
;   OTHER INFORMATION: n equals a,t,g, or c
US-[illegible]-474

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible]

RESULT [illegible]
US-[illegible]
; Sequence 48, Application US/[illegible]
; Publication No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible], Ann M.
;  APPLICANT: [illegible]
;  APPLICANT: Law, Simon W.
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: 2001-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 08/97[illegible],608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/0[illegible]1,[illegible]
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-[illegible]
;  NUMBER OF SEQ ID NOS: 5[illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-09-976-740-48

  Query Match             [illegible]%;  Score 44.4;  DB [illegible];  Length 2561;
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  104;  Conservative    0;  Mismatches   81;  Indels    1;  Gaps    1;

Qy         11 [illegible] 70

Db        620 [illegible] 679

Qy         71 [illegible] 12[illegible]

Db        680 [illegible] 739

Qy        130 [illegible] 18[illegible]

Db        740 [illegible] 799

Qy        190 GGA[illegible] 195

Db        800 [illegible] 805


RESULT 13
US-10-023-529-48
; Sequence 48, Application US/10023529
; Patent No. US20020[illegible]88A1
; GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT: Lees, Robert S.
;  APPLICANT: [illegible], Simon W.
;  APPLICANT: Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/10/023,529
;  CURRENT FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: [illegible]/[illegible]16,2[illegible]
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US [illegible]/517,84[illegible]
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/97[illegible],608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,[illegible]
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-[illegible]
;  NUMBER OF SEQ ID NOS: 5[illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.[illegible]
; SEQ ID NO 48
;   LENGTH: 25[illegible]
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-10-023-529-48

  Query Match             [illegible]%;  Score 44.4;  DB 12;  Length 2561;
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  104;  Conservative    0;  Mismatches   81;  Indels    [illegible];  Gaps    1;

Qy         11 [illegible] 70

Db        620 [illegible] 679

Qy         71 [illegible] 12[illegible]

Db        680 [illegible] 739

Qy        130 [illegible] 18[illegible]

Db        740 [illegible] 799

Qy        190 GGA[illegible] 195

Db        800 [illegible] 805


RESULT 14
US-10-023-[illegible]-48
; Sequence 48, Application US/1[illegible]
; Patent No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT: Lees, Robert S.
;  APPLICANT: [illegible], Simon W.
;  APPLICANT: Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/1[illegible]/[illegible]
;  CURRENT FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: US/0[illegible]/[illegible]
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US [illegible]/517,84[illegible]
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.[illegible]
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-10-023-[illegible]-48

  Query Match             [illegible]%;  Score 44.4;  DB 12;  Length 2561;
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  104;  Conservative    [illegible];  Mismatches   81;  Indels    [illegible];  Gaps    [illegible];

Qy         11 [illegible]

Db        620 [illegible]

Qy         71 [illegible]

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Qy        130 [illegible]

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[illegible]
GENERAL INFORMATION:
APPLICANT: Thomas [illegible] Andreas [illegible] Reinhard K[illegible] M[illegible]
TITLE OF INVENTION: [illegible]
FILE REFERENCE: [illegible]A
CURRENT APPLICATION NUMBER: [illegible]A
CURRENT FILING DATE: [illegible]
NUMBER OF SEQ ID NOS: [illegible]
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                        GenCore version 5.1.4
              Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 23, 2003, 09:34:26 ; Search time 377. Seconds
                                              (without alignments)
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Title:           US-09-866-987-3
Perfect score:   1388
Sequence:         1 atgtcccaccagatggttcca..........aatgaccaatgtcccatctga 1388

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2 54647 seqs, 14559402878 residues

Total number of hits satisfying chosen parameters:       41 826

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 41:   em_htgo_other:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

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    3     1076.4     78.0    2121   9  AK096681                  AK096681 Homo sapi
    4       1049     76.0    2134   9  HSM803792                 AL832781 Homo sapi
    5     1014.4     73.5    1429   9  AK056894                  AK056894 Homo sapi
    6        783     56.7    1382   9  BC009644                  BC009644 Homo sapi
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   22      159.4     11.5     852   9  HSA[illegible]            AJ[illegible] Homo sapi
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c  34       64.8      4.7  [illegible]  2  AC[illegible]         AC[illegible] Rattus n
c  35       62.[illegible]  4.[illegible]  44[illegible]  3  AF[illegible]  AF[illegible] Caenorhab
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c  38       58.2      4.2  [illegible]  2  AC127508              AC127508 Rattus n
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                                 ALIGNMENTS


RESULT 1
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LOCUS       AX352514                 1388 bp    DNA     linear   PAT [illegible]
DEFINITION  Sequence 3 from Patent WO0192491.
ACCESSION   AX352514
VERSION     AX352514.1  GI:[illegible]
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Plowman,G.D., Whyte,D., Sudarsanam,S., Manning,G., Caenepeel,S.,
            Martinez,R., Hill,R.J. and Flanagan,P.
  TITLE     Mammalian protein phosphatases
  JOURNAL   Patent: WO 0192491-A 3 06-DEC-2001;
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FEATURES             Location/Qualifiers
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DEFINITION  Sequence [illegible] from Patent WO[illegible].
ACCESSION   AX[illegible]
VERSION     AX[illegible]  GI:[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   [illegible], Tang,Y.T., Azimzai,Y., Yue,H., Baughn,M.R.,
            Hillman,J.L., [illegible], Walia,[illegible], Gandhi,A.R., [illegible] and
            Mathur,P.
  TITLE     Phosphatases
  JOURNAL   Patent: WO [illegible]-A [illegible]
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..[illegible]
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Db       1381 A 1381


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LOCUS       AK096681                2121 bp    mRNA    linear   [illegible]
DEFINITION  Homo sapiens cDNA [illegible] fis, clone PEBLM2 [illegible]
            [illegible] PROTEIN [illegible] (EC 3.1.3.16).
ACCESSION   AK096681
VERSION     AK096681.1  GI:[illegible]
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens peripheral blood mononuclear cells ([illegible]) cDNA to
            mRNA, clone_lib:PEBLM2 clone:PEBLM2[illegible].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K.,
            Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
            Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
            Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
            Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
            Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B.,
            Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and
            Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2121)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) Takao Isogai, FLJ Project(HRI [illegible]
            Kazusa Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:[illegible])
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
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RESULT 4
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LOCUS       HSM8[illegible]         [illegible] bp    mRNA    [illegible]
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686N[illegible] (from clone DKFZp686N[illegible]).
ACCESSION   AL8[illegible]
VERSION     AL8[illegible]  GI:[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2184)
  AUTHORS   Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible] 2002) [illegible] 85764 Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by DKFZ (German Cancer Research Center
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp686N[illegible]) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg [illegible]
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cdna/.
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RESULT 5
AK056894
LOCUS       AK056894                2429 bp    mRNA    linear   [illegible]
DEFINITION  Homo sapiens cDNA FLJ32332 fis, clone PROST2001211, weakly similar
            to PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16).
ACCESSION   AK056894
VERSION     AK056894.1  GI:16552415
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens prostate cDNA to mRNA, clone_lib:PROST2
            clone:PROST2001211.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ishibashi,T., Kimura,K., Yoshida,M., Watanabe,S., Ishida,S.,
            Ono,Y., Hotta,I., Hiraoka,S., Murakawa,K., Takiguchi,S.,
            Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
            Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
            Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
            Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y.,
            Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A.,
            Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2429)
  AUTHORS   Isogai,T., Otsuki,T. and Sugiyama,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: RAB and
            HRI.
FEATURES             Location/Qualifiers
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Qy        22[illegible] [illegible] 2[illegible]1
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Db          1[illegible] [illegible]
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SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1820)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, [illegible] Center Drive, Room 11A07, Bethesda, MD [illegible],
            USA
  REMARK    NIH-MGC [illegible] http://mgc.nci.nih.gov/
COMMENT     Contact: MGC help desk
            [illegible]
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA [illegible]
            Web site: http://www-shgc.stanford.edu
            Contact: (Dickson, Mark) [illegible]@stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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                     [illegible]AVSK[illegible]
                     [illegible]VVVMA[illegible]VLSNE[illegible]VESF[illegible]
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Qy        598 GATGA[illegible]
Db        225 GATGA[illegible]

Qy        658 [illegible]
Db        [illegible]

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Qy        [illegible]
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Qy        [illegible]
Db        [illegible]
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Qy        898 [illegible] 957
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Db        525 [illegible] 584

Qy        958 AT[illegible] 1017
              [illegible]
Db        585 AT[illegible] 644

Qy       1018 [illegible] 1077
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Qy       1078 GTGCCA[illegible] 1137
              [illegible]
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Qy       1138 [illegible] 1197
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Db        765 [illegible] 824

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Db        825 [illegible]

Qy       1258 [illegible]
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Db        885 [illegible]

Qy       1318 [illegible]
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Db        945 [illegible]

Qy       1378 TGA 1380
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Db       1005 TGA 1007


RESULT 7
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LOCUS       AK094270                1687 bp    mRNA    linear   PRI 15-JUL-2002
DEFINITION  Homo sapiens cDNA [illegible] fis, clone TESTI2012104, [illegible]
            to PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16).
ACCESSION   AK094270
VERSION     AK094270.1  GI:21752092
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens testis cDNA to mRNA, clone_lib:TESTI2
            clone: TESTI2012104.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.,
            Ono,Y., Hotuta,T., Hiraoka,S., [illegible]
            Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
            Yamashita,H., Chiba,Y., [illegible]
            Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
            Saito,K., Nishikawa,T., Kimura,K., [illegible]
            Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A.,
            Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1687)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (JAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: JAB,
            HRI and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            JAB; annotation: HRI and JAB.
FEATURES             Location/Qualifiers
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BASE COUNT      336 a    512 c    513 g    326 t
ORIGIN

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  Matches  723;  Conservative    0;  Mismatches  547;  Indels  [illegible];  Gaps  [illegible];

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Db         [illegible]

Qy         [illegible]
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Db         [illegible]

Qy         [illegible] 264
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Db         [illegible]

Qy        265 [illegible] 324
              [illegible]
Db        374 [illegible]

Qy        325 [illegible] 384
              [illegible]
Db        434 CCTA---[illegible]

Qy        385 [illegible] 444
              [illegible]
Db        [illegible]

Qy        445 GAGG[illegible]--------[illegible]
              [illegible]
Db        [illegible] AAGGAG[illegible]

Qy        494 ATGCCGCTGCATCTGCCCAGTGACCTCAGTTGTGGAG------------ 534
              [illegible]
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Qy        535 ---GAAAA[illegible]
              [illegible]
Db        [illegible]

Qy        [illegible] GAA[illegible]
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Qy        [illegible]
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Qy        712 [illegible]
              [illegible]
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Qy        772 [illegible]
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Qy        [illegible]
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Db        [illegible]
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[illegible]

ACCESSION   [illegible]
DEFINITION  Homo sapiens, Similar to RIKEN cDNA [illegible] gene, clone
            MGC:[illegible] IMAGE:[illegible], mRNA, complete cds.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD [illegible]
            USA
  REMARK    NIH-MGC Project URL: http://[illegible]
COMMENT     Contact: MGC help desk
            Email: [illegible]
            Tissue Procurement: [illegible]
            cDNA Library Preparation: [illegible]
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            [illegible], Maryland
            Web site: http://[illegible]
            Contact: [illegible]
            [illegible]
            [illegible]
            [illegible]
            [illegible]
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            [illegible]

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.[illegible]
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            This clone was selected for full length sequencing because it
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                     /note="Vector: pOTB7"
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  Best Local Similarity     [illegible]
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Db        744 GCACTGGTTGTGATCTACTTGCTAGGCAAGGTGTACGTGG CAATG AGG GATAGCAGG 803

Qy        712 [illegible] 771

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Qy        772 [illegible]

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Qy        832 [illegible] 891

Db        924 [illegible]

Qy        892 [illegible]

Db        984 [illegible]

Qy        952 [illegible]

Db       1044 [illegible]

Qy       1012 [illegible] 1071

Db       1104 [illegible]

Qy       1072 [illegible]

Db       1164 [illegible]

Qy       1132 [illegible]

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Qy       1192 [illegible]

Db       1284 [illegible]

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Qy       1297 [illegible]

Db       1404 [illegible]

Qy       1357 [illegible] 1359

Db       1464 GGT 1466


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DEFINITION  [illegible]
ACCESSION   AX419118
VERSION     AX419118.1  GI:2152[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human protein phosphatase [illegible]-like enzyme
  JOURNAL   Patent: WO 0218565-A 2 07-MAR-2002;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
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BASE COUNT      507 a    768 c    759 g    481 t
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  Matches  [illegible];  Conservative  [illegible];  Mismatches  377;  Indels  [illegible];  Gaps  [illegible];

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Db       1[illegible] [illegible]

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Db       1668 [illegible]

Qy        805 [illegible] 864

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Qy        865 [illegible]

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Qy       1105 [illegible] 1164

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Db       2088 [illegible]
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[illegible]

RESULT [illegible]
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LOCUS       HSM[illegible]                [illegible] bp    mRNA    linear   PRI [illegible]
DEFINITION  Homo sapiens mRNA; cDNA DKFZp[illegible] (from clone DKFZp[illegible]);
            partial cds.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   [illegible]
  TITLE     Direct Submission
  JOURNAL   Submitted [illegible] MIPS, Am Klopferspitz [illegible]
            Martinsried, GERMANY
COMMENT     [illegible] German Cancer
            Research Center (DKFZ); Email: [illegible]
            sequenced by BMFZ (Biomedical Research Center at the Charite,
            Berlin/Germany) within the cDNA sequencing consortium of the German
            Genome Project.
            This clone (DKFZp[illegible]) is available at the RZPD in Berlin.
            Please contact the RZPD: [illegible]
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://[illegible]/cDNA/.
FEATURES             Location/Qualifiers
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                     [illegible]KVYVANA[illegible]
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[illegible]

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DEFINITION  Sequence [illegible] from Patent W[illegible]
ACCESSION   AX[illegible]
VERSION     AX[illegible]
KEYWORDS    .
SOURCE      [illegible]
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human protein phosphatase [illegible]-like enzyme
  JOURNAL   Patent: WO 0218565-A 1 07-MAR-2002;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
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Db         97 [illegible]

Qy        643 [illegible] 702
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Qy        703 [illegible]
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Qy        823 [illegible]
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Qy       1240 [illegible]
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Qy       1288 [illegible]
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Db        817 [illegible]

Qy       1343 [illegible]
Db        877 [illegible]


RESULT 12
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DEFINITION  Sequence 242 from Patent WO0210424.
ACCESSION   AX400071
VERSION     AX400071.1  GI:[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   [illegible]
            Wang,J.R., [illegible]
  TITLE     Nucleic acids and polypeptides
  JOURNAL   Patent: WO 0210424-A 242 07-MAR-2002;
            HYSEQ, INC. (US)
FEATURES             Location/Qualifiers
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                     [illegible]
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                     [illegible]SYS"
BASE COUNT      243 a    3[illegible] c    373 g    252 t
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB 6;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
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Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
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[illegible]
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[illegible]
[illegible]
[illegible]
[illegible]
[illegible]
[illegible]
[illegible]
[illegible]
```

```
[illegible]
LOCUS       A[illegible]         [illegible] bp    DNA     linear   [illegible]
DEFINITION  Homo sapiens [illegible] (Roswell Park Cancer
            Institute Human BAC Library) complete sequence.
ACCESSION   A[illegible]
VERSION     A[illegible]  GI:[illegible]
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Muzny,D.M., Adams,C.Q., Bouck,J., Bonner,T., Chen,G., Chen,Z.,
            Culpepper,B., Ding,Y., Durbin,K.J., Dutton,K.J., Fortune,C.,
            Ghosh,E.B., Garcia,A., Garcia,D.K., Gorrell,H., Gorrell,L.J.,
            He,X., Hernandez,J., Hawkins,L.L., Kowalewski,N., Leal,B.,
            Lichtarge,O., Liu,W., Loque,J., Lu,J., Martinez,E., Moore,S.,
            Morgan,M., Nguyen,N., Oswald,L., Pampolla,L., Parish,R.,
            Perez,L.M., Rashid,N., Rives,C.M., Scherer,S.E., Shen,H.,
            [illegible],M., [illegible], Wei,Y., Williamson,A.C., Worley,K.C., [illegible],
            Naylor,S.L. and Gibbs,R.A.
  TITLE     [illegible]
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to [illegible])
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) Molecular and Human Genetics, Baylor
            College of Medicine, One Baylor Plaza, Houston, TX [illegible], USA
REFERENCE   3  (bases 1 to [illegible])
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (27 FEB [illegible]) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX [illegible], USA
COMMENT     On Mar [illegible] this sequence version replaced gi:[illegible].
            INFORMATION: http://www.hgsc.bcm.tmc.edu/ or e-mail
            [illegible]@bcm.tmc.edu

            CLONE LENGTH: This sequence does not necessarily represent the
            entire insert of this clone. Overlapping portions of clones are only
            sequenced and submitted once. So the sequence for the remainder of
            the insert may be found in the record for the adjacent clones.
            Overlapping clones are noted at the beginning and end of the
            Features listing.

            ANNOTATION OF FEATURES:
              STSs are identified using e-PCR (Genome Res. 7:541 [illegible]) searches
            of a local database that includes entries from dbSTS, GDB, and
            local mapping efforts.
              Repeats are identified using RepeatMasker (A. Smit and P. Green,
            unpublished.) for Human and Mouse sequences.
              Genes and Region of sequence similarity are identified by BLAST
            (Nucl. Acids Res. 25, 3389-3402) similarity (expect < le-[illegible]) to the
            EST and cDNA sequences. Genes demonstrate at least two exons
            flanked by consensus splice sites that maintained sequence
            continuity across the splice junctions. Sequences that are not
            identical matches are annotated as similar.

            SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
            standard of double strand coverage with a minimum of 2 clones and 2
            reads with no ambiguities or 2 chemistries with a minimum of 2
            clones and 3 reads with no ambiguities. If the sequence quality for
            a region does not meet this standard, it will be indicated in the
            annotation as Low Coverage.

            QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
            standards - estimated error rate less than 1 per 10,000 bases.
            Reports of lowest quality individual bases and measures of base
            quality are listed below. Description of the metrics can be found
            at URL: http://[illegible]/quality.[illegible]
            html.

            QUALSTAT Block

                          Summary Statistics
            Contig length:                                      [illegible]
            Phrap values in estimate:                           [illegible]
            Average error rate (ECM Phrap estimate):            [illegible]
            Fraction of Phrap values less than 40 :             [illegible]
            Number of consensus changing edits:                 6
            Number of N's in consensus :                        0

            -                  Consensus changing edits                 -
            Position     Original Context          Edited Context
            [illegible]  [illegible](n)[illegible]  [illegible](c)[illegible]
            [illegible]  acctta[illegible](n)[illegible]  acctta[illegible](a)[illegible]
            [illegible]  attaa[illegible](n)atacatttt  attaa[illegible](a)atacatttt
            [illegible]  [illegible](n)[illegible]  [illegible](a)[illegible]
            [illegible]  ttttatattt(n)atctaatgta  ttttatattt(a)atctaatgta
            [illegible]  [illegible](n)[illegible]  [illegible](t)[illegible]

                      Distribution of quality < 40 Bases

                    1000|                                          *
                     900|                                          *
                     800|                                          *
               #     700|                                          *
              Bases  600|                                    *     *
                     500|                                    *     *
                     400|                                    *     *
                     300|                                    *     *
                     200|                              *     *     *
                     100|                  *     *     *     *     *
                       |    *     *     *     *     *     *     *     *

                         [illegible]   15   [illegible]   25   30   35   4[illegible]
                                  Phrap Value Range

            Version: [illegible]
```

```
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "RPC15-1157M23"
                     /note "Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                     Eutheria; Primates; Catarrhini; Hominidae; Homo."
     repeat_region   1..69
                     /rpt_family "Alu"
     repeat_region   78..379
                     /rpt_family "AluSx"
     gene            complement(join(588..1542,1865..[illegible],2124..2257,
                     2487..255[illegible],2734..2853))
                     /gene "Unigene cluster containing AI378477, [illegible]80596,
                     AA22[illegible], [illegible], AA728[illegible], [illegible], and AA2[illegible]."
     STS             647..783
                     /standard_name "stSG4882"
                     /db_xref "GDB:456642[illegible]"
     STS             695..860
                     /standard_name "[illegible]"
                     /db_xref "dbSTS:32797"
     misc_feature    5021..5289
                     /note "Region: Similar to H.sapiens genomic DNA, X87529."
     repeat_region   5178..5235
                     /rpt_family "GC_rich"
     repeat_region   5290..5532
                     /rpt_family "GC_rich"
     misc_feature    5530..5630
                     /note "Region: Similar to H.sapiens genomic DNA, X8752[illegible]."
     repeat_region   6319..6602
                     /rpt_family "AluSx"
     repeat_region   complement([illegible]..7715)
                     /rpt_family "L1M4"
     repeat_region   complement([illegible])
                     /rpt_family "AluSp"
     repeat_region   8106..8173
                     /rpt_family "MER4A2"
     repeat_region   complement(82[illegible]7..8491)
                     /rpt_family "AluSx"
     repeat_region   complement(8542..8591)
                     /rpt_family "AluSp"
     repeat_region   9144..9289
                     /rpt_family "MER4[illegible]"
     repeat_region   complement(9421..9582)
                     /rpt_family "FRAM"
     repeat_region   complement(9586..9631)
                     /rpt_family "(TAGA)n"
     repeat_region   complement(9663..9894)
                     /rpt_family "AluJo"
     repeat_region   9[illegible]5..10052
                     /rpt_family "MIR"
     repeat_region   complement(1[illegible]24..10266)
                     /rpt_family "L2"
     repeat_region   11050..11126
                     /rpt_family "L2"
     repeat_region   11143..11426
                     /rpt_family "AluSp"
     repeat_region   11960..12050
                     /rpt_family "GC_rich"
     gene            join(12104..12195,16081..[illegible],19065..19243,19956..[illegible],
                     20192..[illegible],21117..[illegible],[illegible]..21526,21986..[illegible])
                     /gene "Unigene cluster containing AI188660, AA77[illegible],
                     W93722, T68451, AA341000, F12[illegible], and AA250126."
     repeat_region   complement(14187..14295)
                     /rpt_family "MIR"
     repeat_region   complement(14866..15168)
                     /rpt_family "AluSq"
     repeat_region   complement(15623..15725)
                     /rpt_family "(TA)n"
     repeat_region   complement(17254..17546)
                     /rpt_family "AluY"
     repeat_region   complement(18160..18451)
                     /rpt_family "AluSp"
     STS             [illegible]
                     /standard_name "[illegible]"
                     /db_xref "[illegible]"
     STS             22320..22490
                     /standard_name "stSG[illegible]"
                     /db_xref "GDB:456442[illegible]"
     repeat_region   complement([illegible])
                     /rpt_family "ML[illegible]"
     repeat_region   complement([illegible]..24822)
                     /rpt_family "L2"
     repeat_region   complement(25824..26124)
                     /rpt_family "AluSp"
     repeat_region   complement([illegible]..30874)
                     /rpt_family "(GGGA)n"

  Query Match             18.[illegible]%;  Score [illegible];  DB 9;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  262;  Conservative    0;  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy        334 [illegible]
              [illegible]
Db       4222 [illegible]

Qy        394 [illegible]
              [illegible]
Db       4162 [illegible]

Qy        454 [illegible]
              [illegible]
Db       4102 [illegible]

Qy        514 [illegible]
              [illegible]
Db       [illegible]

Qy        574 [illegible] 598
              [illegible]
Db       3982 [illegible]


RESULT 14
AC092045/c
LOCUS       AC092045               171343 bp    DNA     linear   PRI [illegible]
DEFINITION  Homo sapiens chromosome [illegible], clone RP11-[illegible], complete sequence.
ACCESSION   AC092045 AC024148
VERSION     AC092045.2  GI:15281257
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171343)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C. and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 171343)
  AUTHORS   Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,[illegible] and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]-JUN-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 171343)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C. and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-AUG-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
COMMENT     On Aug 25, 2001 this sequence version replaced gi:[illegible].
            [illegible] Genome Center
               Center: University of Washington Genome Center
               Center code: UWGC
               Web site: http://www.genome.washington.edu
```

```
                     [illegible]
                     [illegible] Center: BCM
                               Project Information
                     Center project name: [illegible]
                     Center clone name: RP11-[illegible] ([illegible])
                               Summary Statistics
                     Sequencing vector: M13; [illegible] reads
                     Sequencing vector: plasmid; [illegible] reads
                     Chemistry: Dye terminator ET; [illegible] reads
                     Chemistry: Dye primer Bodipy; [illegible] reads
                     Chemistry: Dye terminator Big Dye; [illegible] reads
                     Assembly program: Phrap; version [illegible]
                     Consensus quality: [illegible] bases at least Q[illegible]
                     Consensus quality: [illegible] bases at least Q[illegible]
                     Consensus quality: [illegible] bases at least Q[illegible]
                     Insert size: [illegible]; [illegible] error; [illegible] bp
                     Insert size: [illegible]; sum of contigs
                     Quality coverage: [illegible]x in Q20 bases; [illegible] bp
                     Quality coverage: [illegible]x in Q20 bases; [illegible]

            Overlapping Sequences:
                     5': RP11-[illegible] ([illegible]) A[illegible]
                     3': RP11-[illegible] ([illegible]) A[illegible]

            Sequence Quality Assessment:
             This entry has been annotated with sequence quality
             estimates computed by the Phrap assembly program.
             All manually edited bases have been reduced to quality zero.
             Quality levels above 40 are expected to have less than
             1 error in 10,000 bp.
             Base-by-base quality values are not generally available in the
             GenBank flat file format but are available as part
             of this entry's ASN.1 file.

            This sequence was finished as follows unless otherwise noted:
            all regions were either double stranded or sequenced with an
            alternate chemistry or covered by high quality data (i.e., phred
            quality [illegible] 30); an attempt was made to resolve all sequencing
            problems, such as compressions and repeats; all regions were
            covered by at least one plasmid subclone or more than one M13
            subclone; and the assembly was confirmed by restriction digest.

            Sequence Validation:
             This sequence has been validated by Multiple Complete Digest
             Fingerprinting. Comparison of the experimentally derived digest
             fragments with sequence predicted fragments is given below.
             The electronically digested sequence consists of both insert and
             vector in order to accurately represent the entire clone (BAC).
             Small fragments below a variable cut off (approximately 4[illegible] bp)
             are not resolved in the fingerprint and hence do not appear
             in the table. There are no significant remaining discrepancies
             between the experimental and predicted values. Uniquely ordered
             fragments are separated by dashed lines.
                   BglII                  EcoRI                  HindIII

            SeqberMap  Fingerprint   SeqberMap  Fingerprint   SeqberMap  Fingerprint



                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 2441         2425           6127         6141           4085         [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  8744           [illegible]  [illegible]

                 17140        [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  [illegible]    [illegible]  [illegible]

                 [illegible]  [illegible]    [illegible]  8744           [illegible]  [illegible]

                 [illegible]  [illegible]    18221        18042          [illegible]  [illegible]

                 [illegible]  [illegible]    7            [illegible]    [illegible]  [illegible]

                 1644         [illegible]                                [illegible]  [illegible]

                 [illegible]  [illegible]                                [illegible]  [illegible]

                 [illegible]  [illegible]                                [illegible]  [illegible]

                 [illegible]  [illegible]                                [illegible]  [illegible]

                 [illegible]  [illegible]                                [illegible]  [illegible]

                 [illegible]  [illegible]                                [illegible]  [illegible]

                 [illegible]  [illegible]                                [illegible]  [illegible]

                 [illegible]  [illegible]                                [illegible]  [illegible]

                 [illegible]  [illegible]

                 [illegible]  [illegible]

                 [illegible]  [illegible]

                 [illegible]  [illegible]

                 [illegible]  [illegible]

                 [illegible]  [illegible]

                 [illegible]  [illegible]
FEATURES             Location/Qualifiers
```

```
     SOURCE          1..171343
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="3"
                     /clone="RP11-168J18"
                     /clone_lib="[illegible] BAC Library 11"
BASE COUNT     39231 a  46165 c  45178 g  40769 t
ORIGIN

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length 171343;
  Best Local Similarity   98.9%;  Pred. No. 1.2e-41;
  Matches  2[illegible]2;  Conservative    0;  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy        334 [illegible] 393
              [illegible]
Db     165894 [illegible] 165835

Qy        394 [illegible] 453
              [illegible]
Db     165834 [illegible] 165775

Qy        454 [illegible] 513
              [illegible]
Db     165774 [illegible] 165715

Qy        514 [illegible] 573
              [illegible]
Db     165714 [illegible] 165655

Qy        574 TTGGAGAGTGCCTTTCAGGAATGTG 598
              |||||||||||||||||||||||||
Db     165654 TTGGAGAGTGCCTTTCAGGAATGTG 165630


RESULT 15
AC094021
LOCUS       AC094021               214160 bp    DNA     linear   PRI 27-MAR-2002
DEFINITION  Homo sapiens chromosome 3 clone RP11-80L18, complete sequence.
ACCESSION   AC094021 AC069253
VERSION     AC094021.2  GI:19745[illegible]
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Raymond,C., [illegible] and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-2002) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
COMMENT     On Mar 27, 2002 this sequence version replaced gi:15[illegible]4339.
            ------------ Genome Center
                 Center: University of Washington Genome Center
                 Center Code: UWGC
                 Web site: http://genome.washington.edu
                 Contact: uwgc[illegible]@u.washington.edu
                 Drafting Center: BCM
            ------------ Project Information
                 Center project name: chr-3
                 Center clone name: RP11-80L18 (bc565)
            ------------ Summary Statistics
                 Sequencing vector: M13; L08821; [illegible]% of reads
                 Sequencing vector: plasmid; [illegible]% of reads
                 Chemistry: Dye-terminator ET; [illegible]% of reads
                 Chemistry: Dye-primer Bodipy; 1[illegible]% of reads
                 Chemistry: Dye-terminator Big Dye; [illegible]% of reads
                 Assembly program: Phrap; version [illegible]
                 Consensus quality: 214[illegible] bases at least Q40
                 Consensus quality: 214[illegible] bases at least Q30
                 Consensus quality: 214[illegible] bases at least Q20
                 Insert size: 214160; sum-of-contigs
                 Quality coverage: [illegible]x in Q20 bases; sum-of-contigs
            ------------
            Overlapping Sequences:
                 5': Mapping in progress
                 3': [illegible] (UWGC:[illegible]) AC0[illegible]208
            --------------------
            Sequence Quality Assessment:
             This entry has been annotated with sequence quality
             estimates computed by the Phrap assembly program.
             All manually edited bases have been reduced to quality zero.
             Quality levels above 40 are expected to have less than
             1 error in 10,000 bp.
             Base-by-base quality values are not generally visible from the
             GenBank flat file format but are available as part
             of this entry's ASN.1 file.

            This sequence was finished as follows unless otherwise noted:
            all regions were either double stranded or sequenced with an
            alternate chemistry or covered by high quality data (i.e., Phred
            quality >= 30); an attempt was made to resolve all sequencing
            problems, such as compressions and repeats; all regions were
            covered by at least one plasmid subclone or more than one M13
            subclone; and the assembly was confirmed by restriction digest.
            --------------------
            Sequence Validation:
             This sequence has been validated by Multiple Complete Digest
             Fingerprinting. Comparison of the experimentally derived digest
             fragments with sequence-predicted fragments is given below.
             The electronically digested sequence consists of both insert and
             vector, in order to accurately represent the entire circular BAC.
             Small fragments below a variable cutoff (approximately 1,000 bp)
             are not resolved in the fingerprint and hence don't appear
             in the table. There are no significant remaining discrepancies
             between the experimental and predicted values. Uniquely ordered
             fragments are separated by dashed lines.
                    [illegible]                  [illegible]                [illegible]
            ---------------------------------------------------------------
            SeqPredMap  Fingerprint    SeqPredMap  Fingerprint    SeqPredMap  Fingerprint
            ---------------------------------------------------------------
                [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ----------
                [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ----------
                1[illegible]  [illegible]   48[illegible]  4941   [illegible]  [illegible]
            ----------
                1447[illegible]  14[illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ----------
                [illegible]  [illegible]   16[illegible]  164[illegible]   [illegible]  [illegible]
            ----------
                [illegible]  [illegible]   14[illegible]  144[illegible]   [illegible]  [illegible]
            ----------
                [illegible]  [illegible]   4[illegible]  [illegible]   [illegible]  [illegible]
            ----------
                [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ----------
                4[illegible]  4[illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ----------
                [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ----------
                [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
            ----------
                [illegible]  [illegible]   [illegible]  [illegible]   [illegible]  [illegible]
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[illegible]

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ORIGIN

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Db    [illegible] [illegible]

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Db    [illegible] [illegible]

Qy        574 [illegible]
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Search completed: [illegible]
Job time : [illegible] secs
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                    GenCore version 5.1.3
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         February 23, 2003, 06:59:10 ; Search time [illegible] Seconds
                                        (without alignments)
                                        10122.[illegible] Million cell updates/sec

Title:          US-09-866-987-3
Perfect score:  [illegible]
Sequence:       1 [illegible]..........[illegible]

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2185239 seqs, 1125999155 residues

Total number of hits satisfying chosen parameters:      4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :      N_Geneseq_101002:*
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                2: [illegible]:*
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                22: [illegible]:*
                23: [illegible].DAT:*
                24: [illegible]:*

   Pred. No. is the number of results predicted by chance to have a
   score greater than or equal to the score of the result being printed,
   and is derived by analysis of the total score distribution.

                              SUMMARIES
                       %
Result               Query
  No.    Score   Match Length DB  ID                     Description
------------------------------------------------------------------------------
     1   [illegible]   99.2   1837  22  AAH22961          Human phosphatase
     2   [illegible]   [illegible]    917  24  ABA[illegible]          Human protein [illegible]
     3   [illegible]   [illegible]    547  24  ABL79998          Human [illegible]
     4   [illegible]   [illegible]   [illegible]  24  ABK4[illegible]          DNA encoding human
     5   262.4   19.0   4262  17  AAI38484          Rat pettin cDNA [illegible]
     6   [illegible]   [illegible]   [illegible]  17  AAI384[illegible]          Rat pettin cDNA.
     7   243.4   17.6   1617  23  AAS93640          DNA encoding novel
     8   243.4   17.6   [illegible]  22  AA[illegible]          Human polynucleotide [illegible]
     9   243.4   17.6   5791  21  ABK46163          cDNA encoding [illegible]
    10   [illegible]   [illegible]   [illegible]  2[illegible]  AA[illegible]          Human cDNA sequence
    11     178   12.9   [illegible]  17  AAI38482          Rat pettin cDNA [illegible]
    12   [illegible]    7.[illegible]   [illegible]  2[illegible]  AAA[illegible]          Human [illegible]
    13     103    7.5   [illegible]  20  AAZ12841          Human [illegible] express
    14   102.8    7.4   [illegible]  2[illegible]  AAX[illegible]          Human validated [illegible]
    15   101.2    7.3   [illegible]  2[illegible]  ABL2554[illegible]          Cross-hybridising [illegible]
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    17      98    7.1   [illegible]  21  ABL[illegible]          Human [illegible]
    18      [illegible]    [illegible]   [illegible]  20  AAX98437          Human [illegible]
    19   [illegible]    [illegible]   [illegible]  2[illegible]  AAA[illegible]          Human [illegible]
    20    83.6    6.1    294  21  AAA00279          Human [illegible]
    21    81.[illegible]    [illegible]   [illegible]  2[illegible]  ABV2[illegible]          Human prostate exp
    22    81.2    5.9   2258  23  ABV23186          Human prostate exp
    23    81.[illegible]    [illegible]   [illegible]  2[illegible]  ABV2[illegible]          Human prostate exp
    24    81.2    5.9   2258  23  ABV27[illegible]          Human prostate exp
    25    81.2    [illegible]   [illegible]  2[illegible]  ABV2[illegible]          Human prostate exp
c   26    7[illegible].8    5.[illegible]   [illegible]  22  AAH1[illegible]          Human cDNA clone (
    27      [illegible]    [illegible]    434  17  AAI384[illegible]          Rat pettin cDNA [illegible]
    28    59.4    [illegible].7   [illegible]  22  AAS[illegible]          Anti-tumour [illegible]
c   29    49.8    3.6   [illegible]  21  AAZ45[illegible]          Nucleotide sequence
c   30    49.8    3.6   [illegible]  21  AA[illegible]          Nucleotide sequence
c   31    49.8    3.6   [illegible]  21  AAZ45[illegible]          Nucleotide sequence
c   32    4[illegible].4    3.6   [illegible]  22  AAK7[illegible]          Human immune/haema
    33    49.2    3.6   [illegible]  22  AAI59[illegible]          Human polynucleotide
c   34      49    [illegible]   [illegible]  2[illegible]  ABK47[illegible]          [illegible] phosphatase
c   35    48.6    3.5   1127  24  ABQ68452          Listeria monocytogen
c   36    48.[illegible]    [illegible]   [illegible]  [illegible]  AAN[illegible]          Nucleotide sequence
c   37    48.[illegible]    3.5   2887  24  AAD36[illegible]          Human Smad[illegible] DNA.
c   38      48    [illegible]   [illegible]  2[illegible]  AB[illegible]          [illegible]
    39      48    3.5   [illegible]  24  ABQ[illegible]          [illegible]
    40    47.[illegible]    3.4   [illegible]  22  AAJ[illegible]          HSV [illegible]
c   41    47.[illegible]    3.4   [illegible]  22  AAK754[illegible]          Human immune/haema
    42      47    3.4   [illegible]  2[illegible]  AAZ2[illegible]          Z. mays [illegible]
c   43    [illegible]    3.4   [illegible]  21  ABN[illegible]          Gene [illegible]
c   44    [illegible]    [illegible]   [illegible]  21  [illegible]64982          Lung cancer related
c   45    [illegible]    [illegible]   [illegible]  21  [illegible]          Lung cancer related


                              ALIGNMENTS


RESULT 1
AAH22961
ID   AAH22961 standard; cDNA; 1837 BP.
XX
AC   AAH22961;
XX
DT   17-SEP-2001  (first entry)
XX
DE   Human phosphatase (HI) [illegible] cDNA (clone ID 1724417[illegible]).
XX
KW   Phosphatase; HI; Alzheimer's disease; Huntington's disease; tumour;
KW   immune disorder; cancer; [illegible]; immunomodulatory; cytostatic;
KW   neuroprotective; anticoagulant; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             [illegible]
FT                   /*tag= a
FT                   /product= "phosphatase"
XX
PN   WO200153469-A2.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US02086.
XX
PR   21-JAN-2000; 2000US-0[illegible].
PR   2[illegible]-JAN-2000; 2000US-0[illegible].
PR   2[illegible]-FEB-2000; 2000US-0[illegible].
PR   1[illegible]-MAR-2000; 2000US-0[illegible]142.
XX
```

```
CA   [illegible]
XX
PI   [illegible]
PI   [illegible] Wang B, Gandhi AR, [illegible] Mathur P;
XX
DR   WPI; [illegible]
DR   [illegible] AAB[illegible]
XX
PT   Novel phosphatases useful for treating diseases associated with
PT   decreased expression of functional phosphatases, e.g., Alzheimer's
PT   disease, Huntington's disease, immune disorders, and cancers
XX
PS   Claim [illegible]; Page [illegible]; [illegible]pp; English.
XX
CC   The invention provides human phosphatases (PP) and polynucleotides
CC   [illegible] the phosphatases. The polypeptides can be expressed [illegible]
CC   recombinant methodology. The PP are useful for treating a disease or
CC   condition associated with decreased expression of functional
CC   phosphatases. Compositions [illegible] antagonists [illegible] may
CC   be used to treat a disease associated with increased expression [illegible]
CC   [illegible] Such diseases may include
CC   Alzheimer's disease, Huntington's disease, immune disorders, and
CC   cancers. The present sequence represents a human phosphatase [illegible]
CC   cDNA.
XX
SQ   Sequence [illegible]

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative    [illegible];  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

[illegible]

Db       [illegible]

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Db       1081 [illegible] 1140

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1201 [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       1380 A 1380

Db       1381 A 1381


RESULT [illegible]
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ID   ABA[illegible] standard; cDNA; [illegible] BP.
XX
AC   ABA[illegible];
XX
DT   26-MAR-200[illegible]  (first entry)
XX
DE   Human protein phosphatase SGP[illegible] encoding cDNA.
XX
KW   Protein phosphatase; serine threonine phosphatase; [illegible]
KW   [illegible]
KW   [illegible] neuroprotective; virucide; antibacterial; human;
KW   [illegible] antiinflammatory; [illegible]
KW   [illegible] antiasthmatic; osteopathic; [illegible]
KW   antiarteriosclerotic; [illegible] antidiabetic; [illegible]
KW   [illegible] gene therapy; [illegible]
XX
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```
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "[illegible]"
FT                   /note= "sequence coding for approximately another 154
FT                          amino acid residues in the corresponding protein
FT                          is not printed in the specification "
XX
PN   WO2001[illegible]-A2.
XX
PD   [illegible]-2001.
XX
PF   [illegible]-MAY-2001; 2001WO-US17[illegible].
XX
PR   [illegible]-MAY-2000; 2000US-2082[illegible]P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman GD,  Whyte D,  Sudarsanam S,  Manning G,  Caenepeel S;
PI   Martinez R,  Hill RJ,  Flanagan P;
XX
DR   WPI; 2002-[illegible].
DR   P-PSDB; ABB07[illegible]4.
XX
PT   New phosphatase polypeptides for treating e.g., cancers, immune-related
PT   diseases and disorders, cardiovascular diseases, or brain or
PT   neuronal-associated diseases -
XX
PS   Claim 28; Fig 1A; 1[illegible]pp; English.
XX
CC   The invention relates to human protein phosphatase polypeptides and
CC   polynucleotides. The phosphatase polypeptides are useful for diagnosing
CC   and treating various phosphatase-related diseases and conditions, such as
CC   cancers, immune related diseases and disorders, cardiovascular diseases
CC   (e.g., repertusion restenosis), brain or neuronal-associated diseases,
CC   metabolic disorders [illegible]
CC   nervous system diseases and conditions (e.g., pain, migraine, mood
CC   disorders, hypotension, or hypertension), psychotic and neurological
CC   disorders (e.g., anxiety, schizophrenia), neurodegenerative diseases
CC   (e.g., Alzheimer's or Parkinson's disease), infections caused by viral
CC   (e.g., human immunodeficiency virus (HIV)), bacterial, fungal or prion
CC   agents, ocular diseases, macular degeneration, and inflammatory disorders
CC   (e.g., rheumatoid arthritis, multiple sclerosis, osteoarthritis). The
CC   polypeptides may also be used for screening for small molecule compounds
CC   that inhibit the catalytic activity of the encoded protein phosphatase
CC   with potential use for treating the above-mentioned diseases, for
CC   generating antibodies or hybridomas, and as a diagnostic tool for
CC   detecting a disease or disorder. Genetic sequences of phosphatases are
CC   useful in gene therapy. The present sequence represents a cDNA encoding
CC   a novel human serine threonine phosphatase (STP)-like phosphatase
CC   polypeptide SIP[illegible].
XX
SQ   Sequence 917 BP; 161 A; 276 C; 310 G; 170 T; 0 other;

  Query Match             66.4%;  Score 917;  DB 24;  Length 917;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-[illegible];
  Matches  917;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 [illegible] 60
Db          1 [illegible]

Qy         61 [illegible] 120
Db         61 [illegible] 120

Qy        121 [illegible] 180
Db        121 [illegible] 180

Qy        181 [illegible]
Db        181 [illegible]

Qy        241 [illegible]
Db        241 [illegible]

Qy        301 [illegible]
Db        301 [illegible]

Qy        361 [illegible]
Db        361 [illegible]

Qy        421 [illegible]
Db        421 [illegible]

Qy        481 [illegible]
Db        481 [illegible]

Qy        541 [illegible]
Db        541 [illegible]

Qy        601 [illegible]
Db        601 [illegible]

Qy        661 [illegible] 72
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Qy        721 [illegible] 780
Db        721 [illegible] 780

Qy        781 [illegible] 84
Db        781 [illegible] 84

Qy        841 [illegible]
Db        841 [illegible]

Qy        901 CATATGAGTGGCTGGAT 917
Db        901 CATATGAGTGGCTGGAT 917


RESULT [illegible]
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ID   ABL79990 standard; cDNA; [illegible] BP.
XX
AC   ABL79990;
XX
DT   17-MAY-2002  (first entry)
XX
DE   Human ovarian cancer related cDNA clone SEQ ID NO:2008.
XX
KW   Human; ovarian cancer; ovarian tumour; cytostatic; [illegible].
XX
OS   Homo sapiens.
XX
PN   WO200192[illegible]-A2.
XX
PD   [illegible]-DEC-2001.
XX
PF   29-MAY-2001; 2001WO-US1775[illegible].
XX
PR   2[illegible]-MAY-2000; 2000US-20748[illegible].
```

```
XX
PA    [illegible] cDNA [illegible]
XX
PI    Algate PA, [illegible]
XX
DR    WPI; [illegible]
XX
PT    Composition for therapy and diagnosis of ovarian cancer comprising
PT    [illegible] ovarian tumor polypeptides, polynucleotides encoding
PT    polypeptides, antibody specific to polypeptide or T cell expressing
PT    polypeptide
XX
PS    Claim [illegible]; [illegible] English.
XX
CC    The present invention describes a composition (I) comprising carriers
CC    and immunostimulant and a polypeptide (II) of an ovarian tumor
CC    polypeptide encoded by a polynucleotide (III), having a cDNA sequence
CC    (S1) from the [illegible] nucleotide sequences as given in ABK[illegible]
CC    [illegible] (III) encoding (II) having a sequence (S2), a T cell
CC    population of (II), or antigen presenting cells that express (I).
CC    (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC    (III) can be used for detecting ovarian cancer in a patient's biological
CC    sample preferably serum or ovarian tissue. The method comprises
CC    contacting a biological sample from a patient with (IV), detecting the
CC    amount of polynucleotide hybridising to (IV) and comparing the amount to
CC    a predetermined cut off value and thereby detecting ovarian cancer in the
CC    patient, where the amount of polynucleotide hybridising to (IV) is
CC    detected preferably by polymerase chain reaction (PCR). (I) comprising
CC    (III) and/or (II) is useful for stimulating and/or expanding T cells
CC    specific for an ovarian tumor protein, expressing or interacting T cells
CC    with (III) or (II). (III) is useful in designing and preparation of
CC    [illegible] for inhibiting expression of the tumour polypeptides
CC    [illegible] and [illegible] full length genes from a
CC    [illegible] library, e.g., a tumour cDNA library using well known
CC    techniques
XX
SQ    Sequence [illegible]

  Query Match               [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity     [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

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Qy    [illegible]
Db    [illegible]
Qy    [illegible]
Db    [illegible]

Qy    1272 [illegible]
Db     480 [illegible]

Qy    1332 GTTGTTGA 1339
Db     540 GTTGTTGA 547


RESULT 4
ABK47452
ID    ABK47452 standard; DNA; 2518 BP.
XX
AC    ABK47452;
XX
DT    18-JUN-2002  (first entry)
XX
DE    DNA encoding human protein phosphatase II C-like (PPIIC) enzyme.
XX
KW    Protein phosphatase II C like; agonist; antagonist; apoptosis; AIDS;
KW    Acquired immunodeficiency virus; genetic immunodeficiency; PPIIC;
KW    neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW    retinitis pigmentosa; amyotropic lateral sclerosis; myelodysplasia;
KW    aplastic anaemia; ischaemic injury; myocardial infarction; stroke;
KW    reperfusion injury; toxin-induced disease; cirrhosis; wasting disease;
KW    cachexia; viral infection; hepatitis; osteoporosis; cancer; diabetes;
KW    central nervous system disorder; CNS disorder; cardiovascular disorder;
KW    inflammatory disorder; chronic obstructive pulmonary disease; [illegible];
KW    gene; ds; human.
XX
OS    Homo sapiens.
XX
FH    Key             Location/Qualifiers
FT    CDS             [illegible]
FT                    /*tag= a
FT                    /product= "PPIIC"
FT                    /note= "Protein phosphatase II C like enzyme,
FT                           Specifically claimed in claim 1"
FT    misc_binding    [illegible]
FT                    /*tag= b
FT                    /note= "Bound by the antisense oligonucleotide set out
FT                           in ABK17461"
XX
PN    WO2002[illegible]-A2.
XX
PD    [illegible]-MAR-2002.
XX
PF    29-AUG-2001; 2001WO-EP[illegible].
XX
PR    [illegible]
PR    02-APR-2001; 2001US-[illegible].
XX
PA    (FARB ) BAYER AG.
XX
PI    Xiao Y;
XX
DR    WPI; 2002-[illegible]/[illegible].
DR    P-PSDB; AAU[illegible].
XX
PT    New protein phosphatase IIC like enzyme and polynucleotide, useful for
PT    treating a disease associated with an increase or decrease in
PT    apoptosis, e.g. neurodegenerative diseases, viral infections,
PT    myelodysplasia, cancer, diabetes
XX
PS    Disclosure; Page [illegible]; 1[illegible]pp; English.
XX
CC    The invention describes an isolated polynucleotide (I) which encodes a
CC    protein phosphatase IIC (PPIIC) like enzyme (II). (I) and (II) can be
CC    used in diagnostic assays for detecting diseases and abnormalities or
CC    susceptibility to diseases and abnormalities related to the presence of
CC    mutations in the nucleic acid sequences encoding the enzyme. (I) and (II)
CC    or its antagonists, agonists, or modulators are useful for treating a
CC   disease or disorder associated with an increase in apoptosis such as AIDS
CC   or other infectious or genetic immunodeficiencies, neurodegenerative
CC   diseases (e.g. Alzheimer's disease or Parkinson's disease, retinitis
CC   pigmentosa, or amyotropic lateral sclerosis), myelodysplasia (e.g.
CC   aplastic anaemia), ischaemic injuries (e.g. myocardial infarction, stroke
CC   or reperfusion injury), toxin induced diseases (e.g. alcohol induced
CC   liver damage or cirrhosis), wasting diseases (e.g. cachexia), viral
CC   infections (e.g. hepatitis B or C), and osteoporosis, or a decrease in
CC   apoptosis such as cancer, diabetes, CNS disorders, cardiovascular
CC   disorders, chronic obstructive pulmonary disease (COPD), and inflammatory
CC   disorders. Regulation of human PPIIC-like enzyme can be used to treat
CC   disorders such as diabetes, CNS disorders, cardiovascular disorders,
CC   COPD, and cancers (e.g. leukaemia, lymphoma, or cancers of the organs).
CC   This sequence encodes the novel human protein phosphatase IIC like enzyme
CC   described in the invention.
XX
SQ   Sequence 2519 BP; [illegible] A; 768 C; 759 G; 441 T; [illegible] other;

  Query Match             19.2%;  Score 264.8;  DB 24;  Length 2519;
  Best Local Similarity   57.7%;  Pred. No. 7.8e-52;
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Db       1369 [illegible] 1428

Qy        505 [illegible] 564
Db       1429 [illegible] 1487

Qy        565 [illegible] 624
Db       1488 [illegible] 1547

Qy        625 [illegible] 684
Db       1548 [illegible] [illegible]

Qy        685 [illegible] 744
Db       [illegible] [illegible]

Qy        745 [illegible] 804
Db       1668 [illegible] 1727

Qy        805 [illegible] 864
Db       1728 [illegible] [illegible]

Qy        [illegible] [illegible] 924
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Qy        [illegible] [illegible] 984
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Qy        [illegible] [illegible]
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Qy       1045 [illegible] 1104
Db       1968 [illegible] 2027

Qy       [illegible] [illegible] 1164
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Qy       [illegible] [illegible] 1221
Db       [illegible] [illegible] 2147

Qy       1222 [illegible]
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Qy       [illegible] [illegible]
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Qy       [illegible] [illegible]
Db       [illegible] [illegible]


RESULT [illegible]
AAT38484
ID   AAT38484 standard; cDNA; [illegible] BP.
XX
AC   AAT38484;
XX
DT   16-JAN-[illegible]  (first entry)
XX
DE   Rat potrin cDNA [illegible]
XX
KW   Potrin; neurite outgrowth associated protein; CNS;
KW   central nervous system; myelin; protein phosphatase [illegible]; stroke;
KW   neurodegeneration; gene therapy; ss.
XX
OS   Rattus sp.
XX
FH   Key                 Location/Qualifiers
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FT                       /*tag= [illegible]
FT                       /note= "base [illegible] is given as [illegible] in the
FT                       specification"
XX
PN   [illegible]-A1.
XX
PD   17-OCT-[illegible].
XX
PF   [illegible];   [illegible].
XX
PR   [illegible]-APR-[illegible];   [illegible].
XX
PA   (MOUN-) MOUNT SINAI HOSPITAL CORP.
XX
PI   [illegible] M,  Lozano A,  Roach A,  Roder J;
XX
DR   WPI; [illegible]-477127/47.
DR   P-PSDB; [illegible].
XX
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, Potrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 2; Page [illegible]; [illegible]; English.
XX
CC   A cDNA sequence (AAT38484) encoding potrin (AAW[illegible]), a protein
CC   involved in mediating neurite growth inhibition. It was derived
CC   from fragments [illegible] (see also AAT[illegible]) isolated from an
CC   adult rat brain cDNA library in lambda gt11 by screening with
CC   a monoclonal antibody that blocks the effect on neurons in culture
CC   of CNS myelin inhibitors. The potrin gene is expressed in neurons
CC   in brain tissue, partic. in cerebellum Purkinje cells. It can be
CC   used to produce potrin protein and to prepare probes. Antisense
CC   sequences (see also AAT[illegible]) can be used in gene therapy to enhance
CC   axonal regeneration.
XX
SQ   Sequence 4262 BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible];  Score [illegible];  DB 17;  Length 4262;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy  [illegible]
Db  [illegible]

[illegible]

AA[illegible]
ID   AA[illegible] standard; cDNA [illegible] BP.
XX
AC   AA[illegible];
XX
DT   [illegible] JAN [illegible] (first entry)
XX
DE   [illegible] cDNA.
XX
KW   [illegible]
KW   [illegible] protein phosphatase [illegible]; stroke;
KW   [illegible]
XX
OS   [illegible]
XX
FH   Key             Location/Qualifiers
FT   [illegible]
FT                   /*tag= [illegible]
FT                   [illegible] petrin
FT   misc_difference [illegible]
FT                   /*tag= [illegible]
FT                   /note= "base [illegible] is given as [illegible] in the
FT                          specification"
XX
PN   WO[illegible] A1.
XX
PD   17-[illegible]-1996.
XX
PF   12-APR-1996;   96WO-[illegible].
XX
PR   13-APR-1995;   95US-[illegible].
XX
PA   (MOUN ) MOUNT SINAI HOSPITAL [illegible].
XX
PI   [illegible]
XX
DR   WPI; [illegible].
DR   P-PSDB; AAW[illegible].
XX
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 4; Fig [illegible]; [illegible]pp; English.
XX
CC   A nucleotide sequence (AAT[illegible]) codes for petrin (AAW[illegible]), a protein
CC   involved in mediating neurite growth inhibition. It was isolated
CC   from an adult rat brain cDNA library in lambda gt11 by screening
CC   with probes based on partial petrin clones (see also AAT[illegible]).
CC   The human petrin locus was localised to chromosome 12. The gene
CC   is expressed in neurons in brain tissue, partic. in cerebellum
CC   Purkinje cells. It can be used to produce petrin protein and to
CC   prepare probes. Antisense sequences (see also AAT[illegible]) can be used
CC   in gene therapy to enhance axonal regeneration.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy  [illegible]
Db  [illegible]
```

```
Qy     [illegible]
Db     1511 AIA[illegible]AAAA[illegible]AT[illegible]GAACT[illegible]AA 157[illegible]

Qy     [illegible]CAGA[illegible] 1037
Db     1571 [illegible]

Qy     [illegible]AAACA[illegible]CAGCCTCAAGC[illegible]TGCCACA[illegible] 1097
Db     1631 [illegible]

Qy     [illegible] 1157
Db     [illegible]

Qy     [illegible] 121[illegible]
Db     1751 [illegible]

Qy     1215 [illegible]
Db     1811 [illegible]

RESULT 7
AAS[illegible]
ID   AAS[illegible] standard; cDNA; 1617 BP.
XX
AC   AAS[illegible];
XX
DT   1[illegible]-FEB-20[illegible]2  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #2[illegible]444.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   [illegible] supplement; medical imaging; diagnostic; genetic disorder; [illegible]
XX
OS   Homo sapiens.
XX
PN   W[illegible]
XX
PD   [illegible]
XX
PF   [illegible]-MAR-[illegible]
XX
PR   [illegible]-MAR-20[illegible]; [illegible]US-[illegible]40217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, [illegible]
XX
DR   WPI; 2001-[illegible]
DR   P-PSDB; AB[illegible]
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 1; SEQ ID No 29444; 1[illegible]pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS[illegible]-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1617 BP; [illegible] A; 412 C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible]
  Best Local Similarity   57.9%;  Pred. No. 6.5e-47;
  Matches  452;  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     7[illegible]1 [illegible]

Qy     620 [illegible]
Db     8[illegible]1 [illegible]

Qy     [illegible]
Db     [illegible]

Qy     740 [illegible]
Db     [illegible]

Qy     800 [illegible]
Db     [illegible]

Qy     860 [illegible]
Db     [illegible]

Qy     920 [illegible]
Db     [illegible]

Qy     980 [illegible]
Db     12[illegible]1 [illegible]

Qy     1040 [illegible]
Db     1271 [illegible]

Qy     1100 [illegible]
Db     [illegible]

Qy     1160 [illegible]
Db     1391 [illegible]

Qy     1217 [illegible]
Db     1451 [illegible]

Qy     1277 G 1277
             |
Db     1511 G 1511
```

```
RESULT 8
AA[illegible]
ID   AA[illegible] standard; cDNA; [illegible] BP.
XX
AC   AA[illegible];
XX
DT   [illegible] (first entry)
XX
DE   Human nucleotide SEQ ID NO [illegible].
XX
KW   Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; [illegible] arthritis; inflammation;
KW   [illegible].
XX
OS   Homo sapiens.
XX
PN   WO[illegible]-A1.
XX
PD   [illegible].
XX
PF   [illegible] 2001; 2001WO-[illegible].
XX
PR   [illegible]
PR   [illegible]
PR   [illegible]
PR   [illegible]
PR   [illegible]
PR   [illegible]
PR   [illegible]
PR   [illegible]
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Asundi V, Zhou P, Ma Y, Qian XB, Ren F, Wang D,
PI   Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI   Zhao QA, Chen R, Goodrich R, Drmanac RT;
XX
DR   WPI; [illegible].
DR   P-PSDB; AAM[illegible].
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries
XX
PS   Claim [illegible]; SEQ ID NO [illegible]; [illegible]pp; English.
XX
CC   The invention relates to human nucleic acids (AA[illegible]-AA[illegible]) and
CC   the encoded polypeptides (AAM[illegible]-AAM[illegible]) with neutropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies, and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: immune system suppression,
CC   activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemia and
CC   CNS disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]


RESULT 9
ABK4[illegible]
ID   ABK4[illegible] standard; cDNA; [illegible] BP.
XX
AC   ABK4[illegible];
XX
DT   0[illegible] JUN 2002  (first entry)
XX
DE   cDNA encoding novel human protein, SEQ ID No [illegible].
XX
KW   Human; [illegible]; cancer; immune [illegible];
KW   human therapy; [illegible].
XX
OS   Homo sapiens.
XX
PN   WO[illegible]-A1.
```

```
XX
PD   14-FEB-2002.
XX
PF   31-JUL-2001; 2001WO-US24216.
XX
PR   18-AUG-2000; 2000US-226233P.
PR   28-MAR-2001; 2001US-279763P.
PR   29-JUN-2001; 2001US-302051P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   King GE, Meagher MJ, Xu J, Secrist H;
XX
DR   WPI; 2002-241789/29.
XX
PT   New colon cancer polypeptides and polynucleotides - useful in vaccines,
PT   for diagnosing, preventing, and treating colon cancer, and as markers
PT   for the progression of cancer
XX
PS   Claim 1; SEQ ID No 1714; 147pp; English.
XX
CC   The invention relates to polynucleotides encoding colon tumour proteins.
CC   The polynucleotides and encoded polypeptides are useful in pharmaceutical
CC   compositions, such as vaccines, for the diagnosis, prevention, and
CC   treatment of colon cancer. Polynucleotide sequences may be used as
CC   hybridisation probes or primers and in the design and preparation of
CC   ribozyme molecules for inhibiting expression of tumour polypeptides and
CC   proteins in tumour cells. The compositions are useful for stimulating an
CC   immune response against cancer, particularly for the immunotherapy of
CC   colon cancer, and as markers for the progression of cancer.
CC   [illegible] - [illegible] represent coding sequences of human colon tumour
CC   proteins of the invention.
CC   Note: With the exception of SEQ ID No 1 and 2, the sequence data
CC   for this patent did not form part of the printed specification but was
CC   supplied by the European Patent Office.
XX
SQ   Sequence 5791 BP; 1436 A; 1312 C; 1395 G; 1648 T; 0 other;

  Query Match             17.6%;  Score 243.4;  DB 21;  Length 5791;
  Best Local Similarity   57.9%;  Pred. No. 9.2e-17;
  Matches  452;  Conservative    0;  Mismatches  326;  Indels    3;  Gaps    1;

Qy        500 [illegible] 559

Db        401 [illegible] 460

Qy        560 [illegible] 619

Db        461 [illegible] 520

Qy        620 [illegible] 679

Db        521 [illegible] 580

Qy        680 [illegible] 739

Db        581 [illegible] 640

Qy        740 [illegible] 799

Db        641 [illegible] 700

Qy        800 [illegible] 859

Db        701 [illegible] 760

Qy        860 [illegible] 919

Db        761 [illegible] 820

Qy        920 [illegible] 979

Db        821 [illegible] 880

Qy        980 [illegible] 1039

Db        881 [illegible] 940

Qy       1040 [illegible] 1099

Db        941 [illegible] 1000

Qy       1100 [illegible] 1159

Db       1001 [illegible] 1060

Qy       1160 [illegible] 1216

Db       1061 [illegible] 1120

Qy       1217 [illegible] 1276

Db       1121 [illegible] 1180

Qy       1277 G 1277

Db       1181 G 1181


RESULT 10
AAH17958
ID   AAH17958 standard; cDNA; 1903 BP.
XX
AC   AAH17958;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:17758.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full length cDNAs
XX
PS   Claim 8; SEQ ID 17758; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5' end
CC   [illegible]
CC   polynucleotide which comprises a 3' end sequence, where the
CC   [illegible] comprises at least 15 nucleotides and the [illegible]
CC   the 5' end sequence/3' end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides
CC   particularly full length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full length cDNAs. The primers allow obtaining of the full length
CC   cDNAs easily without any specialised methods. AAH[illegible] to AAH[illegible] and
CC   AAH[illegible] to AAH18[illegible] represent human cDNA sequences; AAH[illegible] to
CC   AAH[illegible] represent human amino acid sequences; and AAH[illegible] to AAH[illegible]
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence [illegible]

  Query Match             [illegible]
  Best Local Similarity   [illegible]  Pred. No. [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]
```

```
RESULT 11
AAI[illegible]
ID   AAI[illegible] standard; cDNA; [illegible] BP.
XX
AC   AAI[illegible];
XX
DT   [illegible] JAN [illegible] (first entry)
XX
DE   Rat petrin cDNA clone [illegible].
XX
KW   Petrin; neurite outgrowth associated protein; CNS;
KW   central nervous system; myelin; protein phosphatase 2C; stroke;
KW   neurodegeneration; gene therapy; ss.
XX
OS   Rattus sp.
XX
PN   W[illegible]-A1.
XX
PD   17-[illegible]-1996.
XX
PF   12-APR-[illegible];   [illegible]
XX
PR   13-APR-1995;   [illegible]
XX
PA   (MOUN-) MOUNT SINAI HOSPITAL CORP.
XX
PI   Labes M, Lozano A, Roach A, Roder J;
XX
DR   WPI; 1996-477127/47.
XX
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, Petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 2; Page [illegible]; [illegible]pp; English.
XX
CC   A cDNA clone (AAI[illegible]), designated [illegible] 413, is a fragment of clone
CC   [illegible] (see also AAI[illegible] and AAI[illegible]) that codes for petrin (AAW[illegible]),
CC   a protein involved in modulating neurite growth inhibition. [illegible]
CC   was isolated from an adult rat brain cDNA library by screening with
CC   a monoclonal antibody capable of neutralising the inhibition of
CC   neurite growth by several neuronal types on CNS myelin substrates.
CC   The gene is expressed in neurons in brain tissue, partic. in
CC   cerebellar Purkinje cells. It can be used to produce petrin
CC   protein and to prepare probes. Antisense sequences (see also
CC   AAI[illegible]) can be used in gene therapy to enhance axonal regeneration.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible]  Score [illegible]  DB [illegible]  Length [illegible]
  Best Local Similarity   [illegible]  Pred. No. [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
```

```
Db        2?7 [illegible] 
Qy       1?54 [illegible] 111?
Db        427 [illegible]
Qy       1114 [illegible] 11??
Db        ?87 [illegible] 1??
Qy       1174 [illegible] 1187
Db        14? [illegible] 46?


RESULT 12
AAA?2?11
ID   AAA??11 standard; cDNA; 729 BP.
XX
AC   AAA??11;
XX
DT   1? MAY-2000  (first entry)
XX
DE   Human colon cancer cell line polynucleotide sequence SEQ ID NO:?2?2.
XX
KW   Human; colon cancer; tumour; diagnosis; gene expression product;
KW   probe; detection, cancerous state, metastasis, identification,
KW   breast cancer; oestrogen receptor-positive breast cancer; therapy;
KW   oestrogen receptor negative breast cancer, lung cancer, ss.
XX
OS   Homo sapiens.
XX
PN   WO2??5?675-A2.
XX
PD   18 NOV 1999.
XX
PF   1? MAY 1999;    99WO-US10692.
XX
PR   14 MAY 1998;    98US-0085426.
PR   15 MAY 1998;    98US-0085?47.
PR   15-MAY 1998;    98US-0085696.
PR   2? ?CT-1998;    98US-010524?.
PR   27-OCT-1998;    98US-0105877.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Williams LT,  Escobedo J,  Innis MA,  Garcia PD,  Sudduth Klinger J;
PI   Reinhard C,  Giese K,  Randazzo F,  Kennedy GC,  Pot D,  Kassam A;
PI   Lamson G,  Drmanac R,  Crkvenjakov R,  Dickson M,  Drmanac S,  Labat I;
PI   Leshkowitz D,  Kita D,  Garcia V,  Jones LW,  Stache Crain B;
XX
DR   WPI; 2000-12??09/11.
XX
PT   Polynucleotide library used to determine cancerous states of mammalian
PT   cells -
XX
PS   Claim 1; Page 30?; 1??7pp; English.
XX
CC   AAA?0?? to AAA?2716 represent polynucleotides isolated from cDNA
CC   libraries constructed from human colon cancer cell lines. The present
CC   invention also describes a method of detecting differentially expressed
CC   genes correlated with a cancerous state of a mammalian cell, comprising
CC   detecting at least one differentially expressed gene product in a test
CC   sample derived from a cell suspected of being cancerous, where detection
CC   of the differentially expressed gene product is correlated with a
CC   cancerous state of the cell from which the test sample was derived.
CC   The polynucleotides sequences can be used in a method for detecting
CC   differentially expressed genes correlated with a cancerous state of a
CC   mammalian cell. The polynucleotides can also be used as probes for
CC   detecting and mapping related genes. They can be used in diagnosis and
CC   prognosis of diseases and disorders (e.g. identification of
CC   pre-metastatic or metastatic cancerous states, stages of cancer, or
CC   responsiveness of cancer to therapy). This is particularly for breast
CC   cancer, oestrogen receptor positive breast cancer, oestrogen receptor
CC   negative breast cancer, lung cancer, and colon cancer.
XX
SQ   Sequence 729 BP; 1?? A; 1?? C; 1?? G; 16? T; ? other;

  Query Match             [illegible];  Score [illegible];  DB 21;  Length 72?;
  Best Local Similarity   5?.0%;  Pred. No. 8.2e-16;
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Qy       1071 [illegible]
Db        2?? [illegible]
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Db        ??7 [illegible]
Qy       121? [illegible] 129?
Db        ?65 [illegible] 444
Qy       12?? [illegible] 1?55
Db        44? [illegible] ?04
Qy       1?56 GGGC 1?59
Db        505 AGGC 508


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AAZ12841
ID   AAZ12841 standard; cDNA; ? BP.
XX
AC   AAZ12841;
XX
DT   12-?CT-1999  (first entry)
XX
DE   Human gene expression product cDNA sequence SEQ ID NO:????.
XX
KW   Human; gene; gene expression product; diagnosis; therapy; probe;
KW   detection; mapping; tissue typing; profiling; forensic; cancer;
KW   genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9938?72-A2.
XX
PD   05 AUG 1999.
XX
PF   28 JAN 1999;    99WO-US01?1?.
XX
PR   0? APR-1998;    98US-00??6??.
PR   28 JAN-1998;    98US-0?72?? .
PR   24-FEB 1998;    98US-0??5??1.
PR   [illegible] MAY 1999;   [illegible].
PR   [illegible] APR 1999;   [illegible].
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Crkvenjakov R,  Dickson M,  Drmanac R,  Drmanac S;
PI   Escobedo J,  Garcia PD,  Garcia V,  Giese K,  Innis MA;
PI   Jones LW,  Kassam A,  Kennedy GC,  Kita D,  Labat I;
PI   Lamson G,  Leshkowitz D,  Pot D,  Randazzo F,  Reinhard C;
PI   Stache-Crain B,  Sudduth Klinger J,  Williams LT;
XX
DR   WPI; [illegible]/11.
XX
PT   Novel human genes and their expression products which are
PT   differentially expressed in different cell types.
XX
PS   Claim 1; Page [illegible]; [illegible]pp; English.
XX
CC   The present invention describes a library of human polynucleotides
CC   comprising the sequences given in AAZ[illegible] to AAZ[illegible]. Also described is
CC   a method of detecting differentially expressed genes correlated with the
CC   cancerous state of a mammalian cell, comprising detecting at least one
CC   differentially expressed gene product in a test sample from a cell
CC   suspected of being cancerous, where the gene product is encoded by one
CC   of the [illegible] polynucleotide sequences given in AAZ[illegible] to AAZ[illegible]. The
CC   polynucleotides can be used as a source of primers and probes, which can
CC   be used for a variety of purposes, e.g. detection of expression in a
CC   specific tissue type, for profiling, forensics, genetic analysis and
CC   detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC   can be used for raising antibodies for experimental, diagnostic and
CC   therapeutic purposes. The polynucleotides may also be used to construct
CC   [illegible] (which may be used to determine function of an
CC   encoded protein) and to detect differences in expression levels between
CC   two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC   identify a genetic predisposition or susceptibility to a disease such as
CC   cancer). The polynucleotides of the invention are especially used in the
CC   diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC   and lung cancer. The polynucleotides can also be used to screen for
CC   peptide agonists and antagonists.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

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Qy   [illegible]
Db   [illegible]


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ID   AAX[illegible] standard; cDNA; [illegible] BP.
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AC   AAX[illegible];
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DT   24-SEP-1999  (first entry)
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DE   Human validated cancer cell derived cDNA #2[illegible].
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KW   Cancer; human; colon; breast; lung; transmembrane receptor; ATPase;
KW   integral membrane protein; aspartyl protease; GATA family; wnt family;
KW   transcription factor; G-protein alpha subunit; protein phosphatase;
KW   phorbolester binding protein; diacylglycerol binding protein; trypsin;
KW   protein kinase; tyrosine phosphatase; developmental signalling protein;
KW   WW/rsp5/WWP domain; therapy; forensic; genetic mapping; diagnostic;
KW   detection; treatment; cervical; melanoma; colorectal adenocarcinoma;
KW   Wilm's tumour; retinoblastoma; sarcoma; myosarcoma; lung carcinoma;
KW   leukemia; lymphoma; dysplasia; hyperplasia; endometrium; adrenal;
KW   prostate; ss.
XX
OS   Homo sapiens.
XX
PN   WO[illegible]-A2.
XX
PD   08-JUL-1999.
XX
PF   22-DEC-1998;   98WO-US27610.
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PR   23-DEC-1997;   98US-0[illegible].
PR   [illegible];   [illegible].
PR   03-APR-1998;   98US-0080664.
PR   [illegible];   [illegible].
PR   27-OCT-1998;   98US-0105877.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Crkvenjakov R,  Dickson M,  Drmanac R,  Drmanac S;
PI   Escobedo J,  Garcia PD,  Garcia V,  Giese K,  Innis MA;
PI   Jones LW,  Kassam A,  Kennedy GC,  Kita D,  Labat I;
PI   Lamson G,  Leshkowitz D,  Pot D,  Randazzo F,  Reinhard C;
PI   Stache-Crain B,  Sudduth Klinger J,  Williams LT;
XX
DR   WPI; 1999-[illegible]/36.
XX
PT   New isolated human polynucleotides
XX
PS   Claim 1; Page 121; [illegible]pp; English.
XX
CC   This invention describes novel isolated human polynucleotides obtained
CC   by screening for differential expression in colon cancer, breast cancer
CC   and lung cancer cell lines. The polynucleotides of the invention are
CC   represented in AAX[illegible] X6[illegible] and encode polypeptides of protein
CC   families selected from 4 transmembrane segments integral membrane
CC   proteins, 7 transmembrane receptors, ATPases associated with various
CC   cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of
CC   transcription factors, G-protein alpha subunit, phorbolesters or
CC   diacylglycerol binding proteins, protein kinase, protein phosphatase 2C,
CC   protein tyrosine phosphatase, trypsin, wnt family of developmental
CC   signalling proteins and WW/rsp5/WWP domain containing proteins. The
CC   encoded polypeptides also have a functional domain selected from Ank
CC   repeat, basic region plus leucine zipper transcription factors,
CC   bromodomain, EF hand, SH3 domain, WD domain/G-beta repeats, zinc finger
CC   (C2H2 type), zinc finger (CCHC class), and zinc binding metalloprotease
CC   domain. The polynucleotides encode polypeptides with similarity to known
CC   protein families and are predicted to have similar properties. The novel
CC   polynucleotides can be used to develop products for use as therapeutic
CC   agents and in forensics, genetic analysis, mapping and diagnostic
CC   applications. In particular, the product can be used for the detection
CC   and management of cancers. They can be used for treating e.g. cervical
CC   cancers, melanomas, colorectal adenocarcinomas, Wilm's tumour, sarcomas,
CC   retinoblastoma, myosarcomas, lung carcinomas, leukemias, such as chronic
CC   myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and
CC   myeloid leukemia, and lymphomas such as histiocytic lymphoma, and; for
CC   hereditary ectodermal dysplasia, congenital alveolar dysplasia,
CC   epithelial dysplasia of the cervix, fibrous dysplasia of bone, and
CC   mammary dysplasia, hyperplasias, e.g. endometrial, adrenal, breast,
CC   prostate or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of
CC   the skin.
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SQ   Sequence 750 BP; 170 A; 203 C; 182 G; 180 T; [illegible] other;

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Qy       1200 [illegible]
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Db        418 [illegible]

Qy       [illegible]
Db        478 [illegible]

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DT   2[illegible]-MAR-2002  (first entry)
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DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 28120.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200[illegible]942 A2.
XX
PD   27-SEP-2001.
XX
PF   2[illegible]-MAR-2001; 2001WO-US0[illegible].
XX
PR   2[illegible]-MAR-2000; 2000US-[illegible]7P.
PR   1[illegible]-JUL-2000; 2000US-0614150.
XX
PA   (GLKE-) PE [illegible] NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-6[illegible]660/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and [illegible]
PT   interactions
XX
PS   Claim 1; SEQ ID NO 28120; 2[illegible]pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL1617[illegible]-ABL30[illegible]), expressed DNA
CC   sequences (ABL0[illegible]-ABL16175) and the encoded proteins
CC   (ABB577[illegible]-ABB[illegible]).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at [illegible]/published_pct_sequences.
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Search completed: February 2[illegible], 2[illegible]
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        Copyright (c) 1993 - 2003 Compugen Ltd.

 OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters:      882724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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     Pred. No. is the number of results predicted by chance to have a
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     and is derived by analysis of the total score distribution.

                              SUMMARIES
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c  2     49.8    3.6   6924  4  US-09-299-141-9             Sequence 9, Appli
c  3     49.8    3.6   6924  4  US-09-299-141-10            Sequence 10, Appl
c  4     49.8    3.6   6924  4  US-09-299-141-11            Sequence 11, Appl
c  5     48.2    3.5   1491  4  US-09-082-032-3             Sequence 3, Appli
c  6     48.2    3.5   1817  4  US-09-288-292A-45           Sequence 45, Appl
   7       47    3.4    349  4  US-09-198-116C-94           Sequence 94, Appl
c  8     46.4    3.4    724  [illegible] US-08-415-615-11 Sequence 11, Appl
c  9     45.2    3.3    645  4  US-09-535-008-30            Sequence 30, Appl
  10     43.6    3.2 152331  3  US-09-128-155-17            Sequence 17, Appl
c 11     43.4    3.1   1488  4  US-09-096-776B-3            Sequence 3, Appli
c 12     43.4    3.1   2534  4  US-09-096-776B-1            Sequence 1, Appli
c 13     43.2    3.1   3546  3  US-09-083-151-1             Sequence 1, Appli
c 14     43.2    3.1   3546  4  US-09-083-352-1             Sequence 1, Appli
c 15       43    3.1   1028  4  US-08-118-200-1             Sequence 1, Appli
c 16       43    3.1   1028  4  US-08-455-745-1             Sequence 1, Appli
  17     42.8    3.1   8460  1  US-08-469-005A-3            Sequence 3, Appli
  18     42.8    3.1   8515  4  US-09-261-067-1             Sequence 1, Appli
c 19     42.4    3.1    320  4  US-09-165-264-7             Sequence 7, Appli
c 20     42.4    3.1    320  4  US-09-165-264-13            Sequence 13, Appl
c 21     42.4    3.0    319  4  US-09-165-264-8             Sequence 8, Appli
  22     41.4    3.0   4252  2  US-08-475-844-4             Sequence 4, Appli
  23     41.4    3.0   4252  5  PCT-US95-08429-4            Sequence 4, Appli
  24     41.2    3.0   1413  4  US-08-984-709A-52           Sequence 52, Appl
  25     41.2    3.0   6453  1  US-08-306-691B-14           Sequence 14, Appl
  26     41.2    3.0   6453  3  US-09-205-658-1             Sequence 10, Appl
  27     41.2    3.0   6453  3  US-09-356-952-3             Sequence 3, Appli
  28     41.2    3.0 [illegible] 1 US-[illegible]A-11       Sequence 11, Appl
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c 30     40.8    3.0   1523  4  US-09-175-716-1             Sequence 1, Appli
c 31     40.4    2.9   3332  4  US-09-423-860-11            Sequence 11, Appl
c 32     40.2    2.9   8438  1  US-07-945-283-1             Sequence 1, Appli
c 33       40    2.9   1413  4  US-09-984-709A-52           Sequence 52, Appl
c 34     39.8    2.9    320  4  US-09-165-264-11            Sequence 11, Appl
c 35     39.6    2.9   7334  1  US-08-232-463-14            Sequence 14, Appl
c 36     39.4    2.9    700  4  US-09-236-097-7             Sequence 7, Appli
c 37     39.4    2.9   2502  1  US-08-[illegible]-7        Sequence 7, Appli
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c 40     39.4    2.9   2502  1  US-08-481-238-7             Sequence 7, Appli
c 41     39.4    2.9   2502  2  US-08-471-666-7             Sequence 7, Appli
c 42     39.4    2.9   2502  2  US-08-484-456-7             Sequence 7, Appli
c 43     39.4    2.9   2502  2  US-08-757-653-7             Sequence 7, Appli
c 44     39.4    2.9   2502  2  US-08-[illegible]-7        Sequence 7, Appli
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                              ALIGNMENTS

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; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: SONG, SIHONG
;  APPLICANT: [illegible]
;  APPLICANT: [illegible], MICHAEL
;  TITLE OF INVENTION: [illegible] GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: 1999-04-23
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 1[illegible]
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 6714
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:[illegible]
;   OTHER INFORMATION: p4[illegible]
US-09-299-141-6

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Db       1532 [illegible] 1473

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Db       1472 C 1472


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; Sequence 9, Application US/09299141
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  Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
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; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
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Db [illegible]


RESULT 4
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; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: 1998-04-24
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;   ORGANISM: Artificial Sequence
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;   OTHER INFORMATION: Description of Artificial Sequence:[illegible]
;   OTHER INFORMATION: [illegible]
US [illegible]

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  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

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Db [illegible]

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; GENERAL INFORMATION:
;     APPLICANT: [illegible]
;     APPLICANT: [illegible], Anita
;     APPLICANT: [illegible]
;       APPLICANT:  Itoh, Susumu
;       APPLICANT:  Afrakhte, Morghan
;       APPLICANT:  Souchelnytskyi, Serhiy
;       APPLICANT:  Brodin, Greger
;       APPLICANT:  Landstrom, Marene
;       APPLICANT:  Heldin, Nils Erik
;       APPLICANT:  Heldin, Carl Henrik
;       APPLICANT:  ten Dijke, Peter
;       TITLE OF INVENTION:  SMAD7 AND USES THEREOF
;       NUMBER OF SEQUENCES:  15
;       CORRESPONDENCE ADDRESS:
;         ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;         STREET:  600 Atlantic Avenue
;         CITY:  Boston
;         STATE:  MA
;         COUNTRY:  U.S.A.
;         ZIP:  02210-2211
;       COMPUTER READABLE FORM:
;         MEDIUM TYPE:  Diskette
;         COMPUTER:  IBM Compatible
;         OPERATING SYSTEM:  DOS
;         SOFTWARE:  FastSEQ for Windows Version 2.0
;       CURRENT APPLICATION DATA:
;         APPLICATION NUMBER:  [illegible]
;         FILING DATE:  20-MAY-1998
;         CLASSIFICATION:
;       PRIOR APPLICATION DATA:
;         APPLICATION NUMBER:  60/047,221
;         FILING DATE:  20-MAY-1997
;         APPLICATION NUMBER:  60/060,465
;         FILING DATE:  30-SEP-1997
;         APPLICATION NUMBER:  60/075,940
;         FILING DATE:  25-FEB-1998
;         APPLICATION NUMBER:  60/077,033
;         FILING DATE:  06-MAR-1998
;       ATTORNEY/AGENT INFORMATION:
;         NAME:  Van Amsterdam, John R.
;         REGISTRATION NUMBER:  40,212
;         REFERENCE/DOCKET NUMBER:  L0461/7032
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE:  617-720-3500
;         TELEFAX:  617-720-2441
;         TELEX:
;     INFORMATION FOR SEQ ID NO:  9:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH:  1491 base pairs
;         TYPE:  nucleic acid
;         STRANDEDNESS:  single
;         TOPOLOGY:  linear
;       MOLECULE TYPE:  cDNA
US-09-082-092-9

  Query Match             3.9%;  Score 48.2;  DB 4;  Length 1491;
  Best Local Similarity   54.1%;  Pred. No. [illegible];
  Matches   98;  Conservative    0;  Mismatches   83;  Indels    0;  Gaps    0;

Qy          5 [illegible] 64
Db         [illegible]2 [illegible] 21[illegible]

Qy         65 [illegible] 124
Db        242 [illegible] 18[illegible]

Qy        125 [illegible] 184
Db        182 [illegible] 12[illegible]

Qy        185 [illegible] 185
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Db        122 [illegible] 122
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RESULT 6
US-09-288-292A 1[illegible]
; Sequence 45, Application US/[illegible]A
; Patent No. [illegible]4
; GENERAL INFORMATION:
;  APPLICANT: Dean A. [illegible]
;  APPLICANT:  Katherine Galvin
;  APPLICANT:  Michael [illegible]
;  APPLICANT:  [illegible] Baszar
;  APPLICANT:  Michael A. Gimbrone, Jr.
;  TITLE OF INVENTION: Compositions and Methods for the Treatment and Diagnosis of
;  TITLE OF INVENTION:  Cardiovascular Disease
;  FILE REFERENCE: [illegible] 14[illegible]
;  CURRENT APPLICATION NUMBER: US/09/288,292A
;  CURRENT FILING DATE:  [illegible]-4-[illegible]
;  PRIOR APPLICATION NUMBER: 08/87[illegible],1[illegible]4
;  PRIOR FILING DATE: 1997-[illegible]
;  PRIOR APPLICATION NUMBER: 08/7[illegible]
;  PRIOR FILING DATE: 1997-02-1[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]/[illegible]1,787
;  PRIOR FILING DATE: 1996-02-1[illegible]
;  PRIOR APPLICATION NUMBER: 08/485,57[illegible]
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: [illegible]/[illegible]36,844
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 4[illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
;   LENGTH: 1617
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-288-292A-45

  Query Match             3.9%;  Score 48.2;  DB 4;  Length 1617;
  Best Local Similarity   54.1%;  Pred. No. [illegible];
  Matches   98;  Conservative    0;  Mismatches   83;  Indels    0;  Gaps    0;

Qy          5 [illegible] 64
Db        456 [illegible]

Qy         65 [illegible]
Db        [illegible]6 [illegible]

Qy        125 [illegible] 184
Db        [illegible]6 [illegible]

Qy        185 [illegible] 185
                |
Db        276 [illegible] 276


RESULT 7
US-09-[illegible]98-[illegible]4
; Sequence 94, Application US/[illegible]
; Patent No. 64[illegible]42[illegible]
; GENERAL INFORMATION:
;  APPLICANT:  Thomashow, Michael
;  APPLICANT:  Stockinger, Eric
;  APPLICANT:  Jaglo-Ottosen, Kirsten
;  APPLICANT:  Gilmour, Sarah
;  APPLICANT:  Zarka, Daniel
;  APPLICANT:  Jiang, Cai Zhong
;  TITLE OF INVENTION:  Plant Having Altered Environmental Stress [illegible]
;  FILE REFERENCE:  [illegible]17.71[illegible] Seq List
;  CURRENT APPLICATION NUMBER: US/[illegible]/1[illegible]
;  CURRENT FILING DATE:  [illegible]
;  PRIOR APPLICATION NUMBER:  US 08/7[illegible],27[illegible]
;  PRIOR FILING DATE:  [illegible]
;  PRIOR APPLICATION NUMBER:  US 09/[illegible]8,2[illegible]
;  PRIOR FILING DATE:  [illegible]
;     PRIOR APPLICATION NUMBER: [illegible]
;     PRIOR FILING DATE: 1998-[illegible]
;     PRIOR APPLICATION NUMBER: [illegible]
;     PRIOR FILING DATE: 1998-[illegible]
;     PRIOR APPLICATION NUMBER: [illegible]
;     PRIOR FILING DATE: 1998-[illegible]
;     PRIOR APPLICATION NUMBER: [illegible]
;     PRIOR FILING DATE: 1998-[illegible]
;     PRIOR APPLICATION NUMBER: [illegible]
;     PRIOR FILING DATE: 1998-[illegible]
;     NUMBER OF SEQ ID NOS: [illegible]
;     SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;    LENGTH: [illegible]
;    TYPE: DNA
;    ORGANISM: [illegible]
;    FEATURE:
;     OTHER INFORMATION: [illegible]
US-[illegible]

  Query Match             [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity   [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]


RESULT 8
US-[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;     APPLICANT: Massague, [illegible]
;     APPLICANT: Lee, Mong-Hong
;     TITLE OF INVENTION: [illegible]
;     TITLE OF INVENTION: p57KIP2, A CYCLIN DEPENDENT KINASE INHIBITOR AND USES [illegible]
;     TITLE OF INVENTION: SAME
;     NUMBER OF SEQUENCES: 15
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Cooper & Dunham
;       STREET: 1185 Avenue of the Americas
;       CITY: New York
;       STATE: New York
;       COUNTRY: United States of America
;       ZIP: [illegible]
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/[illegible]
;       FILING DATE:
;       CLASSIFICATION: 435
;     ATTORNEY/AGENT INFORMATION:
;       NAME: White, John P.
;       REGISTRATION NUMBER: [illegible]
;       REFERENCE/DOCKET NUMBER: [illegible]
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (212) 278-0400
;       TELEFAX: (212) [illegible]
;  INFORMATION FOR SEQ ID NO: [illegible]
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: [illegible] base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     HYPOTHETICAL: NO
;     ANTI-SENSE: NO
US-[illegible]

  Query Match             [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity   [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]


RESULT 9
US-[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: Wong, Alexander K.C.
;  APPLICANT: Tavtigian, Sean V.
;  APPLICANT: Teng, David H.-F.
;  TITLE OF INVENTION: BRG1 IS A TUMOR SUPPRESSOR THAT IS MUTATED IN PROSTATE
;  TITLE OF INVENTION: AND OTHER CANCER TYPES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: 2000-03-2[illegible]
;  EARLIER APPLICATION NUMBER: US 60/12[illegible]
;  EARLIER FILING DATE: 1999-[illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-[illegible]

  Query Match             [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity   [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]

Db   [illegible]


RESULT 1[illegible]
US-[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. 6117654
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;  TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 10464/052001
;  CURRENT APPLICATION NUMBER: US/09/128,155
;  CURRENT FILING DATE: 1998-08-03
;  EARLIER APPLICATION NUMBER: US 60/091,650
;  EARLIER FILING DATE: 1998-07-02
;  EARLIER APPLICATION NUMBER: US 60/054,646
;  EARLIER FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 152331
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(152331)
;    OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

  Query Match             3.2%;  Score 43.6;  DB 3;  Length 152331;
  Best Local Similarity   51.0%;  Pred. No. 0.64;
  Matches  104;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy          3 GTCGGC[illegible] 62
Db      21997 [illegible] 22056

Qy         63 [illegible] 122
Db      22057 [illegible] 22116

Qy        123 [illegible] 182
Db      22117 [illegible] 22176

Qy        183 [illegible] 204
Db      22177 [illegible] 22198


RESULT 11
US-09-096-776B-3/c
; Sequence 3, Application US/09096776B
; Patent No. 6277994
; GENERAL INFORMATION:
;  APPLICANT:  Miyazono, Kohei
;  APPLICANT:  Kawabata, Masahiro
;  TITLE OF INVENTION:   SMAD6 AND USES THEREOF
;  FILE REFERENCE:   L0461/7038
;  CURRENT APPLICATION NUMBER:  US/09/096,776B
;  CURRENT FILING DATE:  1998-06-12
;  PRIOR APPLICATION NUMBER:   US 60/[illegible]
;  PRIOR FILING DATE:   1997-06-13
;  PRIOR APPLICATION NUMBER:   US 60/053,[illegible]
;  PRIOR FILING DATE:   1997-07-18
;  PRIOR APPLICATION NUMBER:   US 60/066,17[illegible]
;  PRIOR FILING DATE:   1997-11-18
;  NUMBER OF SEQ ID NOS:   10
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1488
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-096-776B-3

  Query Match             3.1%;  Score 43.4;  DB 4;  Length 1488;
  Best Local Similarity   52.5%;  Pred. No. 0.2;
  Matches   95;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;
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Qy          5 [illegible] 64
Db        299 [illegible] 2[illegible]

Qy         65 [illegible] 124
Db        239 [illegible] 1[illegible]

Qy        125 [illegible] 184
Db        179 [illegible] 1[illegible]

Qy        185 C 185

Db        119 C 119


RESULT 12
US-09-096-776B-1/c
; Sequence 1, Application US/09096776B
; Patent No. 6277994
; GENERAL INFORMATION:
;  APPLICANT:  Miyazono, Kohei
;  APPLICANT:  Kawabata, Masahiro
;  TITLE OF INVENTION:   SMAD6 AND USES THEREOF
;  FILE REFERENCE:   L0461/7038
;  CURRENT APPLICATION NUMBER: US/09/096,776B
;  CURRENT FILING DATE:  1998-06-12
;  PRIOR APPLICATION NUMBER:   US 60/049,[illegible]
;  PRIOR FILING DATE:   1997-06-13
;  PRIOR APPLICATION NUMBER:   US 60/[illegible]4
;  PRIOR FILING DATE:   1997-07-18
;  PRIOR APPLICATION NUMBER:   US 60/[illegible]
;  PRIOR FILING DATE:   1997-11-18
;  NUMBER OF SEQ ID NOS:   [illegible]
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 2534
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (751)..(2238)
US-09-096-776B-1

  Query Match             3.1%;  Score 43.4;  DB 4;  Length 2534;
  Best Local Similarity   52.5%;  Pred. No. 0.24;
  Matches   95;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy          5 [illegible] 64
Db       1049 [illegible]

Qy         65 [illegible] 124
Db        989 [illegible]

Qy        125 [illegible] 184
Db        929 [illegible]

Qy        185 C 185

Db        869 C 869


RESULT 13
US-09-083-451-1/c
; Sequence 1, Application US/09083451
; Patent No. 6087107
;  GENERAL INFORMATION:
;    APPLICANT:  Sheffield, Val C.
;       APPLICANT:  Alward, Wallace L.M.
;       APPLICANT:  Stone, Edwin M.
;       APPLICANT:  Nishimura, Darryl
;       APPLICANT:  Patil, Shiva
;       TITLE OF INVENTION:  THERAPEUTIC AND DIAGNOSTIC [illegible]
;       TITLE OF INVENTION:  POTENTIAL HEART DISEASE BASED ON A NOVEL HUMAN
;       TITLE OF INVENTION:  TRANSCRIPTION FACTOR
;       NUMBER OF SEQUENCES:  [illegible]
;       CORRESPONDENCE ADDRESS:
;         ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;         STREET:  One Post Office Square
;         CITY:  Boston
;         STATE:  MA
;         COUNTRY:  USA
;         ZIP:  [illegible]
;       COMPUTER READABLE FORM:
;         MEDIUM TYPE:  Floppy disk
;         COMPUTER:  IBM PC compatible
;         OPERATING SYSTEM:  PC-DOS/MS-DOS
;         SOFTWARE:  PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;         APPLICATION NUMBER:  US/09/083,452
;         FILING DATE:  22-MAY-1998
;         CLASSIFICATION:  514
;       ATTORNEY/AGENT INFORMATION:
;         NAME:  Arnold, Beth E.
;         REGISTRATION NUMBER:  [illegible]
;         REFERENCE/DOCKET NUMBER:  UIA-029.01
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE:  617-832-1000
;         TELEFAX:  617-832-[illegible]
;     INFORMATION FOR SEQ ID NO:  [illegible]:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH:  [illegible] base pairs
;         TYPE:  nucleic acid
;         STRANDEDNESS:  single
;         TOPOLOGY:  linear
;       MOLECULE TYPE:  cDNA
;       FEATURE:
;         NAME/KEY:  CDS
;         LOCATION:  [illegible]
US-09-083-452-[illegible]

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  Matches   [illegible];  Conservative    [illegible];  Mismatches   [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy         88 [illegible]
Db        [illegible]

Qy        148 [illegible]
Db        [illegible]

Qy        208 AA[illegible] 22[illegible]
Db        [illegible]


RESULT 14
US-09-083-452-[illegible]
; Sequence [illegible], Application US/09083452
; Patent No. [illegible]
;   GENERAL INFORMATION:
;       APPLICANT:  Sheffield, Val C.
;       APPLICANT:  Alward, Wallace L.M.
;       APPLICANT:  Stone, Edwin M.
;       APPLICANT:  Nishimura, Darryl
;       APPLICANT:  Patil, Shiva
;       TITLE OF INVENTION:  [illegible] THERAPEUTIC TOOLS AND DIAGNOSTIC [illegible]
;       TITLE OF INVENTION:  BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
;       NUMBER OF SEQUENCES:  [illegible]
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;       CORRESPONDENCE ADDRESS:
;         ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;         STREET:  One Post Office Square
;         CITY:  Boston
;         STATE:  MA
;         COUNTRY:  USA
;         ZIP:  [illegible]
;       COMPUTER READABLE FORM:
;         MEDIUM TYPE:  Floppy disk
;         COMPUTER:  IBM PC compatible
;         OPERATING SYSTEM:  PC-DOS/MS-DOS
;         SOFTWARE:  PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;         APPLICATION NUMBER:  US/09/083,452
;         FILING DATE:  22-MAY-1998
;         CLASSIFICATION:  514
;       ATTORNEY/AGENT INFORMATION:
;         NAME:  Arnold, Beth E.
;         REGISTRATION NUMBER:  [illegible]
;         REFERENCE/DOCKET NUMBER:  UIA-029.01
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE:  617-832-1000
;         TELEFAX:  617-832-[illegible]
;     INFORMATION FOR SEQ ID NO:  [illegible]:
;       SEQUENCE CHARACTERISTICS:
;         LENGTH:  [illegible] base pairs
;         TYPE:  nucleic acid
;         STRANDEDNESS:  single
;         TOPOLOGY:  linear
;       MOLECULE TYPE:  cDNA
;       FEATURE:
;         NAME/KEY:  CDS
;         LOCATION:  4[illegible]
US-09-083-452-[illegible]

  Query Match             [illegible];  Score [illegible];  DB 4;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches   78;  Conservative    0;  Mismatches   [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy         88 [illegible]
Db        468 [illegible]

Qy        148 [illegible]
Db        408 [illegible]

Qy        208 AA[illegible] 22[illegible]
Db        [illegible]


RESULT 15
US-08-118-200-[illegible]
; Sequence [illegible], Application US/08118200
; Patent No. [illegible]
;   GENERAL INFORMATION:
;       APPLICANT:  SUTHERLAND, Grant R
;       APPLICANT:  RICHARDS, Robert I
;       APPLICANT:  SCHLESSINGER, David
;       APPLICANT:  NAGARAJA, Ramaiah
;       APPLICANT:  KREMER, Eric J
;       APPLICANT:  YU, Sui
;       APPLICANT:  BAKER, Elizabeth
;       APPLICANT:  MULLEY, John C
;       APPLICANT:  MANDEL, Jean Louis
;       APPLICANT:  PRITCHARD, Melanie April
;       APPLICANT:  LYNCH, Michael
;       TITLE OF INVENTION:  DNA SEQUENCES RELATED TO ISOLATED
;       TITLE OF INVENTION:  FRAGILE X SYNDROME
;       NUMBER OF SEQUENCES:  [illegible]
;       CORRESPONDENCE ADDRESS:
;         ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;       STREET:  P.O. Box 1404
;       CITY:  Alexandria
;       STATE:  Virginia
;       COUNTRY:  United States
;       ZIP:  22313-1404
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/118,205
;       FILING DATE:  09-SEP-1993
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/802,65
;       FILING DATE:  05-DEC-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/672,2[illegible]2
;       FILING DATE:  20-MAR-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/638,518
;       FILING DATE:  04 JAN 1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/[illegible],[illegible]17
;       FILING DATE:  2[illegible]-DEC-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Crane-Feury, Sharon E
;       REGISTRATION NUMBER:  36,113
;       REFERENCE/DOCKET NUMBER:  20160-164
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703) 836-6620
;       TELEFAX:  (703) 836-2021
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1028 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-118-205-1

  Query Match             5.1%;  Score 43;  DB 1;  Length 1028;
  Best Local Similarity   67.4%;  Pred. No. 0.23;
  Matches   97;  Conservative    0;  Mismatches    7 ;  Indels    2;  Gaps    1;

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              [illegible]
Db        373 [illegible] 432

Qy         95 [illegible] 154
              [illegible]
Db        4[illegible] [illegible]

Qy        155 [illegible] 203
              [illegible]
Db        [illegible] [illegible]


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                         GenCore version 5.1.3
              Copyright (c) 1993 - 2003 Compugen Ltd.

 OM nucleic - nucleic search, using sw model

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Title:          US-09-866-987-3
Perfect score:  1380
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Post-processing: Minimum Match 0%
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      Pred. No. is the number of results predicted by chance to have a
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      and is derived by analysis of the total score distribution.

                                  SUMMARIES
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     1      1380   100.0   1380 10  US-09-866-987-3               Sequence 3, Appl
     2  [illegible] [illegible] 547 1[illegible] US-09-867-[illegible]-2968   Sequence 2968, Ap
     3     243.4    17.6   5791 10  US-09-920-800A-1714           Sequence 1714, Ap
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     5        98     7.1    551 10  US-09-867-701-5460            Sequence 5460, Ap
c    6      48.2     3.5   1817 10  US-09-924-417-64              Sequence 64, Appl
     7        47     3.4    349  9  US-09-996-148-94              Sequence 94, Appl
c    8      46.8     3.4  43058 10  US-09-954-456-292             Sequence 292, App
c    9      46.8     3.4  43058 10  US-09-954-456-[illegible]     Sequence [illegible], Ap
c   10      45.8     3.3 [illegible] 10 US-09-880-107-[illegible] Sequence [illegible], Ap
    11      45.4     3.4   3289 10  US-09-925-901-474             Sequence 474, Ap
    12      44.4     3.2   2561  9  US-09-976-740-48              Sequence 48, Appl
    13      44.4     3.2   2561 12  US-10-023-529-48              Sequence 48, App
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c   15      44.2     3.2   4286 10  US-09-809-634A-1              Sequence 1, Appl
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    25        43     3.1  12425  9  US-09-976-740-50              Sequence 50, Appl
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    27        43     3.1  12425 12  US-10-023-528-50              Sequence 50, Appl
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    29      42.2     3.1  42999  9  US-10-125-767-17              Sequence 17, Appl
    30      42.2     3.1  42999  9  US-09-836-911A-17             Sequence 17, Appl
c   31      41.4     3.0  12755  9  US-10-052-593-17              Sequence 17, Appl
c   32      41.4     3.0  12755  9  US-10-052-593-8               Sequence 8, Appl
c   33      41.2     3.0 [illegible] 9 US-10-04[illegible]-717-59 Sequence 59, Appl
c   34        41     3.0 [illegible] 9 US-10-[illegible]-188-6    Sequence 6, Appl
c   35      40.8     3.0   4525  9  US-10-125-158-1               Sequence 1, Appl
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    37      40.4     2.9   1038 10  US-09-917-800A-1479           Sequence 1479, Ap
    38      40.4     2.9   1155 10  US-09-814-777A-21             Sequence 21, Appl
    39      40.4     2.9   1730 10  US-09-814-777A-19             Sequence 19, Appl
    40      40.4     2.9 [illegible] 10 US-09-814-777A-17         Sequence 17, Appl
c   41      40.4     2.9   3342 12  US-10-0[illegible]-864-11     Sequence 11, Appl
c   42      40.2     2.9   1157 10  US-09-778-844-166             Sequence 166, Appl
c   43      40.2     2.9 [illegible] 10 US-09-778-844-167         Sequence 167, Appl
    44        40     2.9   1496 10  US-09-969-708-132             Sequence 132, Appl
    45      39.8     2.9    829 1[illegible] US-09-[illegible]4-878-381 Sequence 381, Appl

                                 ALIGNMENTS

RESULT 1
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; Sequence 3, Application US/09866987
; Patent No. US2002[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: WANG, JENG FEY L.
;  APPLICANT: MARTINEZ, RICARDO
;  APPLICANT: [illegible], DAVID
;  APPLICANT: [illegible], GERARD
;  APPLICANT: [illegible]
;  APPLICANT: CAINELLI, SEAN
;  APPLICANT: HILL, RON
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/866,987
;  CURRENT FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: 60/2[illegible]
;  PRIOR FILING DATE: 2000-05-30
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1380
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: phosphatase nucleotide
US-09-866-987-3

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Db         61 [illegible] 120
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RESULT 2
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; Sequence 2968, Application US/09867701
; Patent No. US2002[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Algate, Paul A.
;  APPLICANT: Jones, Robert
;  APPLICANT: Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: 210121.497
;  CURRENT APPLICATION NUMBER: US/09/867,701
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.
; SEQ ID NO 2968
;   LENGTH: 547
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-867-701-2968

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Db        540 [illegible]GA 547


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US-09-920-506A-1714
; Sequence 1714, Application US/09920506A
; Patent No. US20020[illegible]728A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547
;  CURRENT APPLICATION NUMBER: US/09/920,506A
;  CURRENT FILING DATE:  2001-07-31
;  NUMBER OF SEQ ID NOS: 1789
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1714
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-920-506A-1714

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Qy       1040 [illegible]
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Db       118[illegible] G 118[illegible]


RESULT 4
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; Sequence 1714, Application US/1003[illegible]528
; Patent No. US20[illegible]
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547C1
;  CURRENT APPLICATION NUMBER: US/10/0[illegible]528
;  CURRENT FILING DATE:  2001-12-2[illegible]
;  NUMBER OF SEQ ID NOS: 18[illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
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;   LENGTH: 57[illegible]
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;   ORGANISM: Homo sapiens
US-10-0[illegible]-528-1714

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  Matches  452;  Conservative    0;  Mismatches  326;  Indels    [illegible];  Gaps    [illegible];

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Qy        5[illegible] [illegible]
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Qy        6[illegible] [illegible]
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Qy        7[illegible] [illegible]
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Qy        8[illegible] [illegible]
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Qy        8[illegible] [illegible]
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Qy        9[illegible] [illegible]
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; Patent No. [illegible]
; GENERAL INFORMATION:
;   APPLICANT: [illegible] A.
;   APPLICANT: [illegible], Robert
;   APPLICANT: [illegible]
;   TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;   TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;   FILE REFERENCE: [illegible]
;   CURRENT APPLICATION NUMBER: US/09/866,987
;   CURRENT FILING DATE: [illegible]
;   NUMBER OF SEQ ID NOS: [illegible]
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;   LOCATION: (1)...([illegible])
;   OTHER INFORMATION: [illegible]
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; Sequence [illegible], Application US/09/[illegible]
; Patent No. US200[illegible]
;  GENERAL INFORMATION:
;       APPLICANT: [illegible]
;       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;                           THE TREATMENT AND DIAGNOSIS OF [illegible] VASCULAR
;                           DISEASE
;       NUMBER OF SEQUENCES: [illegible]
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: PENNIE & EDMONDS LLP
;            STREET: 1155 Avenue of the Americas
;            CITY: New York
;            STATE: NY
;            COUNTRY: USA
;            ZIP: [illegible]
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Diskette
;            COMPUTER: IBM Compatible
;            OPERATING SYSTEM: [illegible]
;            SOFTWARE: FastSEQ Version 2.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/[illegible]
;            FILING DATE: [illegible] Aug [illegible]
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/[illegible]
;            FILING DATE: 04 MAR 1998
;            APPLICATION NUMBER: [illegible]
;            FILING DATE: 06 JUN 1997
;            APPLICATION NUMBER: [illegible]
;            FILING DATE: 13 FEB 1997
;            APPLICATION NUMBER: 60/[illegible]
;            FILING DATE: 16 FEB 1996
;            APPLICATION NUMBER: 08/[illegible]
;            FILING DATE: 09 FEB 1996
;            APPLICATION NUMBER: 08/485,[illegible]
;            FILING DATE: 07 JUN 1995
;            APPLICATION NUMBER: 08/386,841
;            FILING DATE: [illegible] FEB 1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: [illegible] A
;            REGISTRATION NUMBER: [illegible]
;            REFERENCE/DOCKET NUMBER: [illegible]
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (212)[illegible]
;            TELEFAX: (212)[illegible]
;            TELEX: [illegible] PENNIE
;    INFORMATION FOR SEQ ID NO: [illegible]:
;         SEQUENCE CHARACTERISTICS:
;            LENGTH: [illegible] base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: both
;            TOPOLOGY: unknown
;         MOLECULE TYPE: DNA
;         SEQUENCE DESCRIPTION: SEQ ID NO: [illegible]:
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  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

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; Sequence 94, Application US/09996140
; Patent No. US20020157136A1
; GENERAL INFORMATION:
;  APPLICANT: Thomashow, Michael
;  APPLICANT:  Stockinger, Eric
;  APPLICANT:  Jaglo-Ottosen, Kirsten
;  APPLICANT:  Gilmour, Sarah
;  APPLICANT:  Zarka, Daniel
;  APPLICANT:  Jiang, Cai-Zhong
;  TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL
;  TITLE OF INVENTION:  STRESS TOLERANCE
;  FILE REFERENCE: MBI0046US
;  CURRENT APPLICATION NUMBER: US/09/996,140
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: 08/706,270
;  PRIOR FILING DATE: 1996-09-04
;  PRIOR APPLICATION NUMBER: 09/018,233
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/017,816
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,235
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/017,575
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,227
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,234
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/198,119
;  PRIOR FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: PCT/US99/01895
;  PRIOR FILING DATE: 1999-01-28
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94
;    LENGTH: 549
;    TYPE: DNA
;    ORGANISM: Zea maize
US-09-996-140-94

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  Best Local Similarity   55.1%;  Pred. No. [illegible];
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RESULT 8
US-09-954-456-292/c
; Sequence 292, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/[illegible],617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,062
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,928
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,[illegible]
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/[illegible]
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/[illegible]
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/[illegible]
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/[illegible]
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/[illegible]
;  PRIOR FILING DATE: 2000-09-27
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;  SOFTWARE: PatentIn version [illegible]
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;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-954-456-292

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Db      25661 [illegible] 25602

Qy        138 [illegible] 187
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Db      25601 [illegible] [illegible]


RESULT 9
US-09-954-456-529/c
; Sequence 529, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/[illegible],617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,062
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,928
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,[illegible]
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/[illegible]
;  PRIOR FILING DATE: [illegible]
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;  NUMBER OF SEQ ID NOS: [illegible]
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;   ORGANISM: Homo sapiens
US-[illegible]

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  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

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; Patent No. US2002014208[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Horne, [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: Gene Expression [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US/[illegible]
;  PRIOR FILING DATE: [illegible]
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;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. [illegible]
US-[illegible]

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Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]
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Qy [illegible]
Db [illegible]


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; Sequence 474, Application US/[illegible]
; Patent No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA106
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]/124,2[illegible]
;  PRIOR FILING DATE: [illegible]
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;   ORGANISM: Homo sapiens
;   FEATURE:
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;   LOCATION: [illegible]
;   OTHER INFORMATION: [illegible]
US-09-925-301-474

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Qy [illegible]
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Qy [illegible]
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Qy [illegible]
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RESULT 12
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; Sequence [illegible], Application US/[illegible]
; Publication No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-09-976-[illegible]-48

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  Best Local Similarity   5[illegible]%;  Pred. No. [illegible];
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Db        620 [illegible] 679

Qy         71 [illegible] 12[illegible]

Db        680 [illegible] 739

Qy        1[illegible] [illegible] 189

Db        740 [illegible] 799

Qy        190 GGACCC 195

Db        800 GCCCGC 805


RESULT 13
US-10-023-529-48
; Sequence 48, Application US/10023529
; Patent No. US20020129888A1
; GENERAL INFORMATION:
;  APPLICANT: Loos, Ann M.
;  APPLICANT:  Loos, Robert S.
;  APPLICANT:  Law, Simon W.
;  APPLICANT:  Arjuna, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION:  PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION:  ATHEROSCLEROSIS
;  FILE REFERENCE: 1-797-014001
;  CURRENT APPLICATION NUMBER: US/10/023,529
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: 09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
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;   LOCATION: (246)...(1895)
US-10-023-529-48

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Qy        190 GGACG[illegible] 195

Db        800 G[illegible] 805


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; Sequence 48, Application US/10023523
; Patent No. US2002[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Loos, Ann M.
;  APPLICANT:  Loos, Robert S.
;  APPLICANT:  Law, Simon W.
;  APPLICANT:  Arjuna, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION:  PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION:  ATHEROSCLEROSIS
;  FILE REFERENCE: 1-797-[illegible]
;  CURRENT APPLICATION NUMBER: US/10/023,523
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: US/09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-10-023-523-48

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Db        620 [illegible]

Qy         71 [illegible]

Db        680 [illegible]

Qy        130 [illegible]

Db        740 [illegible]
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[illegible]


RESULT [illegible]
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; [illegible] APPLICATION [illegible]
; [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible] Andreas [illegible]
;  TITLE OF INVENTION: [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: [illegible]
;   ORGANISM: [illegible]
;   FEATURE:
;   NAME/KEY: [illegible]
;   LOCATION: [illegible]..(1714)
[illegible]

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  Matches [illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]


Search completed: February 24, 2003, [illegible]
Total time [illegible]
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                    GenCore version 5.1.3
          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         February 23, 2003, 19:39:18 ; Search time 2236 Seconds
                                             (without alignments)
                                             9995.426 Million cell updates/sec

Title:          US-09-866-987-3
Perfect score:  1380
Sequence:       1 atgtccgccgqctattcccg..........aataaqcatgaccactaa 1380

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       1[illegible]154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:     [illegible]

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        EST:*
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                2:  em_esthum:*
                3:  em_estin:*
                4:  em_estmu:*
                5:  em_estov:*
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                7:  em_estro:*
                8:  em_htc:*
                9:  gb_est1:*
                10:  gb_est2:*
                11:  gb_htc:*
                12:  gb_est3:*
                13:  gb_est4:*
                14:  gb_est5:*
                15:  em_estfun:*
                16:  em_estom:*
                17:  gb_gss:*
                18:  em_gss_hum:*
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                25:  em_gss_other:*
                26:  em_gss_pro:*
                27:  em_gss_rod:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result              Query
  No.     Score     Match Length DB   ID                              Description
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    1      1027     74.4    1737  11  AK013149                        AK013149 Mus muscu
    2     793.2     57.5     908  13  BI911260                        BI911260 603062811
    3       742     [illegible]  796  10  AW[illegible]               AW[illegible] EST[illegible]
    4     591.6     42.9    1182  11  AK017245                        AK017245 Mus muscu
    5     556.2     40.3     760  13  BI909341                        BI909341 603065418
 c  6       547     39.6     547  14  BM719454                        BM719454 [illegible]
    7   [illegible] 38.8  [illegible] [illegible] AA[illegible]       AA[illegible]
    8     520.6     37.7  [illegible] 12  [illegible]                 [illegible]
    9       498     36.1  [illegible] [illegible] BM[illegible]       BM[illegible] AGENT PRI
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   14     483.4     35.0  [illegible] 13  BI847199                    BI847199 [illegible] MA
   15     478.2     34.7  [illegible] 12  [illegible]                 [illegible]
   16     476.4     34.5  [illegible] [illegible] AW[illegible]       AW[illegible] MA
   17       473     34.3  [illegible]  9  AI[illegible]               AI[illegible]
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   20     451.4     32.7  [illegible] [illegible] [illegible]         [illegible]
   21       447     32.4  [illegible] [illegible] AI[illegible]       AI[illegible]
   22     446.2     32.3  [illegible] 10  [illegible]                 [illegible]
   23       433     31.4  [illegible] 12  [illegible]                 [illegible]
   24       431     31.2  [illegible] 12  [illegible]                 [illegible]
   25     426.4     30.9     798  12  BG754589                        [illegible]
 c 26     425.2     30.8  [illegible] 12  [illegible]                 [illegible]
   27     413.4     30.0  [illegible] [illegible] AW[illegible]       AW[illegible]
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   36     372.2     27.0     607   9  AI236919                        AI236919 EST[illegible]
   37     369.2     26.8  [illegible] 12  BE413984                    BE413984 [illegible]
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   42     356.8     25.9     478   9  AI390672                        AI390672 mt92b09.y
 c 43       356     25.8     626   9  AI[illegible]                 AI[illegible] EST[illegible]
   44       355     25.7  [illegible] 10  AW[illegible]               AW[illegible] MA
   45     351.2     25.4  [illegible] 10  BE486988                    BE486988 [illegible] PA


                              ALIGNMENTS


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LOCUS       AK013149                1737 bp    mRNA    linear   HTC [illegible] JAN [illegible]
DEFINITION  Mus musculus [illegible] days embryo whole body cDNA, RIKEN full-length
            enriched library, clone:[illegible] [illegible] protein phosphatase [illegible]
            containing protein, full insert sequence.
ACCESSION   AK013149
VERSION     AK013149.1  GI:[illegible]
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus ([illegible]) [illegible] days embryo [illegible] cDNA
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            clone:281[illegible]
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. [illegible] (1999)
  MEDLINE   99279253
   PUBMED   1[illegible]
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), [illegible] (2000)
  MEDLINE   20499374
   PUBMED   [illegible]
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REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
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            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
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            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   [illegible]
   PUBMED   [illegible]
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
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            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6822), 685-690 (2001)
  MEDLINE   [illegible]
   PUBMED   [illegible]
REFERENCE   5  (bases 1 to [illegible])
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,H., Arai,A.,
            Arakawa,T., [illegible] Carninci,P.,
            Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
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            Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
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            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa [illegible], Japan ([illegible])
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5'-GAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTTTTVN-3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. cDNA went
            through one round of normalization to Rot=[illegible] and subtraction to
            Rot=[illegible]. Second strand cDNA was prepared with the primer adapter
            of sequence [5'-
            GAGAGAGAGA[illegible]-3'], cDNA was cleaved
            with XhoI and SstI. Cloning sites; 5' end: XhoI; 3' end: SstI.
            Host: [illegible]
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                     /translation="[illegible]
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                     [illegible]"
BASE COUNT     [illegible] a   [illegible] c   [illegible] g   [illegible] t
ORIGIN

  Query Match             [illegible]%;  Score 1027;  DB 11;  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
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Db          2 [illegible]

Qy         [illegible] 148
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Qy        [illegible]
Db        122 [illegible]

Qy        [illegible]
Db        182 [illegible] 241

Qy        [illegible]
Db        242 [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
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Qy        [illegible]
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Qy        [illegible]
Db        [illegible]
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Qy        563 [illegible] 622
Db        542 [illegible] 601

Qy        623 [illegible] 682
Db        602 [illegible] 661

Qy        683 [illegible] 742
Db        662 [illegible] 721

Qy        743 [illegible] 802
Db        722 [illegible] 781

Qy        803 [illegible] 862
Db        782 [illegible] 841

Qy        863 [illegible] 922
Db        842 [illegible] 901

Qy        923 [illegible] 982
Db        902 [illegible] 961

Qy        983 [illegible] 1042
Db        962 [illegible] 1021

Qy       1043 [illegible] 1102
Db       1022 [illegible] 1081

Qy       1103 [illegible] 1162
Db       1082 [illegible] 1141

Qy       1163 [illegible] 1222
Db       1142 [illegible] 1201

Qy       1223 [illegible]
Db       1202 [illegible]

Qy       1283 [illegible]
Db       1262 [illegible]

Qy       1343 [illegible]
Db       1322 [illegible]


RESULT 2
BE911266
LOCUS       BE911266                [illegible] bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible] NIH_MGC_118 Homo sapiens cDNA clone IMAGE:[illegible]
            mRNA sequence.
ACCESSION   BE911266
VERSION     BE911266.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   NIH-MGC [illegible]
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM[illegible]  row: [illegible]  column: [illegible]
            High quality sequence start: [illegible]
            High quality sequence stop: 841.
FEATURES             Location/Qualifiers
     source          [illegible]
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:[illegible]"
                     /clone_lib="NIH_MGC_118"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from [illegible]
                     [illegible] activated [illegible] adult donors. Library is [illegible]
                     and directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.7 kb. Insert size range
                     [illegible] kb. Library is normalized and enriched for
                     full length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code [illegible]. Note:
                     this is a NIH_MGC Library."
BASE COUNT      178 a    [illegible] c    [illegible] g    [illegible] t
ORIGIN

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Qy        203 [illegible]
Db        153 [illegible]

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Db        213 [illegible]

Qy        323 [illegible]
Db        273 [illegible]

Qy        383 [illegible]
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Qy        443 [illegible]
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Qy        563 [illegible]
Db        513 [illegible]

Qy        623 [illegible]
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[illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]


RESULT [illegible]
AW[illegible]
LOCUS       AW[illegible]     [illegible] bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible] MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW[illegible]
VERSION     AW[illegible]  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Hegde,P., Qi,R., Abernathy,K., [illegible], Gaspard,R., [illegible]
            [illegible], Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
  TITLE     Assessment of gene expression patterns in a model of colon tumor
            metastasis using a [illegible] cDNA [illegible]
  JOURNAL   Unpublished (2000)
COMMENT     Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            [illegible]
            [illegible]
            [illegible]
            [illegible]
            [illegible]
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="MAGE resequences, MAGE"
                     /note="Vector: pBluescript_sk[illegible]"
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Qy    545 [illegible]
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Qy    605 [illegible]
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Qy    665 [illegible]
Db    [illegible]

Qy    725 [illegible]
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Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    965 [illegible]
Db    [illegible]

Qy    965 [illegible]
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Qy   1025 [illegible]

Db    781 [illegible]


RESULT [illegible]
AK017245
LOCUS       AK017[illegible]     [illegible] bp    mRNA    linear   HTC [illegible]
DEFINITION  Mus musculus [illegible] days neonate head cDNA, RIKEN full-length enriched
            library, clone:5430400[illegible]:Protein phosphatase 2C containing
            protein, full insert sequence.
ACCESSION   AK017[illegible]
VERSION     AK017[illegible]  GI:[illegible]
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain [illegible]) [illegible] days neonate head cDNA to mRNA,
            clone_lib:RIKEN full-length enriched mouse cDNA library,
            clone:5430400[illegible].
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. [illegible], [illegible]-44 (1999)
  MEDLINE   [illegible]
  PUBMED    [illegible]
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., [illegible]
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., [illegible], Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
    TITLE   RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
    TITLE   Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5  (bases 1 to 1182)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hirozane,K., Hiraoka,T., [illegible]
            [illegible], Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kondo,M., [illegible]
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            [illegible], Ohno,M., Okazaki,Y., [illegible], Quackenbush,J.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., [illegible]
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
    TITLE   Direct Submission
  JOURNAL   Submitted (1? JUL 2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN [illegible]
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
  COMMENT   Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5'-[illegible]-3'], [illegible]
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap trapper. cDNA went
            through one round of normalization to Rot = [illegible] and subtraction to
            Rot = 100.0. Second strand cDNA was prepared with the primer
            adapter of sequence [5'-
            [illegible]-3']. cDNA was cleaved
            with BamHI and XhoI. Vector: a modified pBluescript [illegible], after
            bulk excision from lambda FLC I. Cloning sites: 5' end: [illegible]; 3'
            end: BamHI. Host: DH10B.
FEATURES             Location/Qualifiers
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                     /strain="C57BL/6J"
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                     /db_xref="MGD:MGI:1894715"
                     /db_xref="taxon:10090"
                     /clone="[illegible]"
                     /tissue_type="[illegible]"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="[illegible] days neonate"
     CDS             <1..766
                     /note="Protein phosphatase 2C containing protein
                     [illegible]
                     putative"
                     /codon_start=2
                     /protein_id="BAB[illegible]"
                     /db_xref="GI:[illegible]"
                     /db_xref="MGD:MGI:[illegible]"
                     /translation="[illegible]
                     [illegible]
                     [illegible]
                     [illegible]
                     [illegible]VSVFVIFLHSQAQEGSCH"
     polyA_signal    1161..1166
                     /note="putative"
     polyA_site      1182
                     /note="putative"
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  Best Local Similarity   8?.?%;  Pred. No. [illegible];
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Db          1 [illegible]

Qy        678 [illegible]
Db         [illegible]

Qy        7?8 [illegible]
Db        [illegible]

Qy        7?8 [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        301 [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        421 [illegible]
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[illegible]
Db        [illegible]

Qy     1158 [illegible] 1217
            [illegible]
Db      [illegible]

Qy     [illegible] 1277
            [illegible]
Db      [illegible]

Qy     [illegible] 1337
            [illegible]
Db      [illegible]

Qy     [illegible] 1386
            [illegible]
Db      [illegible] 766

RESULT [illegible]
[illegible]
LOCUS       [illegible]          [illegible] bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible] NIH_MGC_119 Homo sapiens cDNA clone IMAGE:[illegible] 5',
            mRNA sequence.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 766)
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished ([illegible])
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM[illegible] row: [illegible] column: [illegible]
            High quality sequence stop: [illegible].
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_119"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source: leukocytes from anonymous pool of
                     non-activated adult donors. Library is oligo-dT primed
                     and directionally cloned (EcoRV site is destroyed upon
                     ligation). Average insert size 1.7 kb, insert size range
                     [illegible] kb. Library is normalized and enriched for
                     full length clones and was constructed by Life Tech
                     (Invitrogen). Research Genetics tracking code [illegible]. Note:
                     this is a NIH_MGC Library."
BASE COUNT      [illegible] a     [illegible] c     [illegible] g     [illegible] t
ORIGIN

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  Matches [illegible];  Conservative    [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

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Db       61 [illegible] 119

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Db      120 [illegible]

Qy      960 [illegible]
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Qy     1028 [illegible]
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Db      240 [illegible]

Qy     1088 [illegible]
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Db      [illegible]

Qy     1147 [illegible]
            [illegible]
Db      [illegible] 419

Qy     [illegible]
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Db      420 [illegible]

Qy     1267 [illegible]
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Qy     1327 [illegible]
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RESULT [illegible]
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LOCUS       BM[illegible]          [illegible] bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible] Homo sapiens cDNA clone
            [illegible], mRNA sequence.
ACCESSION   BM[illegible]
VERSION     BM[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 584)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: [illegible]
            Fax: [illegible]
            Email: msoares@blue.weeg.uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
            cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
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                     /tissue_type "fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     Choroid"
                     /dev_stage="fetal and adult"
                     /lab_host "DH10B (Life Technologies) (T1 phage resistant)"
                     /note "organ: eye; Vector: pT7T3 Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EJ1 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double-
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3 Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tags for this library are: fetal eyes, AGAATCAAGA
                     ; lens, CGATTAGGGA; eye anterior segment, [illegible];
                     optic nerve, CCATTAAGTG; retina, [illegible]; Retina Foveal and
                     Macular, GTCC; RPE and Choroid, ACCTA. This library was
                     created for the program, Gene Discovery in the Visual
                     System, supported by National Eye Institute (NEI)."
BASE COUNT      117 a    179 c    134 g    117 t
ORIGIN

  Query Match             39.6%;  Score 547;  DB 14;  Length 547;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-[illegible];
  Matches  547;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        672 [illegible] 7[illegible]
              [illegible]
Db        547 [illegible]

Qy        732 TGA[illegible] 791
              [illegible]
Db        487 [illegible] 42[illegible]

Qy        792 [illegible] 851
              [illegible]
Db        427 GCTGGGCTTTGGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCGACTGGAGTTCCCTCG 368

Qy        852 [illegible] 911
              [illegible]
Db        367 [illegible]

Qy        912 [illegible] 971
              [illegible]
Db        307 [illegible] 248

Qy        972 [illegible]
              [illegible]
Db        247 TA[illegible]AGG[illegible]TCGGTTACTAGGAACACTGGCTGT[illegible]TGGGAGACTATCAGCT 188

Qy       1032 CAGAG[illegible] 1091
              [illegible]
Db        187 CAGA[illegible] 128

Qy       1092 [illegible] 1151
              [illegible]
Db        127 [illegible]

Qy       1152 [illegible] 1211
              [illegible]
Db         67 [illegible]GGATGTATGTGTCAAGGAGCAGGTGGCATG[illegible]GGAG[illegible] 8

Qy       1212 TGGAAT 1218
              [illegible]
Db          7 [illegible]GGAA[illegible] 1


RESULT 7
AA292266
LOCUS       AA292266                 547 bp    mRNA    linear   EST [illegible]-APR-1997
DEFINITION  zt50f[illegible] Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGE:[illegible] 5' similar to SW:P2[illegible] ARATH P4[illegible] PROTEIN PHOSPHATASE
            2C [illegible], mRNA sequence.
ACCESSION   AA292266
VERSION     AA292266.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 547)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
            ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
            ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
            Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
            Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO [illegible]
            Tel: 314 286 [illegible]
            Fax: 314 286 [illegible]
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1457   Std Error: 0.00
            Seq primer: [illegible] from Amersham
            High quality sequence stop: 4[illegible].
FEATURES             Location/Qualifiers
     source          1..547
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "IMAGE:[illegible]"
                     /clone_lib "Soares ovary tumor NbHOT"
                     /sex "female"
                     /tissue_type "ovarian tumor"
                     /lab_host "DH10B (ampicillin resistant)"
                     /note "organ: ovary; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: EcoRI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     [illegible]GCGGCCGCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to EcoRI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and EcoRI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo."
BASE COUNT      12[illegible] a    1[illegible] c    17[illegible] g    118 t
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length 547;
  Best Local Similarity   [illegible];  Pred. No. 1.1e-111;
  Matches  547;  Conservative    0;  Mismatches    0;  Indels    [illegible];  Gaps    1;

Qy        792 [illegible]
              [illegible]
Db          1 [illegible]

Qy        852 [illegible]
              [illegible]
Db         61 [illegible] 12[illegible]

Qy        912 [illegible]
              [illegible]
Db        121 [illegible]
```

```
Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]

Db     [illegible]


RESULT [illegible]
[illegible]
LOCUS       [illegible]               bp    cDNA    linear   EST
DEFINITION  [illegible] NIA Mouse [illegible]K cDNA [illegible] Mus musculus cDNA clone
            [illegible] 5', mRNA sequence.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Kargul,G.J., [illegible], Qian,Y., Lim,M.K., [illegible],S.A., Tanaka
            [illegible], Carter,M.G. and Ko,M.S.H.
  TITLE     Verification and initial annotation of NIA mouse [illegible]K cDNA [illegible]
  JOURNAL   Unpublished ([illegible])
COMMENT     Other ESTs: [illegible]
            Contact: George J. Kargul
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            [illegible] Eastern Avenue, Suite [illegible], Baltimore, MD 21224, USA
            [illegible]
            This clone set has been freely distributed to the community. Please
            visit http://lgsun.grc.nia.nih.gov/cDNA/[illegible] for details.
            [illegible]
            Seq primer: [illegible]
            High quality sequence stop: [illegible]
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="Mus musculus"
                     /strain="[illegible]"
                     /db_xref="taxon:[illegible]"
                     /db_xref="[illegible]"
                     /clone="[illegible]"
                     /clone_lib="NIA Mouse [illegible]K cDNA Clone Set"
                     /sex="[illegible] arrayed from a variety of cDNA libraries"
                     /dev_stage="Clones arrayed from a variety of cDNA
                     libraries"
                     /lab_host="[illegible]"
                     /note="Vector: pSPORT1; [illegible] This
                     clone is among a rearrayed set of 15,247 clones from 11
                     [illegible] cDNA libraries (including preimplantation stage
                     embryos from unfertilized egg to blastocyst, embryonic
                     part of E7.5 embryos, extraembryonic part of E7.5 embryos
                     , and E12.5 female mesonephros/gonad) and one newborn
                     [illegible] cDNA library. Average insert size 1.5 kb. All
                     source libraries are cloned unidirectionally with [illegible](dT
                     ) Not primers. References include: (1) Genome-wide
                     expression profiling of mid-gestation placenta and embryo
                     using a 15,000 mouse developmental cDNA microarray [illegible]
                     Proc. Natl. Acad. Sci. U.S.A. 97: 9127-9132; (2)
                     Large-scale cDNA analysis reveals phased gene expression
                     patterns during preimplantation mouse development. [illegible]
                     Development. 127: 1737-1749; (3) Genome-wide mapping of
                     unselected transcripts from extraembryonic tissue of
                     [illegible] mouse embryos reveals enrichment in the [illegible]
                     and under-representation on the X chromosome. [illegible] Hum
                     Mol Genet [illegible]"
BASE COUNT  [illegible]
ORIGIN

  Query Match             [illegible]  Score [illegible]  DB [illegible]  Length [illegible]
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]


RESULT 9
[illegible]
LOCUS       [illegible]               bp    mRNA    linear   EST
DEFINITION  AGENCOURT [illegible] NIH_MGC_[illegible] Homo sapiens cDNA clone IMAGE:[illegible]
```

```
            5', mRNA sequence.
ACCESSION   BM563697
VERSION     BM563697.1  GI:18810842
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 997)
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1916  row: l  column: 12
            High quality sequence stop: 697.
FEATURES             Location/Qualifiers
     source          1..997
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "IMAGE:5441819"
                     /clone_lib "NIH_MGC_98"
                     /tissue_type "astrocytoma grade IV, cell line"
                     /lab_host "DH10B (phage resistant)"
                     /note "Organ: brain; Vector: pOT87; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed by Lina Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      245 a    274 c    271 g    207 t
ORIGIN

  Query Match             36.1%;  Score 498;  DB 13;  Length 997;
  Best Local Similarity   100.0%;  Pred. No. [illegible];
  Matches  498;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        883 [illegible] 942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTTTTGTTTAGCCATCAGCACATGAGTGGCTGGAGCTACAAACGTGTGGAGAAATGGGAT 60

Qy        943 [illegible] 1002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 [illegible] 120

Qy       1003 [illegible] 1062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 [illegible] 180

Qy       1063 [illegible] 1122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 [illegible] 240

Qy       1123 [illegible]
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 [illegible]

Qy       1183 [illegible]
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 [illegible]

Qy       1243 [illegible]
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 [illegible]
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Qy       1303 [illegible]
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 [illegible] 480

Qy       1363 GAGAGAGTGACTACTGA 1380
              ||||||||||||||||||
Db        481 GAGAGAGTGACTACTGA 498


RESULT 15
BM563742
LOCUS       BM563742                [illegible] bp    mRNA    linear   EST [illegible]
DEFINITION  AGENT [illegible] NIH_MGC_98 Homo sapiens cDNA clone IMAGE:[illegible]
            5', mRNA sequence.
ACCESSION   BM563742
VERSION     BM563742.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1916  row: m  column: 14
            High quality sequence stop: [illegible].
FEATURES             Location/Qualifiers
     source          1..1018
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "IMAGE:[illegible]"
                     /clone_lib "NIH_MGC_98"
                     /tissue_type "astrocytoma grade IV, cell line"
                     /lab_host "DH10B (phage resistant)"
                     /note "Organ: brain; Vector: pOT87; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed by Lina Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      [illegible] a    [illegible] c    [illegible] g    [illegible] t
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB 13;  Length [illegible];
  Best Local Similarity   100.0%;  Pred. No. [illegible];
  Matches  [illegible];  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        883 [illegible]
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 [illegible]

Qy        943 [illegible]
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 [illegible]

Qy       1003 [illegible]
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 [illegible]

Qy       1063 [illegible]
```

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[illegible]

RESULT 11
AW[illegible]
LOCUS       AW[illegible]         [illegible] bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible] NMIF Mus musculus cDNA clone IMAGE:[illegible]
            similar to [illegible] mRNA
            sequence.
ACCESSION   AW[illegible]
VERSION     AW[illegible]  GI:[illegible]
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   NIH-MGC [illegible]
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40RP from Gibco
            High quality sequence stop: [illegible]
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="Mus musculus"
                     /strain="[illegible]"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:[illegible]"
                     /clone_lib="[illegible] NMIF"
                     /sex="male"
                     /dev_stage="newborn"
                     /lab_host="[illegible]"
                     /note="Organ: [illegible] Vector: pT7T3D [illegible]
                     Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed
                     with a Not I - oligo(dT) primer [illegible]
                     [illegible]
                     3'], double-stranded cDNA was [illegible]
                     (Pharmacia), digested with Not I and cloned into the Not
                     I and Eco RI sites of the modified pT7T3 vector. Library
                     is normalized and was constructed and donated by Bento
                     Soares and M.Fatima Bonaldo (University of Iowa) and R.
                     Hardisty, A. Varela-Carver, D. Mburu, and S.D.M. Brown (MRC
                     UK Mouse Genome Centre and Mammalian Genetics Unit,
                     Harwell, UK)."
BASE COUNT  [illegible]
ORIGIN
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```
  Query Match            [illegible]
  Best Local Similarity  [illegible]
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

[illegible]
```

```
RESULT 12
BF[illegible]
LOCUS       BF[illegible]         [illegible] bp    mRNA    linear   EST [illegible]
DEFINITION  7k61h07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:[illegible]
            similar to [illegible] KIAA[illegible] PROTEIN ;, mRNA sequence.
ACCESSION   BF[illegible]
VERSION     BF[illegible]  GI:10881[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   NCI-CGAP [illegible]
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            R. Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequenced by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL: send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 467.
FEATURES             Location/Qualifiers
     source          1..494
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone="IMAGE:3480069"
                     /clone_lib "NCI_CGAP_GC6"
                     /tissue_type "pooled germ cell tumors"
                     /lab_host "DH10B"
                     /note "Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site 2: EcoRI; Plasmid DNA
                     from the normalized library NCI CGAP_GC4 was prepared, and
                     ss circles were made in vitro. Following HAP purification
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (clone ids
                     1257096-1258651, 1469064-1470883, and 1475592-147674).
                     Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT      [illegible] a    [illegible] c    153 g    [illegible] t     1 others
ORIGIN

  Query Match             65.7%;  Score 4[illegible];  DB 12;  Length 494;
  Best Local Similarity   99.8%;  Pred. No. 6.7e-102;
  Matches  4[illegible];  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         75 [illegible] 134
Db          1 TCCCAGCCCCGTGCCCTACCGACGGCCCCGCTTCCTTCGGCGGCTCCAGCTCCAGCCCCGG 60

Qy        135 [illegible] 194
Db         61 [illegible] 120

Qy        195 [illegible] 254
Db        121 [illegible] 180

Qy        255 [illegible] 314
Db        181 [illegible] 240

Qy        315 [illegible] 374
Db        241 AGAGTGGCTGACCCTGGCCCAGAGGAGTTCCTGACAGTCTATTACTGGGTACTGTTGGA 300

Qy        375 TGGGCAGGGCGGTCCTGCAGCAGCCATCTTGGCTGGCAACACCCTGCACTCCTGCTTGCCT 434
Db        301 TGGGCAGGGCGGTCCTGCAGCAGCCATCTTGGCTGGCAACACCCTGCACTCCTGCTTGCCT 360

Qy        435 [illegible] 494
Db        361 [illegible] 420

Qy        495 [illegible] 554
Db        421 [illegible] 480

Qy        555 AGACTTGGTGATCG 568
Db        481 AGACTTGGTGATCG 494


RESULT 13
BI344088
LOCUS       BI344088                 597 bp    mRNA    linear   EST [illegible] 2001
DEFINITION  472441 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BI344088
VERSION     BI344088.1  GI:15[illegible]
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 597)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4[illegible]
            Fax: 402 762 4[illegible]
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and quality trimmed with phred
            v0.980904.e. Vector identified by cross_match with the minscore 20
            and minmatch 12 options.
            PCR PRimers
            FORWARD: [illegible]
            BACKWARD: [illegible]
            Plate: 117  row: B  column: 22
            Seq primer: ATTTAGGTGACACTATAT.
FEATURES             Location/Qualifiers
     source          1..597
                     /organism "Sus scrofa"
                     /db_xref "taxon:9823"
                     /clone_lib "MARC 2PIG"
                     /tissue_type "pooled"
                     /lab_host "DH10B"
                     /note "Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from testis, ovary,
                     endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT      114 a    [illegible] c    [illegible] g    [illegible] t
ORIGIN

  Query Match             [illegible]%;  Score [illegible];  DB 15;  Length 597;
  Best Local Similarity   89.9%;  Pred. No. 7.2e-101;
  Matches  537;  Conservative    0;  Mismatches   54;  Indels    [illegible];  Gaps    [illegible];

Qy        237 [illegible] 296
Db          1 [illegible] 60

Qy        297 TGAGTTTGGGGCTGAAT----AAGATT[illegible] 350
Db         61 [illegible] 120

Qy        351 [illegible] 410
Db        121 AGGTCATTATTGGGCACTGTTTGATGGGCATGGGGTCCAGCTGAGCTATCCTGGTT[illegible] 180

Qy        411 CAACACCCT[illegible] 470
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DEFINITION  [illegible] MARC [illegible] Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE [illegible], USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and QC trimmed with phred
            [illegible]. Vector identified by cross match with the [illegible]
            and minmatch 12 options.
            PCR PRIMERS
            FORWARD: [illegible]
            BACKWARD: [illegible]
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LOCUS       BF415112                   [illegible] bp    mRNA    linear   EST [illegible]
DEFINITION  UI-R-BJ2-bou-h-04-0-UI.s1 UI-R-BJ2 Rattus norvegicus cDNA clone
            UI-R-BJ2-bou-h-04-0-UI 3', mRNA sequence.
ACCESSION   BF415112
VERSION     BF415112.1  GI:11403101
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   [illegible] and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), [illegible] (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares MB
            [illegible] and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA [illegible] USA
            Tel: [illegible]
            Fax: [illegible]
            Email: [illegible]
            [illegible] not found. Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab [illegible] clones will be available [illegible]
            Research Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=N.
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                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
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                     tissues: heart, atrium at [illegible] dpc, ventricle at [illegible]
                     atrium at [illegible] dpc, ventricle at [illegible] dpc, ventricle at [illegible]
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                    dpc, AV canal at 15 dpc.  For a detailed description of
                    the library from which this clone was derived, please
                    visit our web site at [illegible]. The
                    subtraction has been previously described in (Bonaldo,
                    Lennon and Soares, Genome Research 6:791-806, 1996)
                    TAG_SEQ None found"
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Qy        [illegible] [illegible] [illegible]

Db        [illegible] [illegible] 242

Qy        736 [illegible] 795

Db        [illegible] [illegible] [illegible]

Qy        796 [illegible] 855

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Qy        [illegible] [illegible] [illegible]

Db        [illegible] [illegible] 422

Qy        [illegible] [illegible] [illegible]

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Qy        [illegible] [illegible] [illegible]

Db        [illegible] [illegible] 542

Qy       1036 [illegible] 1082

Db        [illegible] [illegible] 584

Search completed: February 24, 2003, [illegible]
Job time : [illegible] secs
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                    GenCore version 5.1.3
            Copyright (c) 1993 - 2003 Compugen Ltd.

 OM nucleic - nucleic search, using sw model

Run on:          February 24, 2003, [illegible] ; Search time [illegible] Seconds
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Title:           US-09-866-987-3
Perfect score:   1386
Sequence:        1 atgtcccgccgactgattcc..........aaaaagcgatgacccactgt 1386

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters:        4108280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        GenEmbl:*
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                 2:   gb_htg:*
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                 26:   em_ro:*
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                 39:   em_htgo_hum:*
                 40:   em_htgo_mus:*
                 41:   em_htgo_other:*

   Pred. No. is the number of results predicted by chance to have a
   score greater than or equal to the score of the result being printed,
   and is derived by analysis of the total score distribution.

                               SUMMARIES
                  %
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    2    1365    98.5   1887  6  AX20[illegible]              AX20[illegible] Sequence
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    4    1049    76.0   2134  9  HSM80[illegible]792           AL832404 Homo sapi
    5  1014.4  [illegible] 24[illegible] 9 AK[illegible]     AK[illegible] Homo sapi
    6     783    56.7   1825  9  BC000044                     BC000044 Homo sapi
    7   281.8    20.4   1687  9  AK[illegible]                AK[illegible] Homo sapi
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c  32    68.6     5.0 125020  9  AF425515                     AF425515 Homo sapi
   33    66.2     4.8 125[illegible] 9 AF42[illegible]        AF42[illegible] Homo sapi
c  34    64.8     4.7 157[illegible] 2 AC115[illegible]       AC115[illegible] Rattus no
c  35    62.6     4.5  44686  3  AF043695                     AF043695 Caenorhab
c  36    61.[illegible] 4.4 [illegible] 2 AC128114             AC128114 Rattus no
   37    58.6     4.2 141747  2  AC129004                     AC129004 Rattus no
c  38    58.2     4.2 12[illegible] 2 AC127[illegible]8       AC127[illegible] Rattus no
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                               ALIGNMENTS

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DEFINITION  Sequence [illegible] from Patent WO[illegible].
ACCESSION   AX352514
VERSION     AX352514.1  GI:[illegible]
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Flanagan,[illegible], Wright,[illegible], [illegible], Mandal,[illegible], [illegible]
            Martinez,R., [illegible] and Flanagan,P.
  TITLE     Mammalian protein phosphatases
  JOURNAL   Patent: WO [illegible]-A [illegible]
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            [illegible] Inc. (US)
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DEFINITION  Sequence [illegible] from Patent W[illegible].
ACCESSION   AX[illegible]
VERSION     AX[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Bandman,O., Tang,Y.T., Azimzai,Y., Yue,H., Baughn,M.R.,
            [illegible]
            [illegible]
  TITLE     Phosphatases
  JOURNAL   Patent: W[illegible]
            Incyte Genomics, Inc. (US)
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Qy        301 TTTGGGGCTGAAGAAGA[illegible] 360
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Qy        361 [illegible] 420
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Qy        421 [illegible] 480
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Db        661 GCTGTGTCCCTGCAGGGAAAG[illegible] 720

Qy        721 [illegible] 780
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Qy        781 [illegible] 840
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Qy        841 [illegible] 900
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Qy        901 [illegible] 960
Db        901 [illegible] 960

Qy        961 [illegible] 1020
Db        961 [illegible] 1020

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Qy       1201 [illegible] 1259
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Qy       1320 [illegible] 1379
Db       1321 [illegible] 1380

Qy       1380 A 1380
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Db       1381 A 1381


RESULT 3
AK096681
LOCUS       AK096681                2121 bp    mRNA    linear   PRI [illegible]
DEFINITION  Homo sapiens cDNA FLJ[illegible] fis, clone PEBLM2[illegible], weakly similar
            to PROTEIN PHOSPHATASE 2C [illegible] (EC 3.1.3.16).
ACCESSION   AK096681
VERSION     AK096681.1  GI:21756[illegible]
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens peripheral blood mononuclear cells (HPBMC [illegible]) cDNA to
            mRNA, clone_lib:PEBLM2 clone:PEBLM2005282.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   [illegible]
            Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
            Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
            Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
            Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
            Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B.,
            Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and
            Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2121)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) Takao Isogai, FLJ Project(HRI Team); [illegible]
            Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-[illegible], Fax:81-438-52-[illegible])
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            [illegible] cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            [illegible]); 5' & 3' end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
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Qy   1359 [illegible]AAGAGA[illegible]ACTGA 1380
Db   1319 [illegible]

RESULT 4
HSM803752
LOCUS       HSM[illegible]   2154 bp    mRNA    linear   [illegible]
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686N2219 (from clone DKFZp686N2219).
ACCESSION   AL[illegible]
VERSION     AL[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2154)
  AUTHORS   [illegible]
  TITLE     Direct Submission
  JOURNAL   Submitted [illegible] Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by DKFZ (German Cancer Research Center,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp686N2219) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin, Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://[illegible]
FEATURES             Location/Qualifiers
     source          1..2154
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686N2219"
                     /tissue_type="cDNA [illegible]"
                     /clone_lib="686 (synonym: hlcc3). Vector pSport1. Site host
                     [illegible] sites SfiIA + SfiIB"
                     /dev_stage="[illegible]"
     polyA_signal    2084..2089
     polyA_site      [illegible]
BASE COUNT     [illegible] a   [illegible] c   [illegible] g   [illegible] t
ORIGIN

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length 2154;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
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Db        128 [illegible]AGATGTGAGTTTGGGGCTGAAGAAGACTGGCTGA[illegible]TGTGCCCAGAGGACTT 187

Qy        345 CCTGACAGG[illegible]CATTACTGGGCACTGTTCGATGGGCACGGCGGTCCTGCAGCAGCCATCTT 404

Db        188 GCTGACAGGCCATTACTGGGCACTGTTCGATGGGCACGGCGGTCCTGCAGCAGCCATCTT 247

Qy        405 [illegible] 464

Db        248 [illegible]

Qy        465 GGTGGCCACTCAGCCCCCATGCACCTCAATGGCC[illegible] 524

Db        308 GGTGGCCACTCAGCCCCCATGCACCTCAATGGCCGCTGCATCTGCCCCAGTGACCCTCA 367

Qy        525 [illegible]

Db        368 [illegible] 427

Qy        585 [illegible] 644

Db        428 [illegible] 487

Qy        645 CTGCACAGCCCTGGTGGCTGTGTCCCTGCAGGGAAAGCTGTACATGGCCAATGCTGGGGA 704

Db        488 CTGCACAGCCCTGGTGGCTGTGTCCCTGCAGGGAAAGCTGTACATGGCCAATGCTGGGGA 547

Qy        705 TAGCAGGGCCATCTTGGTGCGGAGACATGAGATAC[illegible] 764

Db        548 [illegible] 607

Qy        765 AGAGACTGAGCGGCAGCGGATCCAGCAGCT----------------------------- 794

Db        608 AGAGACTGAG[illegible] 667

Qy        795 ------------------------------------------------------------ 794

Db        668 [illegible] 727

Qy        795 -------GGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCC 847

Db        728 CAGCCCAGCCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCC 787

Qy        848 [illegible] 907

Db        788 [illegible] 847

Qy        908 GTGGCTGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGAC 967

Db        848 [illegible] 907

Qy        968 [illegible] 1027

Db        908 [illegible] 967

Qy       1028 [illegible] 1087

Db        968 [illegible] 1027

Qy       1088 TGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAA 1147

Db       1028 TGACTGTGCTGCATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAA [illegible]

Qy       1148 [illegible] 1207

Db       1088 [illegible] 1147

Qy       1208 [illegible] 1267

Db       1148 [illegible] 1207

Qy       1268 [illegible] [illegible]

Db       1208 [illegible] [illegible]
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Qy       1328 [illegible]

Db       1268 [illegible]


RESULT 5
AK056894
LOCUS       AK056894                2429 bp    mRNA    linear   PRI [illegible]
DEFINITION  Homo sapiens cDNA FLJ32332 fis, clone PROST2005121, weakly similar
            to PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16).
ACCESSION   AK056894
VERSION     AK056894.1  GI:16552415
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens prostate cDNA to mRNA, clone_lib:PROST2
            clone:PROST2005121.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ishibashi,T., Kanehori,K., Yoshida,M., Watanabe,S., Ishida,S.,
            Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S.,
            Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
            Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
            Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
            Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y.,
            Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A.,
            Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2429)
  AUTHORS   Isogai,T., Otsuki,T. and Sugiyama,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            [illegible]
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: RAB and
            HRI.
FEATURES             Location/Qualifiers
     source          1..2429
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="PROST2005121"
                     /tissue_type="prostate"
                     /clone_lib="PROST2"
                     /note="cloning vector: pME18SFL3"
     CDS             405..1217
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="BAB71302.1"
                     /db_xref="GI:16552416"
                     /translation="[illegible]
                     [illegible]
                     [illegible]
                     [illegible]
                     [illegible]ASSKEK"
BASE COUNT      527 a    658 c    706 g    538 t
ORIGIN

  Query Match             [illegible];  Score 1014.4;  DB 9;  Length 2429;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches 1015;  Conservative    0;  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy        [illegible] [illegible]

Db        [illegible] [illegible]
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[illegible]

LOCUS       [illegible]                    [illegible] bp    mRNA    linear   [illegible]
DEFINITION  Homo sapiens, clone MGC:[illegible] IMAGE:[illegible], mRNA, complete cds.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (2[illegible]-JUN-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA [illegible]
            Web site: http://www-shgc.stanford.edu
            Contact: (Dickson, Mark) mrd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: [illegible] Row: [illegible] Column: [illegible].
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_71"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             [illegible]
                     /codon_start=1
                     /product="Unknown (protein for MGC:[illegible])"
                     /protein_id="AAH[illegible]"
                     /db_xref="GI:16307111"
                     /translation="[illegible]
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                     [illegible]
                     [illegible]VVVMA[illegible]
                     [illegible]VSYDDVSVEVIPLHSQGQESSDH"
BASE COUNT      [illegible] a    [illegible] c    [illegible] g    [illegible] t
ORIGIN

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. 1.4e-144;
  Matches  [illegible];  Conservative    [illegible];  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

[illegible]
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Qy        898 [illegible] 957
Db        525 [illegible] 584

Qy        958 [illegible] 1017
Db        585 [illegible] 644

Qy       1018 [illegible] 1077
Db        645 [illegible] 704

Qy       1078 [illegible] 1137
Db        705 [illegible] 764

Qy       1138 [illegible] 1197
Db        765 [illegible] 824

Qy       1198 [illegible] 1257
Db        825 [illegible] 884

Qy       1258 [illegible] 1317
Db        885 [illegible] 944

Qy       1318 [illegible] 1377
Db        945 [illegible] 1004

Qy       1378 TGA 1380
Db       1005 TGA 1007


RESULT 7
AK093270
LOCUS       AK093270                1687 bp    mRNA    linear   PRI 15-JUL-2002
DEFINITION  Homo sapiens cDNA FLJ35951 fis, clone TESTI2012104, weakly similar
            to PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16).
ACCESSION   AK093270
VERSION     AK093270.1  GI:21752092
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens testis cDNA to mRNA, clone_lib:TESTI2
            clone:TESTI2012104.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ishikashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.,
            Ono,Y., Hotuta,T., Hiraoka,S., [illegible]
            Kasano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
            Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
            Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
            Saito,K., Nishikawa,T., Kimura,K., [illegible] Nakamura,Y.,
            Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A.,
            Oshima,A., [illegible] Kawakami,B., [illegible]
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1687)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute [illegible]
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="TESTI2012104"
                     /tissue_type="testis"
                     /clone_lib="TESTI2"
                     /note="cloning vector: pME18SFL3"
BASE COUNT      336 a    512 c    513 g    326 t
ORIGIN

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  Best Local Similarity   [illegible]  Pred. No. [illegible]
  Matches  723;  Conservative  [illegible];  Mismatches  547;  Indels  [illegible];  Gaps  [illegible];

Qy         87 [illegible] 146
Db        194 [illegible]

Qy        147 [illegible] 204
Db        254 [illegible]

Qy        205 [illegible] 264
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Qy        265 [illegible] 324
Db        374 [illegible]

Qy        325 [illegible] 384
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Qy        385 [illegible] 444
Db        [illegible]

Qy        445 [illegible] 493
Db        [illegible]

Qy        494 [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        592 [illegible]
Db        [illegible]

Qy        652 [illegible]
Db        [illegible]

Qy        712 [illegible]
Db        [illegible]

Qy        772 [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]
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[illegible]

DEFINITION  Homo sapiens, similar to RIKEN cDNA [illegible] gene, clone
            MGC:[illegible] IMAGE:[illegible], mRNA, complete cds.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD [illegible],
            USA
  REMARK    NIH-MGC Project URL: http://[illegible]
COMMENT     Contact: MGC help desk
            Email: [illegible]
            Tissue Procurement: [illegible]
            cDNA Library Preparation: Rubin Laboratory,
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://[illegible]
            Contact: [illegible]
            [illegible], Y., Wetherby, K., Beckstrom-Sternberg, S.M.,
            [illegible]
            [illegible]
            [illegible]
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            [illegible]
            Zhang,L.H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 27 Row: p Column: 10
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: [illegible].
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_48"
                     /lab_host="DH10B"
                     /note="Vector: pOTB7"
     CDS             [illegible]..1478
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                     /product="Similar to RIKEN cDNA [illegible] gene"
                     /protein_id="AAH[illegible].1"
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                     /translation="MASELLHRHIREQLKDLVEILQ[illegible]
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                     [illegible]
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BASE COUNT     [illegible] a    [illegible] c    [illegible] g    [illegible] t
ORIGIN

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches [illegible];  Conservative    0;  Mismatches [illegible];  Indels [illegible];  Gaps    [illegible];

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Qy     147 [illegible]
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Qy         [illegible]
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Qy         [illegible]
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Qy         [illegible]
Db         [illegible]

Qy         [illegible]
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Qy         [illegible]
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Qy        652 [illegible] 711

Db        744 [illegible] 803

Qy        712 [illegible] 771

Db        804 [illegible] 863

Qy        772 [illegible] 831

Db        864 [illegible] 923

Qy        832 [illegible] 891

Db        924 [illegible] 983

Qy        892 [illegible] 951

Db        984 [illegible] 1043

Qy        952 [illegible] 1011

Db       1044 [illegible] 1103

Qy       1012 [illegible] 1071

Db       1104 [illegible] 1163

Qy       1072 [illegible] 1131

Db       1164 [illegible] 1223

Qy       1132 [illegible] 1191

Db       1224 [illegible] 1283

Qy       1192 [illegible]

Db       1284 [illegible]

Qy       1249 [illegible]

Db       1344 [illegible]

Qy       1297 [illegible]

Db       1404 [illegible]

Qy       1357 [illegible]

Db       1464 [illegible]


RESULT [illegible]
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LOCUS       [illegible]     2518 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  [illegible]
ACCESSION   AX4[illegible]
VERSION     AX4[illegible].1  GI:[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human protein phosphatase IIc-like enzyme
  JOURNAL   Patent: WO 0218565-A 3 07-MAR-2002;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
     CDS             141..[illegible]
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="[illegible]"
                     /db_xref="GI:[illegible]"
                     /translation="MASE[illegible]
                     [illegible]"
BASE COUNT      507 a    768 c    759 g    484 t
ORIGIN

  Query Match             [illegible];  Score 264.8;  DB 6;  Length 2518;
  Best Local Similarity   57.7%;  Pred. No. 2.7e-42;
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy        445 [illegible] 504

Db       1368 [illegible] 1428

Qy        505 [illegible]

Db       1428 [illegible]

Qy        565 [illegible] 624

Db       1488 [illegible]

Qy        625 [illegible] 684

Db       1548 [illegible]

Qy        685 [illegible]

Db       [illegible]

Qy        745 [illegible] 804

Db       1668 [illegible]

Qy        805 [illegible] 864

Db       1728 [illegible] 1787

Qy        865 [illegible] 924

Db       [illegible]

Qy        925 [illegible] 984

Db       1848 [illegible]

Qy        985 [illegible]

Db       [illegible]

Qy       1045 [illegible]

Db       1968 [illegible]

Qy       1105 [illegible]

Db       2028 [illegible]

Qy       1165 [illegible]

Db       [illegible] 2147
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Qy     [illegible]
Db     [illegible]

Qy     [illegible] AGGAAGACATGTCACAGAGGAAGGGA[illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]


RESULT 1[illegible]
HUMP[illegible]
LOCUS       [illegible]          [illegible] bp    mRNA            [illegible]
DEFINITION  Homo sapiens mRNA; cDNA DKFZp[illegible] (from clone DKFZp[illegible]);
            partial cds.
ACCESSION   A[illegible]
VERSION     A[illegible]
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., [illegible] and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-[illegible]) MIPS, Am Klopferspitz 18a, D-8215[illegible]
            Martinsried, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by BMFZ (Biomedical Research Center at the Charite,
            Berlin/Germany) within the cDNA sequencing consortium of the German
            Genome Project.
            This clone (DKFZp434[illegible]14) is available at the RZPD in Berlin.
            Please contact the RZPD: Resourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://www.mips.biochem.mpg.de/proj/cDNA/.
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp434[illegible]"
                     /tissue_type="testis"
                     /clone_lib="434 (synonym: hte3). Vector pSport1; host
                     DH10B; sites NotI + SalI"
                     /dev_stage="adult"
     gene            [illegible]
                     /gene="DKFZp434[illegible]"
     CDS             [illegible]
                     /gene="DKFZp434[illegible]"
                     /note="similarity to [illegible] (unspliced)"
                     /codon_start=1
                     /product="hypothetical protein"
                     /protein_id="CAB[illegible]"
                     /db_xref="[illegible]"
                     /translation="MA[illegible]
                     [illegible]ALVVIYLLGKVYVANA[illegible]
                     [illegible]
                     [illegible]
                     [illegible]
                     NK[illegible]VFV[illegible]"
     polyA_signal    [illegible]
     polyA_site      [illegible]
BASE COUNT    [illegible]
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length 2[illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];
```

```
Qy      445 [illegible]
Db     1[illegible]

Qy      505 [illegible]
Db     1[illegible]

Qy      565 [illegible]
Db     1488 [illegible]

Qy      625 [illegible]
Db     1548 [illegible]

Qy      685 [illegible]
Db     1608 [illegible]

Qy      745 [illegible] 804
Db     1668 [illegible]

Qy      805 [illegible]
Db     1728 [illegible]

Qy      865 [illegible] 924
Db     1788 AAGGAGCTGGGGCAGAGGATGTTGTACGGGACCAGAACATGACCGGCTGGGCTACAAA 1847

Qy      925 [illegible] 984
Db     1848 [illegible]GGGAGGG AAAAAG[illegible]

Qy      985 TTACTAGGAACACTGG[illegible]TGTCTCCCGGGGCTGGGAGACCATCAGCTCAGAGTCCTGGAC 1044
Db     1908 [illegible]GGAGGCTTGGGAGACCACAGC[illegible]TAAGG[illegible]

Qy     1045 [illegible]
Db     1968 [illegible]

Qy     1105 [illegible]
Db     2028 [illegible]

Qy     1165 [illegible]
Db     2088 [illegible]

Qy     1225 [illegible]
Db     2148 [illegible]

Qy     1285 [illegible]
Db     2208 [illegible]

Qy     1345 [illegible]
Db     2268 [illegible] 2297


RESULT 11
AX419116
LOCUS       AX419116             [illegible] bp    DNA     linear   PAT [illegible]
DEFINITION  Sequence 1 from Patent WO[illegible].
ACCESSION   AX419116
VERSION     AX419116.1  GI:[illegible]
KEYWORDS    .
SOURCE      human.
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human protein phosphatase IIc like enzyme
  JOURNAL   Patent: WO 0218565 A 1 07-MAR-2002;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1..900
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
BASE COUNT      1[illegible] a    247 c    282 g    18[illegible] t
ORIGIN

  Query Match             1[illegible].2%;  Score 264.4;  DB [illegible];  Length 900;
  Best Local Similarity   58.8%;  Pred. No. 3.8e-42;
  Matches  5[illegible];  Conservative    0;  Mismatches  [illegible];  Indels   15;  Gaps    2;

Qy        52[illegible] [illegible] 5[illegible]
Db         37 [illegible] 9[illegible]

Qy        583 [illegible] 642
Db         97 [illegible] 156

Qy        643 [illegible] 702
Db        157 [illegible] 216

Qy        7[illegible] [illegible] 762
Db        217 [illegible] 276

Qy        763 [illegible] 822
Db        277 [illegible] [illegible]

Qy        823 [illegible] 882
Db        337 [illegible] [illegible]

Qy        883 [illegible] 942
Db        397 [illegible] 45[illegible]

Qy        94[illegible] [illegible] 1[illegible]2
Db        457 [illegible] 5[illegible]

Qy       1003 [illegible]
Db        517 [illegible]

Qy       106[illegible] [illegible]
Db        577 [illegible]

Qy       112[illegible] [illegible]
Db        637 [illegible]

Qy       118[illegible] [illegible]
Db        697 [illegible]

Qy       124[illegible] [illegible]
Db        757 [illegible]

Qy       1288 [illegible]

Db        817 [illegible] 876

Qy       1348 [illegible] 1359

Db        877 [illegible] 888


RESULT 12
AX40007
LOCUS       AX400071                1198 bp    DNA     linear   PAT [illegible]-2002
DEFINITION  Sequence 242 from Patent WO0218424.
ACCESSION   AX400071
VERSION     AX400071.1  GI:[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   [illegible]
            Wang,[illegible], Zhao,[illegible]A., Wang,[illegible], Liu,[illegible] and [illegible]
  TITLE     Nucleic acids and polypeptides
  JOURNAL   Patent: WO 0218424 A 242 07-MAR-2002;
            HYSEQ, INC. (US)
FEATURES             Location/Qualifiers
     source          1..1198
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
     CDS             182..1198
                     /note "unnamed protein product"
                     /codon_start 1
                     /protein_id "[illegible]"
                     /db_xref "GI:[illegible]"
                     /translation "MA[illegible]
                     [illegible]
                     [illegible]KVYVANAG[illegible]RA[illegible]VRN[illegible]PMSREF[illegible]PE[illegible]ERQRL[illegible]LLQF[illegible]KPELLGSFFIHLEFP
                     FRVLPKELQ[illegible]RMLYRIQNMTGWAYKK[illegible]
                     [illegible]
                     [illegible]
                     [illegible]"
BASE COUNT      243 a    [illegible] c    [illegible]73 g    252 t
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length 11[illegible];
  Best Local Similarity   [illegible];  Pred. No. 8.3e-42;
  Matches  [illegible];  Conservative    [illegible];  Mismatches  329;  Indels   15;  Gaps    2;

Qy        [illegible] [illegible] [illegible]
Db        [illegible] [illegible] [illegible]

Qy        [illegible] [illegible] [illegible]
Db        [illegible] [illegible] [illegible]

Qy        [illegible] [illegible] [illegible]
Db        [illegible] [illegible] [illegible]

Qy        [illegible] [illegible] [illegible]
Db        [illegible] [illegible] [illegible]

Qy        [illegible] [illegible] [illegible]
Db        [illegible] [illegible] [illegible]

Qy        [illegible] [illegible] [illegible]
Db        [illegible] [illegible] [illegible]

Qy        [illegible] [illegible] [illegible]
```

```
[illegible]

LOCUS       [illegible]                bp    DNA     linear   PRI [illegible]
DEFINITION  Homo sapiens [illegible] (Roswell Park Cancer
            Institute Human BAC Library) complete sequence.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   [illegible]
            Williamson,A.[illegible], Worley,K.[illegible], Zhou,X.,
            [illegible] and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to [illegible])
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) Molecular and Human Genetics, Baylor
            College of Medicine, One Baylor Plaza, Houston, TX [illegible], USA
REFERENCE   3  (bases 1 to [illegible])
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX [illegible], USA
COMMENT     On [illegible] this sequence version replaced [illegible].
            INFORMATION: [illegible]
            [illegible]

            [illegible]
```

[illegible] the insert may be found in the record for the adjacent [illegible]. Overlapping clones are noted at the beginning and end of the features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. [illegible]) searches of a local database that includes entries from dbSTS, the [illegible] local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nat. Genet. [illegible]) similarity (expect [illegible]) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as low coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality_info/genbank_metrics.html.

QUALITY REPORT

```
                     Summary Statistics
Total Length:                                        [illegible]
Phrap values in estimate:                            [illegible]
Average error rate (BCM Phrap estimate):             [illegible]
Fraction of Phrap values less than 40 :              [illegible]
Number of consensus changing edits:                  [illegible]
Number of N's in consensus :                         [illegible]


                 Consensus changing edits
Position         Original Context             Edited Context
[illegible]      [illegible](n)[illegible]    [illegible]([illegible])[illegible]
[illegible]      [illegible](n)[illegible]    [illegible]([illegible])[illegible]
[illegible]      [illegible](n)[illegible]    [illegible]([illegible])[illegible]
[illegible]      [illegible](n)[illegible]    [illegible]([illegible])[illegible]
[illegible]      [illegible](n)[illegible]    [illegible]([illegible])[illegible]
[illegible]      [illegible](n)[illegible]    [illegible]([illegible])[illegible]


         Distribution of quality < 40 Bases

                                                       *
                                                       *
                                                       *
                                                       *
                                                  *    *
                                                  *    *
   #                                              *    *
 Bases                                            *    *
                                             *    *    *
                               *    *        *    *    *
                 *    *    *   *    *        *    *    *

                       Phrap Value Range


[illegible]
```

```
FEATURES             Location/Qualifiers
     source          1..82098
                     /organism "Homo sapiens"
                     /db_xref "taxon:[illegible]"
                     /clone "RP11-115?M2?"
                     /note "Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
                     Eutheria; Primates; Catarrhini; Hominidae; Homo."
     repeat_region   1..169
                     /rpt_family "Alu"
     repeat_region   78..[illegible]
                     /rpt_family "AluSx"
     gene            complement(join(588..1542,1965..201?,2124..2237,
                     2487..2550,2734..285?))
                     /note "Unigene cluster containing AI?78477, [illegible],
                     AA22759?, [illegible], AA72?09?, [illegible], and AA292266."
     STS             647..78?
                     /standard_name "stSG4882"
                     /db_xref "GDB:4566425"
     STS             6?5..860
                     /standard_name "[illegible]"
                     /db_xref "dbSTS:32797"
     misc_feature    5021..5289
                     /note "Region: Similar to H.sapiens genomic DNA, X87529."
     repeat_region   5178..5245
                     /rpt_family "GC_rich"
     repeat_region   5290..5582
                     /rpt_family "GC_rich"
     misc_feature    55??..5656
                     /note "Region: Similar to H.sapiens genomic DNA, X87529."
     repeat_region   6?1?..[illegible]
                     /rpt_family "AluSx"
     repeat_region   complement(7?72..7745)
                     /rpt_family "L1M4"
     repeat_region   complement(7747..7929)
                     /rpt_family "AluSp"
     repeat_region   8[illegible]..817?
                     /rpt_family "MER4A2"
     repeat_region   complement(8207..8491)
                     /rpt_family "AluSx"
     repeat_region   complement(8542..8591)
                     /rpt_family "AluSp"
     repeat_region   9144..9289
                     /rpt_family "MER4?"
     repeat_region   complement(9421..9582)
                     /rpt_family "FRAM"
     repeat_region   complement(9586..9631)
                     /rpt_family "(TAGA)n"
     repeat_region   complement(9663..9894)
                     /rpt_family "AluJo"
     repeat_region   9[illegible]..10?52
                     /rpt_family "MIR"
     repeat_region   complement(10124..10260)
                     /rpt_family "L2"
     repeat_region   11059..11126
                     /rpt_family "L2"
     repeat_region   111??..11?2?
                     /rpt_family "AluSp"
     repeat_region   11960..1205?
                     /rpt_family "GC_rich"
     gene            join(12104..12195,1608?..1615?,1906?..19243,199??..2??6?,
                     20192..20317,21137..21267,211??..21526,21986..22?75)
                     /note "Unigene cluster containing AI1?86??, AA??????,
                     W??722, [illegible], AA?11??, [illegible], and AA298126."
     repeat_region   complement(14187..1429?)
                     /rpt_family "MIR"
     repeat_region   complement(14866..15168)
                     /rpt_family "AluSq"
     repeat_region   complement(15?2?..15725)
                     /rpt_family "(CA)n"
     repeat_region   complement(17254..1754?)
                     /rpt_family "AluY"
     repeat_region   complement(18160..18451)
                     /rpt_family "AluSp"
     STS             1?2??..1?8??
                     /standard_name "[illegible]"
                     /db_xref "dbSTS:7608"
     STS             2??2?..224??
                     /standard_name "[illegible]"
                     /db_xref "GDB:4564423"
     repeat_region   complement(228??..2??2?)
                     /rpt_family "MER[illegible]"
     repeat_region   complement(24093..24822)
                     /rpt_family "L2"
     repeat_region   complement(25824..26124)
                     /rpt_family "AluSp"
     repeat_region   complement([illegible]..[illegible]74)
                     /rpt_family "(GGGA)n"

  Query Match             [illegible];  Score [illegible];  DB 9;  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. 1.5e-41;
  Matches  262;  Conservative    [illegible];  Mismatches    3;  Indels    0;  Gaps    0;

Qy        [illegible]
              [illegible]
Db     4222 [illegible]

Qy        344 [illegible]
              [illegible]
Db     4162 GCAGGCAT[illegible]AA[illegible]ACTC[illegible]GCCGGGG[illegible]

Qy        454 [illegible]
              [illegible]
Db     4102 [illegible]

Qy        [illegible]
              [illegible]
Db     4?42 [illegible]

Qy        [illegible]
              [illegible]
Db     3982 [illegible] 3958


RESULT 14
AC092045/c
LOCUS       AC092045               171343 bp    DNA     linear   [illegible]
DEFINITION  Homo sapiens chromosome [illegible] clone RP11-168J?8, complete sequence.
ACCESSION   AC092045 A[illegible] 24118
VERSION     AC092045.2  GI:15281257
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171343)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C. and
            Hansen,E.J.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 171343)
  AUTHORS   Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J., [illegible] and
            Hansen,E.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (1?-JUN-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 171343)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C. and
            Hansen,E.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-OCT-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
COMMENT     On Aug 23, 2001 this sequence version replaced gi:1[illegible].
                 [illegible] Genome Center
               Center: University of Washington Genome Center
               Center code: UWGC
               Web site: http://www.genome.washington.edu
```

```
 [illegible] Washington University [illegible]
 [illegible]
              Project Information
 Center project name: [illegible]
 Center clone name: [illegible]
              Summary Statistics
 Sequencing vector: M13; [illegible] of reads
 Sequencing vector: plasmid; [illegible] of reads
 Chemistry: Dye-terminator [illegible] of reads
 Chemistry: Dye-primer Bodipy; [illegible] of reads
 Chemistry: Dye-terminator [illegible] of reads
 Assembly program: Phrap; version [illegible]
 Consensus quality: [illegible] bases at least Q40
 Consensus quality: [illegible] bases at least Q30
 Consensus quality: [illegible] bases at least Q20
 Insert size: [illegible]; agarose-fp
 Insert size: [illegible]; sum-of-contigs
 Quality coverage: [illegible] in Q20 bases; agarose-fp
 Quality coverage: [illegible] in Q20 bases; sum-of-contigs

Overlapping Sequences:
 5': [illegible] (BWB[illegible]) A[illegible]
 3': [illegible] (BWB[illegible]) A[illegible]

Sequence Quality Assessment:
 This entry has been annotated with sequence quality
 estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than
 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the
 GenBank flat file format but are available as part
 of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13
subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
 This sequence has been checked by Multiple Complete Digest
 Fingerprinting. Comparison of the experimentally derived digest
 fragments with those predicted fragments as listed below
 [illegible]
 [illegible] in order to accurately represent the entire [illegible] BAC
 [illegible]
 [illegible] appear
 in the [illegible]. There are no significant remaining discrepancies
 between the experimental and predicted [illegible]
 fragments are separated by dashed lines.
          BglII                  [illegible]                HindIII

SeqMap   Fragment      SeqMap   Fragment      SeqMap   Fragment

```

SeqMap	Fragment	SeqMap	Fragment	SeqMap	Fragment
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
1864	1862	227	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]				
[illegible]	[illegible]				
[illegible]	[illegible]				
[illegible]	[illegible]				
[illegible]	[illegible]				
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[illegible]	[illegible]				

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FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /chromosome="3"
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                     /clone_lib="RPCI human BAC library 11"
BASE COUNT    39231 a  46165 c  45178 g  40769 t
ORIGIN

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Db     165894 [illegible] 165835

Qy        394 [illegible] 453
              [illegible]
Db     165834 [illegible] 165775

Qy        454 GTGGAAGGCTTGGTGGCCACTCAGGC[illegible]CCATGCAC[illegible]AATG[illegible]TGCATCTGCCCC 513
              [illegible]
Db     165774 GTGGAAGGCTTGGTGGCCACTCAGGC[illegible]CCATGCAC[illegible]AATG[illegible]TGCATCTGCCCC 165715

Qy        514 [illegible] 573
              [illegible]
Db     165714 AGTGACCCTCAGTTTGTGGAGGAAAAGGGCATCAGGGCAGAAGACTTGGTGATCGGGGCA 165655

Qy        574 TTGGAGAGTGGCTTTCAGGAATGTG 598
              ||||||| |||||||||||||||||
Db     165654 TTGGAGATTGGCTTTCAGGAATGTG 165630


RESULT 15
AC094021
LOCUS       AC094021               214160 bp    DNA     linear   PRI 27-MAR-2002
DEFINITION  Homo sapiens chromosome 3 clone RP11-801L18, complete sequence.
ACCESSION   AC094021 AC069253
VERSION     AC094021.2  GI:19745061
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-2002) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
COMMENT     On Mar 27, 2002 this sequence version replaced gi:15594339.
            ------------ Genome Center
                Center: University of Washington Genome Center
                Center Code: UWGC
                Web site: http://www.genome.washington.edu
                Contact: uwgchtgs@u.washington.edu
                Drafting Center: BCM
            ------------ Project Information
                Center project name: chr-3
                Center clone name: RP11-801L18 (bc0565)
            ------------ Summary Statistics
                Sequencing vector: M13; L08821; 19% of reads
                Sequencing vector: plasmid; 51% of reads
                Chemistry: Dye-terminator ET; [illegible]% of reads
                Chemistry: Dye-primer Bodipy; 11% of reads
                Chemistry: Dye-terminator Big Dye; 53% of reads
                Assembly program: Phrap; version 0.990319
                Consensus quality: 213971 bases at least Q40
                Consensus quality: 214159 bases at least Q30
                Consensus quality: 214[illegible] bases at least Q20
                Insert size: 214160; sum-of-contigs
                Quality coverage: 6.8x in Q20 bases; sum-of-contigs
            ------------
            Overlapping Sequences:
                5': Mapping in progress
                3': [illegible] (UWGC:[illegible]) AC[illegible]
            ------------
            Sequence Quality Assessment:
             This entry has been annotated with sequence quality
             estimates computed by the Phrap assembly program.
             All manually edited bases have been reduced to quality zero.
             Quality levels above 40 are expected to have less than
             1 error in 10,000 bp.
             Base-by-base quality values are not generally visible in the
             GenBank flat file format but are available as part
             of this entry's ASN.1 file.

            This sequence was finished as follows unless otherwise noted:
            all regions were either double stranded or sequenced with an
            alternate chemistry or covered by high quality data (i.e., Phred
            quality >= 30); an attempt was made to resolve all sequencing
            problems, such as compressions and repeats; all regions were
            covered by at least one plasmid subclone or more than one M13
            subclone; and the assembly was confirmed by restriction digest.
            ------------
            Sequence Validation:
             This sequence has been validated by Multiple Complete Digest
             Fingerprinting. Comparison of the experimentally derived digest
             fragments with sequence predicted fragments is given below.
             The electronically digested sequence consists of both insert and
             vector, in order to accurately represent the entire circular BAC.
             Small fragments below a variable cutoff (approximately 400-800 bp)
             are not resolved in the fingerprint and hence do not appear
             in the table. There are no significant remaining discrepancies
             between the experimental and predicted values. Uniquely ordered
             fragments are separated by dashed lines.
                    BglII                    EcoRI                  HindIII
            ---------------------   ---------------------   ---------------------
            SeqMap    FngrPrnt      SeqMap    FngrPrnt      SeqMap    FngrPrnt
            ---------------------   ---------------------   ---------------------

                                    ------
             [illegible] [illegible]  8[illegible]  8[illegible]  4[illegible]  [illegible]
            ------                  ---
             20[illegible]  [illegible]  6[illegible]  [illegible]  [illegible]  [illegible]
            ------                  ---                     ---
             10268     10181         4872      4941        [illegible]  [illegible]
            ------                  ---
             14477     14184         [illegible]  7[illegible]  41[illegible]  [illegible]
            ------                  ---                     ---
              6169      6264         1627      1647        [illegible]  [illegible]
            ------                  ---
             11239     1[illegible]  1465      1443        2481[illegible]  [illegible]
            ------                  ---                     ---
             16[illegible]  157[illegible]  4[illegible]  4941  [illegible]  [illegible]
            ------
              1601      1579         5201      5277         4137      4167
            ------                  ---
              4210      418[illegible]  60[illegible]  604[illegible]  [illegible]  [illegible]
            ------                  ------                  ---
              142[illegible]  [illegible]  80[illegible]  8002  2[illegible]  2[illegible]
            ------                  ---                     ------
              1[illegible]  [illegible]800  753  [illegible]800  7228  72[illegible]
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              59[illegible]  [illegible]  8244  8387  2[illegible]  2[illegible]
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[illegible]

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ORIGIN

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Qy        334 [illegible]
Db      [illegible] [illegible]

Qy        394 [illegible]
Db      [illegible] [illegible]

Qy        454 [illegible]
Db      [illegible] [illegible]

Qy        514 [illegible]
Db      [illegible] [illegible]

Qy        574 [illegible]
Db      [illegible] [illegible]

Search completed: February 24, [illegible]
Job time : [illegible] secs
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                         GenCore version 5.1.[illegible]
                 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 23, 2003, 05:51:08 ; Search time 319 Seconds
                                                (without alignments)
                                                9742.187 Million cell updates/sec

Title:           US-09-866-987-3
Perfect score:   1386
Sequence:        1 atgtccaccgactggttccg..........aagaagcagtgaccactga 1386

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2185237 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters:      4370474

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       N_Geneseq_101002:*
              1:  [illegible]:*
              2:  [illegible]:*
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    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                                SUMMARIES
                       %
Result               Query
   No.     Score   Match Length DB  ID                          Description
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      1  [illegible]  [illegible]  [illegible]  22  AAH22961    Human phosphatase
      2      917    66.4    917  24  ABA94426                   Human protein phos
      3  [illegible]  38.8    547  24  ABL79990                 Human ovarian canc
      4  [illegible]  [illegible]  2518  24  ABK47452           DNA encoding human
      5    262.4    19.0   4262  17  AAI38484                   Rat petrin cDNA ci
      6    262.1    19.0   4515  17  AAI38486                   Rat petrin cDNA.
      7    243.4    17.6   1617  23  AAS93640                   DNA encoding novel
      8    243.4    17.6   1887  22  AAI58166                   Human polynucleoti
      9    243.4    17.6   [illegible]  24  ABK46163            cDNA encoding col
     10    242.4    17.6   [illegible]  22  AAH17958            Human cDNA sequenc
     11      178    12.9   [illegible]  [illegible]  AAI38482   Rat petrin cDNA cl
     12    109.2     7.9    729  21  AAA02311                   Human colon cancer
     13      103     7.5   [illegible]  2[illegible]  AAZ12841  Human gene express
     14    102.8     7.4   [illegible]  2[illegible]  AAX89954  Human cultured ca
     15    101.2     7.3   2087  23  ABL25549                   Drosophila melanog
     16    101.2     7.3   [illegible]  23  ABL25548            Drosophila melanog
     17       98     7.1   [illegible]  24  ABL32482            Human ovarian canc
     18       95     6.9    300  20  AAX98437                   Human cancer cell
     19     87.6     6.3    794  21  AAA[illegible]             Human colon cancer
     20     83.6     6.1    294  21  AAA00279                   Human colon cancer
     21     81.2     5.9   2258  23  ABV22179                   Human prostate exp
     22     81.2     5.9   2258  23  ABV25186                   Human prostate exp
     23     81.2     5.9   2258  23  ABV27918                   Human prostate exp
     24     81.2     5.9   2258  23  ABV27965                   Human prostate exp
     25     81.2     5.9   2258  23  ABV2[illegible]            Human prostate exp
c    26     76.8     5.6    582  22  AAH1[illegible]            Human cDNA [illegible]
     27       68     4.9    454  17  AAI38488                   Rat petrin cDNA cl
     28     [illegible]  3.7  [illegible]  2[illegible]  AAS[illegible]  Acid [illegible]
c    29     49.8     3.6   6714  21  AAZ45[illegible]           Nucleotide sequenc
c    30     49.8     3.6   [illegible]  2[illegible]  AAZ45933  Nucleotide sequenc
c    31     49.8     3.6   [illegible]  2[illegible]  AAZ4[illegible]  Nucleotide sequenc
c    32     49.4     3.6   2698  22  AAK[illegible]             Human immune/haema
     33     49.2     3.6   [illegible]  22  AAI[illegible]      Human polynucleoti
c    34       49     3.5   [illegible]  21  ABK1[illegible]     Protein phosphatase
c    35     48.8     3.5   1327  24  ABQ68452                   Listeria monocytog
c    36     48.2     3.5   [illegible]  2[illegible]  AAX[illegible]  Nucleotide sequenc
c    37     48.2     3.5   28[illegible]  21  AA[illegible]     Human brain cDNA.
c    38       48     3.5    953  24  ABQ37014                   Oligonucleotide fo
     39       48     3.5    953  24  ABQ37015                   Oligonucleotide fo
     40     [illegible]  [illegible]  [illegible]  [illegible]  AAQ11243  HPV 28K gene [illegible]
     41     [illegible]  [illegible]  [illegible]  22  AAK[illegible]  Human immune/haema
     42     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  C. mays SH3 domai
c    43     [illegible]  [illegible]  [illegible]  21  ABN[illegible]  [illegible] used [illegible]
c    44     [illegible]  [illegible]  [illegible]  21  ABL[illegible]  Human cancer relate
     45     [illegible]  [illegible]  [illegible]  21  ABL65214        Human cancer relate

                                ALIGNMENTS

RESULT 1
AAH22961
ID   AAH22961 standard; cDNA; 1837 BP.
XX
AC   AAH22961;
XX
DT   17-SEP-2001  (first entry)
XX
DE   Human phosphatase (PP) full length cDNA (clone ID 1723447CB1).
XX
KW   Phosphatase; PP; Alzheimer's disease; Huntington's disease; human;
KW   immune disorder; cancer; neotropic; immunomodulatory; cytostatic;
KW   neuroprotective; anticonvulsant; ss.
XX
OS   Homo sapiens.
XX
FH   Key                 Location/Qualifiers
FT   CDS                 [illegible]
FT                       /*tag=  a
FT                       /product= "phosphatase"
XX
PN   WO200153467-A2.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US02088.
XX
PR   21-JAN-2000; 2000US-[illegible].
PR   28-JAN-2000; 2000US-178998.
PR   2[illegible]-FEB-2000; 2000US-184[illegible].
PR   17-MAR-2000; 2000US-190[illegible].
XX
```

```
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   [illegible] Azimzai Y, Yue H, Baughn MR, Bandman O;
PI   [illegible] Walia NK, Gandhi AR, [illegible]
XX
DR   WPI; [illegible]
DR   N-PSDB; AAB[illegible]
XX
PT   Novel phosphatases useful for treating diseases associated with
PT   decreased expression of functional phosphatases, e.g. Alzheimer's
PT   disease, Huntington's disease, immune disorders, and cancers
XX
PS   Claim [illegible]; Page [illegible]; [illegible] pp; English.
XX
CC   The invention provides human phosphatases (PP) and polynucleotides
CC   which encode the phosphatases. The polypeptides can be expressed by standard
CC   recombinant methodology. The PP are useful for treating a disease or
CC   condition associated with decreased expression of functional
CC   phosphatases. Compositions containing agonists or antagonists of PP may
CC   be used to treat a disease associated with decreased expression or
CC   overexpression of PP, respectively. Such diseases may include
CC   Alzheimer's disease, Huntington's disease, immune disorders, and
CC   cancers. The present sequence represents a human phosphatase encoding
CC   cDNA.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy          [illegible]
Db          [illegible]

Qy          [illegible]
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Qy          [illegible]
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Qy          [illegible]
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Qy          [illegible]
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Qy          [illegible]
Db          [illegible]

Qy          [illegible]
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Qy          [illegible]
Db          [illegible]

Qy          [illegible]
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Qy          [illegible]

Db      [illegible]

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Db      661 [illegible]

Qy      [illegible]
Db      [illegible]

Qy      781 [illegible]
Db      781 [illegible]

Qy      841 [illegible]
Db      841 [illegible]

Qy      901 [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy     1021 [illegible]
Db     1021 [illegible]

Qy     1081 [illegible]
Db     1081 [illegible]

Qy     1141 [illegible] 1200
Db     1141 [illegible]

Qy     1201 [illegible]
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Qy     1261 [illegible]
Db     1261 [illegible]

Qy     1321 [illegible]
Db     1321 [illegible]

Qy     [illegible] A [illegible]
            |
Db     [illegible] A [illegible]


RESULT 2
ABA44129
ID   ABA44129 standard; cDNA; [illegible] BP.
XX
AC   ABA44129;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human protein phosphatase [illegible] encoding cDNA.
XX
KW   Protein phosphatase; serine threonine phosphatase; PTP; STP; [illegible]
KW   cytostatic; immunosuppressive; vasotropic; analgesic; hypertensive;
KW   hypotensive; nootropic; neuroprotective; virucide; antibacterial; [illegible]
KW   fungicide; ophthalmological; antiinflammatory; cardiant; antimigraine;
KW   antiarthritic; muscular; antiasthmatic; osteopathic; antipsoriatic;
KW   antiarteriosclerotic; antiallergic; antidiabetic; tranquilizer; cancer;
KW   neuroleptic; antiparkinsonian; anorectic; gene therapy; ss.
XX
```

```
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..917
FT                   /*tag=  a
FT                   /product= "[illegible]"
FT                   /note= "sequence coding for approximately another 154
FT                          amino acid residues in the corresponding protein
FT                          is not printed in the specification"
XX
PN   WO200192491-A2.
XX
PD   06-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US17305.
XX
PR   30-MAY-2000; 2000US-208291P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman GD,  Whyte D,  Sudarsanam S,  Manning G,  Caenepeel S;
PI   Martinez R,  Hill RJ,  Flanagan P;
XX
DR   WPI; 2002-111340/15.
DR   P-PSDB; ABB67304.
XX
PT   New phosphatase polypeptides for treating e.g., cancers, immune-related
PT   diseases and disorders, cardiovascular diseases, or brain or
PT   neuronal-associated diseases -
XX
PS   Claim 28; Fig 1A; 161pp; English.
XX
CC   The invention relates to human protein phosphatase polypeptides and
CC   polynucleotides. The phosphatase polypeptides are useful for diagnosing
CC   and treating various phosphatase related diseases and conditions, such as
CC   cancers, immune-related diseases and disorders, cardiovascular diseases
CC   (e.g., reperfusion restenosis), brain or neuronal-associated diseases,
CC   metabolic disorders (e.g., diabetes or obesity), central or peripheral
CC   nervous system diseases and conditions (e.g., pain, migraine, mood
CC   disorders, hypotension, or hypertension), psychotic and neurological
CC   disorders (e.g., anxiety, schizophrenia), neurodegenerative diseases
CC   (e.g., Alzheimer's or Parkinson's disease), infections caused by viral
CC   (e.g., human immunodeficiency virus (HIV)), bacterial, fungal or prion
CC   agents, [illegible]
CC   (e.g., rheumatoid arthritis, multiple sclerosis, osteoarthritis). The
CC   polypeptides may also be used for screening for small molecule compounds
CC   that inhibit the catalytic activity of the encoded protein phosphatase
CC   with potential use for treating the above-mentioned diseases, for
CC   generating antibodies or hybridomas, and as a diagnostic tool for
CC   detecting a disease or disorder. Genetic sequences of phosphatases are
CC   useful in gene therapy. The present sequence represents a cDNA encoding
CC   a novel human serine threonine phosphatase (STP)-like phosphatase
CC   polypeptide SGP050.
XX
SQ   Sequence 917 BP; 161 A; 276 C; 310 G; 170 T; 0 other;

  Query Match             66.4%;  Score 917;  DB 21;  Length 917;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-[illegible];
  Matches  917;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCGCCGGCTGGTTCCGGCGCCGCTTCCTGCCTGGGAGCCGCTGCCCGCCGCGGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCGCCGGCTGGTTCCGGCGCCGCTTCCTGCCTGGGAGCCGCTGCCCGCCGCGGCGG 60

Qy         61 [illegible] 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 [illegible] 120

Qy        121 [illegible] 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 [illegible] 180

Qy        181 [illegible] 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 [illegible] 240

Qy        241 [illegible] 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 [illegible] 300

Qy        301 [illegible] 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 [illegible] 360

Qy        361 [illegible] 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 [illegible] 420

Qy        421 [illegible] 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 [illegible] 480

Qy        481 [illegible] 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 [illegible] 540

Qy        541 [illegible] 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 [illegible] 600

Qy        601 [illegible] 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 [illegible] 660

Qy        661 [illegible] 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 [illegible] 720

Qy        721 [illegible] 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 [illegible] 780

Qy        781 [illegible] 840
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Db        781 [illegible] 840

Qy        841 [illegible] 900
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Db        841 [illegible] 900

Qy        901 CACATGAGGGCTGGAC 917
              ||||||||||||||||
Db        901 CACATGAGGGCTGGAC 917


RESULT 3
ABL79990
ID   ABL79990 standard; cDNA; 547 BP.
XX
AC   ABL79990;
XX
DT   15-MAY-2002  (first entry)
XX
DE   Human ovarian cancer related cDNA clone SEQ ID NO:2968.
XX
KW   Human; ovarian cancer; ovarian tumour; cytostatic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200192581-A2.
XX
PD   06-DEC-2001.
XX
PF   29-MAY-2001; 2001WO-US17394.
XX
PR   29-MAY-2000; 2000US-207484P.
```

```
XX
PA    [illegible] ORIXA [illegible]
XX
PI    [illegible]
XX
DR    WO [illegible]
XX
PT    Composition for therapy and diagnosis of ovarian cancer comprising
PT    [illegible] polypeptides, polynucleotide [illegible]
PT    [illegible] specific to polypeptide [illegible] expressing
PT    polypeptide
XX
PS    [illegible] English.
XX
CC    The present invention describes a composition (I) comprising [illegible]
CC    and [illegible]; and a polypeptide (II) of an ovarian tumour
CC    polypeptide encoded by a polynucleotide (III) having a cDNA sequence
CC    [illegible] the [illegible] nucleotide sequences as given in [illegible]
CC    [illegible] (III) encoding (II) having a sequence (S2), [illegible]
CC    population of (II), or antigen presenting cells that express (II).
CC    (I) [illegible] activity. An oligonucleotide (IV) that hybridises to
CC    (III) can be used for detecting ovarian cancer in a patient's biological
CC    sample, preferably serum or ovarian tissue. The method comprises
CC    [illegible] a biological sample from a patient with (IV), detecting the
CC    amount of polynucleotide hybridising to (IV) and comparing the amount to
CC    a predetermined cutoff value and thereby detecting ovarian cancer in the
CC    patient, where the amount of polynucleotide hybridising to (IV) is
CC    detected preferably by polymerase chain reaction (PCR). (I) comprising
CC    (III) and/or (II) is useful for stimulating and/or expanding T cells
CC    [illegible] an ovarian tumour protein [illegible] T cells
CC    with (III) or (II). (III) is useful in design and preparation of
CC    ribozyme molecules for inhibiting expression of the tumour polypeptides
CC    and proteins in tumour cells and to [illegible] full length gene [illegible]
CC    [illegible] cDNA [illegible]
CC    techniques.
XX
SQ    Sequence [illegible]

  [illegible] Match [illegible]
  [illegible]
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible]
```

```
Qy    1272 A[illegible]
Db    480 ACAGGAAA[illegible]

Qy    [illegible]
Db    [illegible]


RESULT 4
ABK[illegible]
ID    ABK[illegible] standard; DNA; [illegible] BP.
XX
AC    ABK[illegible];
XX
DT    18-JUN-2002  (first entry)
XX
DE    DNA encoding human protein phosphatase [illegible] like (PP[illegible]) enzyme.
XX
KW    Protein phosphatase [illegible] like; agonist; antagonist; apoptosis; AIDS;
KW    Acquired immunodeficiency virus; genetic immunodeficiency; [illegible];
KW    neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW    retinitis pigmentosa; amyotrophic lateral sclerosis; myelodysplasia;
KW    aplastic anaemia; ischaemic injury; myocardial infarction; stroke;
KW    reperfusion injury; toxin induced disease; cirrhosis; wasting disease;
KW    cachexia; [illegible] infection; hepatitis; osteoporosis; cancer; diabetes;
KW    central nervous system disorder; CNS disorder; cardiovascular disorder;
KW    inflammatory disorder; chronic obstructive pulmonary disease; [illegible];
KW    gene; ds; human.
XX
OS    Homo sapiens.
XX
FH    Key             Location/Qualifiers
FT    CDS             [illegible]
FT                    /*tag= a
FT                    /product= "PP[illegible]"
FT                    /note= "Protein phosphatase [illegible] like enzyme.
FT                            Specifically claimed in claim [illegible]"
FT    misc_binding    [illegible]
FT                    /*tag= b
FT                    /note= "Bound by the antisense oligonucleotide shown
FT                            in ABK[illegible]"
XX
PN    WO[illegible]-A2.
XX
PD    07-MAR-2002.
XX
PF    [illegible]-AUG-2001; 2001WO-EP[illegible].
XX
PR    [illegible]-AUG-2000;   2000US-[illegible].
PR    02-APR-2001;   2001US-[illegible].
XX
PA    (FARB ) BAYER AG.
XX
PI    Xiao Y;
XX
DR    WPI; 2002-[illegible]/[illegible].
DR    P-PSDB; AAU[illegible].
XX
PT    New protein phosphatase [illegible] like enzyme and polynucleotides, useful for
PT    treating a disease associated with an increase or decrease in
PT    apoptosis, e.g. [illegible] degenerative diseases, viral infections,
PT    myelodysplasia, cancer, diabetes
XX
PS    Disclosure; [illegible]; English.
XX
CC    The invention describes an isolated polynucleotide (I) which encodes a
CC    protein phosphatase [illegible] (PP[illegible]) like enzyme (II). (I) and (II) can be
CC    used in diagnostic assays for detecting diseases and abnormalities or
CC    susceptibility to diseases and abnormalities related to the presence of
CC    mutations in the nucleic acid sequences encoding the enzyme. (I) and (II)
CC    or its antagonists, agonists, or modulators are useful for treating a
CC   disease or disorder associated with an increase in apoptosis such as AIDS
CC   or other infections or genetic immunodeficiencies, neurodegenerative
CC   diseases (e.g. Alzheimer's disease or Parkinson's disease, retinitis
CC   pigmentosa, or amyotropic lateral sclerosis), myelodysplasia (e.g.
CC   aplastic anaemia), ischaemic injuries (e.g. myocardial infarction, stroke
CC   or reperfusion injury), toxin induced diseases (e.g. alcohol induced
CC   liver damage or cirrhosis), wasting diseases (e.g. cachexia), viral
CC   infections (e.g. hepatitis B or C), and osteoporosis, or a decrease in
CC   apoptosis such as cancer, diabetes, CNS disorders, cardiovascular
CC   disorders, chronic obstructive pulmonary disease (COPD), and inflammatory
CC   disorders. Regulation of human PP1IC-like enzyme can be used to treat
CC   disorders such as diabetes, CNS disorders, cardiovascular disorders,
CC   COPD, and cancers (e.g. leukaemia, lymphoma, or cancers of the organs).
CC   This sequence encodes the novel human protein phosphatase IIC-like enzyme
CC   described in the invention.
XX
SQ   Sequence 2518 BP; 507 A; 768 C; 759 G; 484 T; 0 other;

  Query Match             19.2%;  Score 264.8;  DB 24;  Length 2518;
  Best Local Similarity   57.7%;  Pred. No. 7.6e-52;
  Matches  537;  Conservative    0;  Mismatches  377;  Indels   16;  Gaps    8;

Qy        445 [illegible]
Db       1369 [illegible] 1428

Qy        505 [illegible]
Db       1429 AT? GCATATCGAGAGCAGTAAAGGACCTGAAGGAAGTGAGCCACGAGAGCCTGGTA 1487

Qy        565 [illegible]
Db       1488 [illegible]

Qy        625 [illegible] 684
Db       1548 [illegible]

Qy        685 [illegible] 744
Db       1608 [illegible]

Qy        745 [illegible] 804
Db       1668 [illegible] 1727

Qy        805 [illegible] 864
Db       1728 [illegible]

Qy        865 [illegible] 924
Db       1788 [illegible] 1847

Qy        925 [illegible] 984
Db       1848 AAGAT?GA[illegible]GGAGGATCTGAGGTTTCCTCTGGTCTGTGGGGAGGGCAAAAAGGCTCGG 1907

Qy        985 [illegible]
Db       1908 [illegible] 1967

Qy       1045 [illegible]
Db       1968 [illegible] 2027

Qy       1105 [illegible] 1164
Db       2028 [illegible] 2087

Qy       1165 [illegible] 1224
Db       2088 [illegible] 2147

Qy       [illegible]
Db       2148 [illegible]

Qy       [illegible]
Db       2208 [illegible]

Qy       [illegible] 1359
Db       2268 [illegible] 2297


RESULT 5
AAT38484
ID   AAT38484 standard; cDNA; 4262 BP.
XX
AC   AAT38484;
XX
DT   16-JAN-1997  (first entry)
XX
DE   Rat petrin cDNA clone 11.
XX
KW   Petrin; neurite outgrowth associated protein; CNS;
KW   central nervous system; myelin; protein phosphatase 2C; stroke;
KW   neurodegeneration; gene therapy; ss.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 3825
FT                   /*tag=  a
FT                   /note= "base 3825 is given as b in the
FT                   specification"
XX
PN   WO9632476-A1.
XX
PD   17-OCT-1996.
XX
PF   11-APR-1996;   96WO-CA00214.
XX
PR   11-APR-1995;   95US-0421764.
XX
PA   (MGUN ) MCGILL UNIV ROYAL INST ADVANCEMENT LEARNING.
XX
PI   Lubeck M,  Gonzalez A,  Roach A,  Roder J;
XX
DR   WPI; 1996-477127/47.
DR   P-PSDB; AAW04327.
XX
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 2; Page 50-52; 119pp; English.
XX
CC   A cDNA sequence (AAT38484) coding for petrin (AAW04327), a protein
CC   involved in modulating neurite growth inhibition.  It was derived
CC   from fragments of clone 11 (see also AAT38483) isolated from an
CC   adult rat brain cDNA library in lambda gt11 by screening with
CC   a monoclonal antibody that blocks the effect on neurons in culture
CC   of CNS myelin inhibitors.  The petrin gene is expressed in neurons
CC   in brain tissue, particul. in cerebellum Purkinje cells.  It can be
CC   used to produce petrin protein and to prepare probes.  Antisense
CC   sequences (see also AAT38485) can be used in gene therapy to enhance
CC   axonal regeneration.
XX
SQ   Sequence 4262 BP; 924 A; 1164 C; 1170 G; 1002 T; 2 other;

  Query Match             19.0%;  Score 262.4;  DB 17;  Length 4262;
  Best Local Similarity   53.8%;  Pred. No. 5.2e-51;
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible] 977
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]


RESULT [illegible]
AAI[illegible]
ID   AAI[illegible] standard; cDNA; [illegible] BP.
XX
AC   AAI[illegible];
XX
DT   [illegible]-JAN-[illegible]  (first entry)
XX
DE   Rat petrin cDNA.
XX
KW   [illegible] protein; CNS;
KW   central nervous system; [illegible] protein phosphatase [illegible]
KW   [illegible] gene therapy; [illegible]
XX
OS   [illegible]
XX
FH   Key                 Location/Qualifiers
FT   [illegible]         [illegible]
FT                       /*tag= [illegible]
FT                       /product= "petrin"
FT   misc_difference     [illegible]
FT                       /*tag= [illegible]
FT                       /note= "Base [illegible] is given as N in the
FT                       specification"
XX
PN   WO[illegible]-A1.
XX
PD   [illegible].
XX
PF   12-APR-1996;   96WO-[illegible].
XX
PR   13-APR-1995;   95US-[illegible].
XX
PA   (MOUN-) MOUNT SINAI HOSPITAL CORP.
XX
PI   Lubes M,  [illegible] A,  [illegible] A,  [illegible]
XX
DR   WPI; 1996-[illegible].
DR   P-PSDB; AAW[illegible].
XX
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 4; Fig 23; 119pp; English.
XX
CC   A nucleotide sequence (AAI38486) codes for petrin (AAW04527), a protein
CC   involved in modulating neurite growth inhibition.  It was isolated
CC   from an adult rat brain cDNA library in lambda gt11 by screening
CC   with probes based on partial petrin clones (see also AAI38479-84).
CC   The human petrin locus was localised to chromosome 12.  The gene
CC   is expressed in neurons in brain tissue, partic. in cerebellum
CC   Purkinje cells.  It can be used to produce petrin protein and to
CC   prepare probes.  Antisense sequences (see also AAI38487) can be used
CC   in gene therapy to enhance axonal regeneration.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]
```

```
Qy        918 [illegible] 977

Db       1511 [illegible]

Qy        978 [illegible] 1037

Db       1571 [illegible]

Qy       1038 [illegible]

Db       1631 [illegible]

Qy       1098 [illegible] 1157

Db       1691 [illegible]

Qy       1158 [illegible] 1217

Db       1751 [illegible]

Qy       1218 [illegible] 1262

Db       1811 [illegible]


RESULT 7
AAS[illegible]
ID   AAS99640 standard; cDNA; 1617 BP.
XX
AC   AAS99640;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #29444.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US[illegible].
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639672/73.
DR   P-PSDB; [illegible]
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 1; SEQ ID No 29444; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) [illegible]
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS[illegible]-AAS[illegible] represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1617 BP; [illegible] A; 442 C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible]%;  Score [illegible];  DB 23;  Length 1617;
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  452;  Conservative    [illegible];  Mismatches  326;  Indels  [illegible];  Gaps  [illegible];

Qy        [illegible]

Db        731 [illegible]

Qy        560 [illegible]

Db        791 [illegible]

Qy        620 [illegible]

Db        851 [illegible]

Qy        [illegible]

Db        911 [illegible]

Qy        740 [illegible]

Db        971 [illegible]

Qy        800 [illegible]

Db       1031 [illegible]

Qy        860 [illegible]

Db       1091 [illegible]

Qy        920 [illegible]

Db       1151 [illegible]

Qy        980 [illegible]

Db       1211 [illegible]

Qy       1040 [illegible]

Db       1271 [illegible]

Qy       1100 [illegible]

Db       1331 [illegible]

Qy       1160 [illegible]

Db       1391 [illegible]

Qy       1217 [illegible]

Db       1451 [illegible]

Qy       1277 G 1277
              |
Db       1511 G 1511
```

```
[illegible]
AAI[illegible]
ID   AA[illegible] standard; DNA; [illegible] BP.
XX
AC   AA[illegible];
XX
DT   [illegible] (first entry)
XX
DE   Human polynucleotide SEQ ID NO [illegible].
XX
KW   Human; [illegible]; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy Drager Syndrome; chemotactic;
KW   [illegible]; thrombolytic; [illegible]; arthritis; inflammation;
KW   [illegible].
XX
OS   Homo sapiens.
XX
FN   [illegible] A.
XX
FT   [illegible]
XX
FT   [illegible]
XX
PR   [illegible]
PR   [illegible]
PR   [illegible]
PR   [illegible]
PR   [illegible]
PR   [illegible]
PR   [illegible]
PR   [illegible]
XX
PA   [illegible] INC.
XX
PI   [illegible] Y, [illegible], [illegible] V, [illegible]
PI   Wang [illegible], Wang [illegible], Wehrman [illegible], Xu [illegible], Xue A[illegible], Yu [illegible] Y, Zhang [illegible];
PI   [illegible]
XX
DR   WPI; [illegible].
DR   P-PSDB; AAM[illegible].
XX
PT   [illegible] polypeptides [illegible] treating [illegible]
PT   [illegible] central nervous system injuries
XX
PS   [illegible]
XX
CC   The invention relates to human nucleic acids (AA[illegible] AA[illegible]) and
CC   the encoded polypeptides (AAM[illegible] AAM[illegible]) with neotropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A [illegible] polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system such as peripheral nervous injuries, peripheral neuropathy and
CC   [illegible] neuropathies and central nervous system disorders such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy Drager Syndrome. Other uses include the
CC   [illegible] of the activities such as immune system suppression,
CC   [illegible] activity, chemotactic/chemokinetic activity, haemostatic
CC   [illegible] activity, tumor [illegible] and therapy, [illegible]
CC   [illegible] receptor activity, arthritis and inflammation, leukaemia and
CC   CNS disorders.
CC   [illegible]
CC   [illegible]
XX
SQ   [illegible]

  [illegible]
  Best [illegible]
  Matches [illegible]
```

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Qy    [illegible]
Db    677 [illegible]

Qy    [illegible]
Db    737 [illegible]

Qy    [illegible]
Db    797 [illegible]

Qy    [illegible]
Db    857 [illegible]

Qy    [illegible]
Db    917 [illegible]

Qy    [illegible]
Db    977 [illegible]

Qy    [illegible]
Db    1037 [illegible]

Qy    [illegible]
Db    1097 [illegible]

Qy    [illegible]
Db    1157 [illegible]

Qy    [illegible]
Db    1217 [illegible]

Qy    [illegible]
Db    1277 [illegible]

Qy    [illegible]
Db    1337 [illegible]

Qy    [illegible]
Db    1397 [illegible]

Qy    [illegible]
Db    1457 [illegible] 1457
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RESULT [illegible]
ABK4[illegible]
ID   ABK4[illegible] standard; cDNA; [illegible] BP.
XX
AC   ABK4[illegible];
XX
DT   [illegible] JUN [illegible] (first entry)
XX
DE   cDNA [illegible] human [illegible] protein, SEQ ID NO [illegible].
XX
KW   Human; [illegible]; cancer; immuno[illegible];
KW   immunotherapy; [illegible].
XX
OS   Homo sapiens.
XX
FN   [illegible] A.
```

```
XX
PD   14-FEB-2002.
XX
PF   31-JUL-2001; 2001WO-US24218.
XX
PR   31-AUG-2000; 2000US-[illegible].
PR   28-MAR-2001; 2001US-[illegible].
PR   29-JUN-2001; 2001US-[illegible].
XX
PA   (CORI-) CORIXA CORP.
XX
PI   King GE,  Meagher MJ,  Xu J,  Secrist H;
XX
DR   WPI; 2002-241709/29.
XX
PT   New colon cancer polypeptides and polynucleotides, useful as vaccines,
PT   for diagnosing, preventing, and treating colon cancer, and as markers
PT   for the progression of cancer -
XX
PS   Claim 1; SEQ ID NO 1714; 147pp; English.
XX
CC   The invention relates to polynucleotides encoding colon tumour proteins.
CC   The polynucleotides and encoded polypeptides are useful in pharmaceutical
CC   compositions, such as vaccines, for the diagnosis, prevention, and
CC   treatment of colon cancer. Polynucleotide sequences may be used as
CC   hybridisation probes or primers, and in the design and preparation of
CC   ribozyme molecules for inhibiting expression of tumour polypeptides and
CC   proteins in tumour cells. The compositions are useful for stimulating an
CC   immune response against cancer, particularly for the immunotherapy of
CC   colon cancer, and as markers for the progression of cancer.
CC   ABK44450-ABK46237 represent coding sequences of human colon tumour
CC   proteins of the invention.
CC   Note: With the exception of SEQ ID No 1 and 2, the sequence data
CC   for this patent did not form part of the printed specification but was
CC   supplied by the European Patent Office.
XX
SQ   Sequence 5791 BP; 1456 A, 1312 C, 1395 G, [illegible] T; 0 other;

  Query Match             17.6%;  Score 243.4;  DB 24;  Length 5791;
  Best Local Similarity   57.9%;  Pred. No. 9.2e-47;
  Matches  452;  Conservative    0;  Mismatches  326;  Indels  [illegible];  Gaps    1;

Qy     500 GCTGCATCTGCCCAGTGAC[illegible] 559
Db     401 [illegible]

Qy     560 [illegible] 619
Db     461 [illegible]

Qy     620 [illegible] 679
Db     521 [illegible]

Qy     680 [illegible]
Db     581 [illegible]

Qy     740 [illegible]
Db     641 [illegible]

Qy     800 [illegible]
Db     701 [illegible]

Qy     860 [illegible]
Db     761 [illegible]

Qy     920 [illegible]
Db     821 [illegible]
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```
Qy     980 [illegible]
Db     881 [illegible]

Qy    1040 [illegible]
Db     941 [illegible]

Qy    1100 [illegible] 1159
Db    1001 [illegible]

Qy    1160 [illegible]
Db    1061 [illegible]

Qy    1217 [illegible]
Db    1121 [illegible]

Qy    1277 G 1277

Db    1181 G 1181


RESULT [illegible]
AAH17958
ID   AAH17958 standard; cDNA; [illegible] BP.
XX
AC   AAH17958;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:[illegible].
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-[illegible].
XX
PR   29-JUL-1999;   99JP-[illegible].
PR   27-AUG-1999;   99JP-[illegible].
PR   11-JAN-2000; 2000JP-[illegible].
PR   02-MAY-2000; 2000JP-[illegible].
PR   09-JUN-2000; 2000JP-[illegible].
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-[illegible].
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full length cDNAs
XX
PS   Claim 8; SEQ ID [illegible]; [illegible]pp; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   [illegible]
CC   [illegible] complementary [illegible]
CC   [illegible] 5' end sequence, where the
CC   [illegible] comprises at least [illegible] nucleotides and the [illegible] of
CC   the 3' end sequence/5' end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full length cDNAs. The primers allow obtaining of the full length
CC   cDNAs easily without any specialised methods. AAH[illegible] to AAH[illegible] and
CC   AAH[illegible] to AAH[illegible] represent human cDNA sequences; AAH[illegible] to
CC   AAH[illegible] represent human amino acid sequences; and AAH[illegible] to AAH[illegible]
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence [illegible] BP; [illegible]

  Query Match             [illegible]
  Best Local Similarity   [illegible]
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible]
```

```
RESULT 11
AAI98482
ID   AAI98482 standard; cDNA; 4[illegible] BP.
XX
AC   AAI98482;
XX
DT   1[illegible]-JAN-200[illegible]  (first entry)
XX
DE   Rat petrin cDNA clone [illegible] 413.
XX
KW   Petrin; neurite outgrowth associated protein; CNS;
KW   central nervous system; myelin; protein phosphatase 2C; stroke;
KW   neurodegenerative; gene therapy; ss.
XX
OS   Rattus sp.
XX
PN   WO[illegible]-A1.
XX
PD   [illegible].
XX
PF   1[illegible]-APR-[illegible]; [illegible]WO-[illegible].
XX
PR   1[illegible]-APR-[illegible]; [illegible]US-[illegible].
XX
PA   (MO[illegible]N-) MOUNT SINAI [illegible] SPITAL [illegible].
XX
PI   Filbin M, [illegible] A, [illegible] A, [illegible] J;
XX
DR   WPI; 200[illegible]-[illegible]/4[illegible].
XX
PT   Assay for substance that modulates response of neuronal cells [illegible] and
PT   neurite growth associated protein, Petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 2[illegible]; Page [illegible]; [illegible]pp; English.
XX
CC   A cDNA clone (AAI98482), designated [illegible] 413, is a fragment of clone
CC   [illegible] (see also AAI98479-84 and AAI98480) that codes for petrin (AAW[illegible]),
CC   a protein involved in modulating neurite growth inhibition. [illegible]
CC   was isolated from an adult rat brain cDNA library by screening with
CC   a monoclonal antibody capable of neutralising the inhibition of
CC   neurite growth by several neuronal types on CNS myelin substrates.
CC   The gene is expressed in neurons in brain tissue, partic. in
CC   cerebellum Purkinje cells. It can be used to produce petrin
CC   protein and to prepare probes. Antisense sequences (see als
CC   AAI98[illegible]) can be used in gene therapy to enhance axonal regeneration.
XX
SQ   Sequence 4[illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible]; Score [illegible]; DB [illegible]; Length 4[illegible];
  Best Local Similarity   [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible]
```

```
Db        267 ACTATTGGATTACAAAGGGATTGGGGACCATGAGCGGAAGGTGCATGACTCAAGATC 326

Qy       1054 CAGTTCAAGGCCTTCTTGGTCTCTGTGCCACAGGTGACTGTGCTGGATGTGGACCAGCTG 1113

Db        327 [illegible] 386

Qy       1114 GAGTTACAGGAGGATGATGTGGTTGTCATGGTAACTGATGGATGTGGCCATGTACTG[illegible] 1173

Db        387 [illegible] 446

Qy       1174 AATTACTATTTCCC 1187

Db        447 AATGAATAAATTATT 46[illegible]


RESULT 12
AAA02311
ID   AAA02311 standard; cDNA; 729 BP.
XX
AC   AAA02311;
XX
DT   13-MAY-2000  (first entry)
XX
DE   Human colon cancer cell line polynucleotide sequence SEQ ID NO:2[illegible].
XX
KW   Human; colon cancer; tumour; diagnosis; gene expression product;
KW   probe; detection; cancerous state; metastasis; identification;
KW   breast cancer; oestrogen receptor-positive breast cancer; therapy;
KW   oestrogen receptor-negative breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9958675-A2.
XX
PD   18-NOV-1999.
XX
PF   13-MAY-1999;   99WO-US10632.
XX
PR   14-MAY-1998;   98US-0085426.
PR   15-MAY-1998;   98US-0085537.
PR   15-MAY-1998;   98US-0085636.
PR   21-OCT-1998;   98US-0105234.
PR   27-OCT-1998;   98US-0105877.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Williams LT,  Escobedo J,  Innis MA,  Garcia PD,  Sudduth-Klinger J;
PI   Reinhard C,  Giese K,  Randazzo F,  Kennedy G,  Pot D,  Kassam A;
PI   Lamson G,  Drmanac R,  Crkvenjakov R,  Dickson M,  Drmanac S,  Labat I;
PI   Leshkowitz D,  Kita D,  Garcia V,  Jones LW,  Stache-Crain B;
XX
DR   WPI; 2000-116369/11.
XX
PT   Polynucleotide library used to determine cancerous states of mammalian
PT   cells -
XX
PS   Claim 1; Page 909; 1097pp; English.
XX
CC   AAA0[illegible] to AAA02716 represent polynucleotides isolated from cDNA
CC   libraries constructed from human colon cancer cell lines. The present
CC   invention also describes a method of detecting differentially expressed
CC   genes correlated with a cancerous state of a mammalian cell, comprising
CC   detecting at least one differentially expressed gene product in a test
CC   sample derived from a cell suspected of being cancerous, where detection
CC   of the differentially expressed gene product is correlated with a
CC   cancerous state of the cell from which the test sample was derived.
CC   The polynucleotides sequences can be used in a method for detecting
CC   differentially expressed genes correlated with a cancerous state of a
CC   mammalian cell. The polynucleotides can also be used as probes for
CC   detecting and mapping related genes. They can be used in diagnosis and
CC   prognosis of diseases and disorders (e.g. identification of
CC   premetastatic or metastatic cancerous states, stages of cancer, or
CC   responsiveness of cancer to therapy). This is particularly for breast
CC   cancer, oestrogen receptor-positive breast cancer, oestrogen receptor
CC   negative breast cancer, lung cancer, and colon cancer.
XX
SQ   Sequence 729 BP; [illegible] A; [illegible] C; [illegible] G; 161 T; 0 other;

  Query Match             7.9%;  Score 109.2;  DB 21;  Length 729;
  Best Local Similarity   55.0%;  Pred. No. 8.2e-16;
  Matches  266;  Conservative    0;  Mismatches  2[illegible];  Indels  1[illegible];  Gaps    2[illegible];

Qy        891 [illegible] 950

Db         25 [illegible]TAGAAAAA[illegible] 84

Qy        951 CCCACTGATCCATGGACAGG[illegible]TAGGAA[illegible] 1010

Db         85 TCCTCTGGTCTGTGGGGAGGGAAAAA[illegible] 144

Qy       1011 [illegible] 1070

Db        145 [illegible] 204

Qy       1071 [illegible] 1130

Db        205 [illegible] 264

Qy       1131 [illegible] 1190

Db        265 [illegible] 324

Qy       1191 [illegible]AAAGGACCTA[illegible]AAA[illegible] 1247

Db        325 [illegible] 384

Qy       1248 [illegible] 1295

Db        385 [illegible] 444

Qy       1296 AGAGGAA[illegible] 1355

Db        445 [illegible] 504

Qy       1356 GGGC 1359
               |||
Db        505 AGGC 508


RESULT 13
AAZ12841
ID   AAZ12841 standard; cDNA; [illegible] BP.
XX
AC   AAZ12841;
XX
DT   [illegible]  (first entry)
XX
DE   Human gene expression product cDNA sequence SEQ ID NO:3[illegible].
XX
KW   Human; gene; gene expression product; diagnosis; therapy; probe;
KW   detection; mapping; tissue typing; profiling; forensic; cancer;
KW   genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9938972-A2.
XX
PD   05-AUG-1999.
XX
PF   28-JAN-1999;   99WO-US0[illegible].
XX
PR   03-APR-1998;   98US-0[illegible].
PR   28-JAN-1998;   98US-[illegible].
PR   24-FEB-1998;   98US-0075954.
PR   [illegible] MAR 1998;   98US-[illegible].
PR   [illegible] APR 1999;   99US-[illegible].
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Drkvenjakov R,  Dickson M,  Drmanac R,  Drmanac S;
PI   Escobedo J,  Garcia PD,  Garcia V,  Giese K,  Innis MA;
PI   Jones LW,  Kassam A,  Kennedy GC,  Kita D,  Labat I;
PI   Lamson G,  Leshkowitz D,  Pot D,  Randazzo F,  Reinhard C;
PI   Stache-Crain B,  Suddath-Klinger J,  Williams LT;
XX
DR   WPI; [illegible].
XX
PT   Novel human genes and their expression products which are
PT   differentially expressed in different cell types
XX
PS   Claim 1; Page [illegible]; [illegible]pp; English.
XX
CC   The present invention describes a library of human polynucleotides
CC   comprising the sequences given in AAZ[illegible] to AAZ[illegible]. Also described is
CC   a method to determine differentially expressed genes correlated with the
CC   cancerous state of a mammalian cell, comprising detecting at least one
CC   differentially expressed gene product in a test sample from a cell
CC   suspected of being cancerous, where the gene product is encoded by one
CC   of the [illegible] polynucleotide sequences given in AAZ1[illegible]32 to AAZ[illegible]. The
CC   polynucleotides can be used as a source of primers and probes, which can
CC   be used for a variety of purposes, e.g. detection of expression levels,
CC   mapping, tissue typing or profiling, forensics, genetic analysis and
CC   detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC   can be used for raising antibodies for experimental, diagnostic and
CC   therapeutic purposes. The polynucleotides may also be used to construct
CC   arrays for transcripts (which may be used to determine function of an
CC   encoded protein); and to detect differences in expression levels between
CC   two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC   identify a genetic predisposition or susceptibility to a disease such as
CC   cancer). The polynucleotides of the invention are especially used in the
CC   diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC   and lung cancer. The polynucleotides can also be used to screen for
CC   peptide mimetics and antagonists.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative    [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy   [illegible]
Db   [illegible] 60

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible] 180

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]


RESULT [illegible]
AAX[illegible]
ID   AAX[illegible] standard; cDNA; [illegible] BP.
XX
AC   AAX[illegible];
XX
DT   24 SEP 1999  (first entry)
XX
DE   Human validated cancer cell derived cDNA #2[illegible].
XX
KW   Cancer; human; colon; breast; lung; transmembrane receptor; ATPase;
KW   integral membrane protein; aspartyl protease; GATA family; wnt family;
KW   transcription factor; G-protein alpha subunit; protein phosphatase;
KW   phorbolester binding protein; diacylglycerol binding protein; trypsin;
KW   protein kinase; tyrosine phosphatase; developmental signalling protein;
KW   WW/rsp5/WWP domain; therapy; forensic; genetic mapping; diagnostic;
KW   detection; treatment; cervical; melanoma; colorectal adenocarcinoma;
KW   Wilm's tumour; retinoblastoma; sarcoma; myosarcoma; lung carcinoma;
KW   leukemia; lymphoma; dysplasia; hyperplasia; endometrium; adrenal;
KW   prostate; ss.
XX
OS   Homo sapiens.
XX
PN   WO[illegible]-A1.
XX
PD   [illegible] [illegible] 1999.
XX
PF   22 DEC 1998;   98WO-US[illegible].
XX
PR   21 DEC 1998;   98US-0217471.
PR   23 DEC 1997;   97US-[illegible].
PR   [illegible] APR 1998;   98US-[illegible].
PR   21 OCT 1998;   98US-0105234.
PR   27 OCT 1998;   98US-[illegible].
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Drkvenjakov R,  Dickson M,  Drmanac R,  Drmanac S;
PI   Escobedo J,  Garcia PD,  Garcia V,  Giese K,  Innis MA;
PI   Jones LW,  Kassam A,  Kennedy GC,  Kita D,  Labat I;
PI   Lamson G,  Leshkowitz D,  Pot D,  Randazzo F,  Reinhard C;
PI   Stache-Crain B,  Suddath-Klinger J,  Williams LT;
XX
DR   WPI; 1999-[illegible].
XX
PT   New isolated human polynucleotides
XX
PS   Claim 1; Page 5[illegible]; 5[illegible]pp; English.
XX
CC   This invention describes novel isolated human polynucleotides obtained
CC   by screening for differential expression in colon cancer, breast cancer
CC   and lung cancer cell lines. The polynucleotides of the invention are
CC   represented in AAX98275-X99118 and encode polypeptides of protein
CC   families selected from 4 transmembrane segments integral membrane
CC   proteins, 7 transmembrane receptors, ATPases associated with various
CC   cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of
CC   transcription factors, G protein alpha subunit, phorbolesters or
CC   diacylglycerol binding proteins, protein kinase, protein phosphatase 2C,
CC   protein tyrosine phosphatase, trypsin, wnt family of developmental
CC   signalling proteins and WW/rsp5/WWP domain containing proteins. The
CC   encoded polypeptides also have a functional domain selected from Ank
CC   repeat, basic region plus leucine zipper transcription factors,
CC   bromodomain, EF hand, SH3 domain, WD domain/G beta repeats, zinc finger
CC   (C2H2 type), zinc finger (C3HC4 class), and zinc binding metalloprotease
CC   domain. The polynucleotides encode polypeptides with similarity to known
CC   protein families and are predicted to have similar properties. The novel
CC   polynucleotides can be used to develop products for use as therapeutic
CC   agents and in forensics, genetic analysis, mapping and diagnostic
CC   applications. In particular, the product can be used for the detection
CC   and management of cancers. They can be used for treating e.g. cervical
CC   cancers, melanomas, colorectal adenocarcinomas, Wilm's tumour, sarcomas,
CC   retinoblastoma, myosarcomas, lung carcinomas, leukemias, such as chronic
CC   myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and
CC   myeloid leukemia, and lymphomas such as histiocytic lymphoma, and/or
CC   hereditary ectodermal dysplasia, congenital alveolar dysplasia,
CC   epithelial dysplasia of the cervix, fibrous dysplasia of bone, and
CC   mammary dysplasia, hyperplasias, e.g. endometrial, adrenal, breast,
CC   prostate or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of
CC   the skin.
XX
SQ   Sequence 750 BP; 170 A; 203 C; 182 G; 180 T; 15 other;

  Query Match             7.4%;  Score 102.8;  DB 20;  Length 750;
  Best Local Similarity   54.4%;  Pred. No. 2.5e-14;
  Matches  257;  Conservative    0;  Mismatches  [illegible];  Indels   1[illegible];  Gaps    2;

Qy        904 ATGAGTGGCTGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTCATCCAT 963
Db         58 AGGACCGGCTGGGCCTACAAAAAGATCGAGCTGGAGGATCTCAGGTTTCCTCTGCTCTGT 117

Qy        964 GGACAGGTAGGCAGGCTCGGTTACTAGGAACACTGGCTGTCTGGGGGGCCTGGGAGAC 1023
Db        118 GGGGAGCCCAAAAAGCTTCGGGTCATGCCCACCATTGGGTTGACCCGAGGCTGGGAGAC 177

Qy       1024 [illegible]
Db        178 [illegible] 237

Qy       1084 [illegible]
Db        2[illegible] [illegible]

Qy       1144 [illegible]
Db        2[illegible] [illegible]

Qy       1[illegible] [illegible]
Db        [illegible] [illegible] 417

Qy       1260 [illegible]
Db        418 GGTCCTGGGGCCCGGGTA[illegible] 477

Qy       1308 GGTGTCCTACGATGACCTCTCTGTTCGTCATTCCCTTCCACATTCAGCC 135[illegible]
Db        47[illegible] [illegible] 52[illegible]


RESULT 15
ABL25549
ID   ABL25549 standard; DNA; 2087 BP.
XX
AC   ABL25549;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID No 28120.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   [illegible]
XX
OS   Drosophila melanogaster.
XX
PN   WO[illegible]171042 A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US0[illegible].
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell cell
PT   interactions -
XX
PS   Claim 1; SEQ ID No 28120; 21pp; Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2087 BP; [illegible] A; [illegible] C; [illegible] G; 401 T; 0 other;

  Query Match             7.[illegible]%;  Score 101.2;  DB 23;  Length 2087;
  Best Local Similarity   5[illegible].9%;  Pred. No. 7.9e-14;
  Matches  287;  Conservative    0;  Mismatches  25[illegible];  Indels   [illegible];  Gaps    [illegible];

Qy        7[illegible] [illegible] 8[illegible]
Db       1[illegible] [illegible] 1171

Qy        8[illegible] [illegible] 8[illegible]
Db       1[illegible] [illegible] 1231

Qy        8[illegible] [illegible] [illegible]
Db       1[illegible] [illegible] 1291

Qy        9[illegible] [illegible] 98[illegible]
Db       1292 [illegible] 1351

Qy        9[illegible] [illegible]AGACCAT[illegible]CAGAGTCCT 1040
Db       1352 TCCCTTGCTGGCTACGTTGGCCCTCACCCTCCCTTTCCGGATCATGAGTTCCTTGCCCAT 1411

Qy       1041 GGACACAAACATCCAGCTCAAGCCCTTCTTGCTCTCTGTGCCACAGGTGATTGTGCTGGA 1100
Db       1412 [illegible] 1471

Qy       1101 TGTGGACCAGCTGGAGCTACAGGAGGATGA------------------------GTGGT 113[illegible]
Db       1472 [illegible] 15[illegible]1

Qy       11[illegible] [illegible] 11[illegible]
Db       1[illegible] [illegible] 1591

Qy       1197 GCGG[illegible] 125[illegible]
Db       1592 [illegible] 1651

Qy       1257 [illegible] 1280
Db       16[illegible]2 GCTGGTGGCCCCTGCTCGTGGCAA 1675


Search completed: February 23, 2003, 09:18:10
Job time : 344 secs
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OM nucleic - nucleic search, using sw model

Run on:         February 23, 2003, 07:31:46 ; Search time 65 Seconds
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                                              651.344 Million cell updates/sec

Title:          US-09-866-987-3
Perfect score:  1380
Sequence:       1 atgtcccgccggctaattccg..........[illegible] 1380

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters:      882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
                1: [illegible]
                2: [illegible]
                3: [illegible]
                4: [illegible]
                5: [illegible]
                6: [illegible]

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES
                        %
Result                Query
   No.     Score     Match Length  DB  ID                          Description
---  ---  ------   ------- ------ ---  ------------------------    -------------
c    1     49.8     3.6    6714   4   US-09-299-141-6             Sequence 6, Appl
c    2     49.8     3.6    6924   4   US-09-299-141-9             Sequence 9, Appl
c    3     49.8     3.6    6924   4   US-09-299-141-10            Sequence 10, Appl
c    4     49.8     3.6    6924   4   US-09-299-141-11            Sequence 11, Appl
c    5     48.2     3.5    1491   4   US-09-082-092-9             Sequence 9, Appl
c    6     48.2     3.5    1817   1   US-09-288-292A-45           Sequence 45, Appl
     7     47       3.4     349   4   US-09-198-119C-94           Sequence 94, Appl
c    8     46.4     3.4     774   3   US-08-415-655-11            Sequence 11, Appl
c    9     45.2     3.3     645   4   US-09-535-008-30            Sequence 30, Appl
    10     43.6     3.2  152331   3   US-09-128-155-16            Sequence 16, Appl
c   11     43.4     3.1    1488   4   US-09-096-776B-3            Sequence 3, Appl
c   12     43.4     3.1    2534   4   US-09-096-776B-1            Sequence 1, Appl
c   13     43.2     3.1    3946   3   US-09-083-351-1             Sequence 1, Appl
c   14     43.2     3.1    3946   4   US-09-083-352-1             Sequence 1, Appl
c   15     43       3.1    1028   4   US-08-118-207-1             Sequence 1, Appl
c   16     43       3.1    1028   4   US-08-458-745-1             Sequence 1, Appl
    17     42.8     3.1    8460   1   US-08-469-005A-9            Sequence 9, Appl
    18     [illegible]                                            Sequence 1, Appl
c   19     42.4     3.1     328   4   US-09-165-264-7             Sequence 7, Appl
c   20     42.4     3.1     328   4   US-09-165-264-13            Sequence 13, Appl
c   21     41.4     3.0     329   4   US-09-165-264-8             Sequence 8, Appl
    22     41.4     3.0    4252   2   US-08-475-844-4             Sequence 4, Appl
    23     41.4     3.0    4252   5   PCT-US95-08429-4            Sequence 4, Appl
    24     41.2     3.0    1413   4   US-08-984-709A-52           Sequence 52, Appl
    25     41.2     3.0    6453   1   US-08-336-691B-14           Sequence 14, Appl
    26     41.2     3.0    6453   3   US-09-209-668-10            Sequence 10, Appl
    27     41.2     3.0    6453   3   US-09-356-952-8             Sequence 8, Appl
    28     41.2     3.0   [illegible] 1   US-08-458-[illegible]A-11   Sequence 11, Appl
c   29     40.8     3.0   [illegible]     US-08-72[illegible]-211-1   Sequence 1, Appl
c   30     40.8     3.0    4524   4   US-09-473-716-1             Sequence 1, Appl
c   31     40.4     2.9   [illegible] 1   US-0[illegible]-428-895-11  Sequence 11, Appl
c   32     40.2     2.9    8458   1   US-07-945-285-1             Sequence 1, Appl
c   33     40       2.9    1413   4   US-08-984-709A-52           Sequence 52, Appl
c   34     39.8     2.9     332   4   US-09-165-264-11            Sequence 11, Appl
c   35     39.6     2.9    7218   1   US-08-232-463-14            Sequence 14, Appl
c   36     39.4     2.9    7000   4   US-09-236-097-7             Sequence 7, Appl
c   37     39.4     2.9    2502   1   US-08-273-[illegible]-7     Sequence 7, Appl
c   38     39.4     2.9    2502   1   US-08-254-159A-7            Sequence 7, Appl
c   39     39.4     2.9    2502   1   US-08-486-[illegible]-7     Sequence 7, Appl
c   40     39.4     2.9    2502   1   US-08-481-238-7             Sequence 7, Appl
c   41     39.4     2.9    2502   2   US-08-471-066B-7            Sequence 7, Appl
c   42     39.4     2.9    2502   2   US-08-484-956-7             Sequence 7, Appl
c   43     39.4     2.9    2502   2   US-08-757-655-7             Sequence 7, Appl
c   44     39.4     2.9    2502   2   US-08-599-491-7             Sequence 7, Appl
c   45     39.4     2.9    2502   2   US-08-756-386-7             Sequence 7, Appl

                                ALIGNMENTS

RESULT 1
US-09-299-141-6/c
; Sequence 6, Application US/09299141
; Patent No. 646[illegible]
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: [illegible]
;  APPLICANT: [illegible], MICHAEL
;  [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: 60/083,025
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 6714
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p43CB A1
US-09-299-141-6

  Query Match             3.6%;  Score 49.8;  DB 4;  Length 6714;
  Best Local Similarity   54.7%;  Pred. No. [illegible];
  Matches   99;  Conservative    0;  Mismatches   82;  Indels [illegible];  Gaps [illegible];

Qy         19 [illegible] 78
              [illegible]
Db       1652 [illegible] 1593

Qy         79 [illegible] 138
              [illegible]
Db       1592 [illegible] 1533

Qy        139 [illegible] 198
              [illegible]
Db       1532 [illegible] 1473

Qy        199 C 199
              |
Db       1472 [illegible] 1472


RESULT 2
US-09-299-141-9/c
; Sequence 9, Application US/09299141
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: 1999-04-23
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:[illegible]
;   OTHER INFORMATION: [illegible]
US-09-299-141-[illegible]

  Query Match [illegible]; Score [illegible]; DB 4; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy   [illegible]

Db   [illegible]

Qy   [illegible]

Db   [illegible]

Qy   [illegible]

Db   [illegible]

Qy   [illegible]

Db   [illegible]


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; Sequence [illegible], Application US/09299141
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: 1999-04-23
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:[illegible]
;   OTHER INFORMATION: [illegible]
US-09-299-141-[illegible]

  Query Match [illegible]; Score [illegible]; DB 4; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy   [illegible]

Db   [illegible]

Qy   [illegible]

Db   [illegible]

Qy   [illegible]

Db   [illegible]

Qy   [illegible]

Db   [illegible]


RESULT 4
US-09-299-141-11/c
; Sequence 11, Application US/09299141
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: 1999-04-23
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO 11
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:[illegible]
;   OTHER INFORMATION: [illegible]
US-09-299-141-11

  Query Match [illegible]; Score [illegible]; DB 4; Length [illegible];
  Best Local Similarity 54.[illegible]%; Pred. No. [illegible];
  Matches 99; Conservative 0; Mismatches 82; Indels [illegible]; Gaps [illegible];

Qy   [illegible]

Db   [illegible]

Qy   [illegible]

Db   [illegible]

Qy   [illegible]

Db   [illegible]

Qy   [illegible]

Db   [illegible]


RESULT 5
US-[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;    APPLICANT: [illegible]
;    APPLICANT: [illegible]
;    APPLICANT: [illegible]
;     APPLICANT:  Itoh, Susumu
;     APPLICANT:  [illegible]
;     APPLICANT:  Souchelnytskyi, Serhiy
;     APPLICANT:  Bredin, Greger
;     APPLICANT:  Landstrom, Marene
;     APPLICANT:  Heldin, Nils Erik
;     APPLICANT:  Heldin, Carl-Henrik
;     APPLICANT:  ten Dijke, Peter
;     TITLE OF INVENTION:  SMAD7 AND USES THEREOF
;     NUMBER OF SEQUENCES:  15
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;       STREET:  600 Atlantic Avenue
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  U.S.A.
;       ZIP:  02210-2211
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette
;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  [illegible]
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  [illegible]
;       FILING DATE:  [illegible]
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/047,221
;       FILING DATE:  20-MAY 1997
;       APPLICATION NUMBER:  60/[illegible]
;       FILING DATE:  30-SEP-1997
;       APPLICATION NUMBER:  60/075,940
;       FILING DATE:  25-FEB-1998
;       APPLICATION NUMBER:  60/077,032
;       FILING DATE:  06-MAR 1998
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Van Amsterdam, John R.
;       REGISTRATION NUMBER.  40,212
;       REFERENCE/DOCKET NUMBER.  10461/7022
;     TELECOMMUNICATION INFORMATION.
;       TELEPHONE:  617-720-3500
;       TELEFAX:  617 720 2441
;       TELEX:
;   INFORMATION FOR SEQ ID NO: [illegible]
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1491 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US [illegible]

  Query Match             3.5%;  Score 48.2;  DB 1;  Length 1491;
  Best Local Similarity   54.1%;  Pred. No. [illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy          5 [illegible] 64

Db        [illegible] 243

Qy         65 [illegible] 124

Db        242 [illegible] 183

Qy        125 [illegible] 184

Db        182 [illegible] 123

Qy        185 [illegible] 185
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Db        122 [illegible] 122
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RESULT [illegible]
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; Sequence 45, Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: Dean A. Falk
;  APPLICANT:  Katherine [illegible]
;  APPLICANT:  Michael Donovan
;  APPLICANT:  Dennis Buszar
;  APPLICANT:  Michael A. [illegible]
;  TITLE OF INVENTION: Compositions and Methods for the Treatment and Diagnosis [illegible]
;  TITLE OF INVENTION:  Cardiovascular Disease
;  FILE REFERENCE: 7853 [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE:  [illegible]
;  PRIOR APPLICATION NUMBER: 08/[illegible],434
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: 08/7[illegible]
;  PRIOR FILING DATE: 1997-02-13
;  PRIOR APPLICATION NUMBER: 60/011,[illegible]
;  PRIOR FILING DATE: 1996-02-16
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/[illegible],841
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
;    LENGTH: 1817
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-268-292A-45

  Query Match             3.5%;  Score 48.2;  DB 4;  Length 1817;
  Best Local Similarity   54.1%;  Pred. No. 0.016;
  Matches  98;  Conservative  [illegible];  Mismatches  83;  Indels  [illegible];  Gaps  [illegible];

Qy          5 [illegible] 64

Db        456 [illegible]

Qy         65 [illegible] 124

Db        [illegible]

Qy        125 [illegible] 184

Db        [illegible]

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Db        276 [illegible] 276


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; Sequence 94, Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT:  Thomashow, Michael
;  APPLICANT:  Stockinger, Eric
;  APPLICANT:  [illegible], Kirsten
;  APPLICANT:  Gilmour, Sarah
;  APPLICANT:  Zarka, Daniel
;  APPLICANT:  [illegible]
;  TITLE OF INVENTION:  Plant having Altered Environmental Stress [illegible]
;  FILE REFERENCE:  [illegible] Seq List
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE:  1998-[illegible]
;  PRIOR APPLICATION NUMBER:  US [illegible]
;  PRIOR FILING DATE:  1998-09-04
;  PRIOR APPLICATION NUMBER:  US [illegible]
;  PRIOR FILING DATE:  [illegible]
;    PRIOR APPLICATION NUMBER: [illegible]
;    PRIOR FILING DATE: [illegible]
;    PRIOR APPLICATION NUMBER: US 09/[illegible]
;    PRIOR FILING DATE: 1998-02-[illegible]
;    PRIOR APPLICATION NUMBER: [illegible]
;    PRIOR FILING DATE: 1998-[illegible]
;    PRIOR APPLICATION NUMBER: [illegible]
;    PRIOR FILING DATE: 1998-02-[illegible]
;    PRIOR APPLICATION NUMBER: [illegible]
;    PRIOR FILING DATE: 1998-[illegible]
;    NUMBER OF SEQ ID NOS: [illegible]
;    SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: [illegible]
;   FEATURE:
;   OTHER INFORMATION: [illegible]
US-[illegible]

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  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy  [illegible]
Db  [illegible]

Qy  [illegible]
Db  [illegible]

Qy  [illegible]
Db  [illegible]

RESULT [illegible]
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; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;     APPLICANT: [illegible]
;     APPLICANT: [illegible]
;     TITLE OF INVENTION: [illegible] NUCLEIC ACID [illegible]
;     TITLE OF INVENTION: p[illegible]KIP[illegible], A CYCLIN DEPENDENT KINASE INHIBITOR AND USES [illegible]
;     TITLE OF INVENTION: SAME
;     NUMBER OF SEQUENCES: [illegible]
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: Cooper & Dunham
;       STREET: 1185 Avenue of the Americas
;       CITY: New York
;       STATE: New York
;       COUNTRY: United States of America
;       ZIP: [illegible]
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.[illegible]
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/[illegible]
;       FILING DATE:
;       CLASSIFICATION: [illegible]
;     ATTORNEY/AGENT INFORMATION:
;       NAME: White, John P.
;       REGISTRATION NUMBER: [illegible]
;       REFERENCE/DOCKET NUMBER: [illegible]
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: (212) [illegible]
;       TELEFAX: (212) [illegible]
;   INFORMATION FOR SEQ ID NO: [illegible]
;     SEQUENCE CHARACTERISTICS:
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;       LENGTH: [illegible] base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: [illegible]NA
;     HYPOTHETICAL: N
;     ANTI-SENSE: N
US-08-415-655-[illegible]

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy  [illegible]
Db  772 [illegible]

Qy  [illegible]
Db  712 [illegible]

Qy  [illegible]AGAGA[illegible]
Db  652 [illegible]AAGAGA[illegible] 613

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; Sequence [illegible], Application US/09[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: Wong, Alexander K.[illegible]
;  APPLICANT: Tavtigian, Sean V.
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: [illegible] IS A TUMOR SUPPRESSOR THAT IS MUTATED IN [illegible]
;  TITLE OF INVENTION: AND OTHER CANCER TYPES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/[illegible]
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: U.S. [illegible]/12[illegible]
;  EARLIER FILING DATE: 199[illegible]-23
;  NUMBER OF SEQ ID NOS: 7[illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-[illegible]

  Query Match             [illegible];  Score [illegible];  DB 4;  Length 64[illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy        6 [illegible]
Db  [illegible]

Qy  [illegible]
Db  [illegible]

Qy  [illegible]
Db  [illegible]

Qy      [illegible] ACGA[illegible]
Db  [illegible]

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; Sequence [illegible], Application US/[illegible]
; Patent No. 6117654
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;  TITLE OF INVENTION: NOVEL MOLECULES OF THE TANGO-77 RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 10404/052001
;  CURRENT APPLICATION NUMBER: US/09/128,155
;  CURRENT FILING DATE: 1998-08-03
;  EARLIER APPLICATION NUMBER: US 60/091,650
;  EARLIER FILING DATE: 1998-07-02
;  EARLIER APPLICATION NUMBER: US 60/054,646
;  EARLIER FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 152331
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(152331)
;   OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

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  Matches  103;  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy          3 GTCCGCCGGCTGGTTCGGGCGCCGCTTCCTGCCTGGGAGCCGCTCCCGGCGCCCGGCC 62

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Qy         63 [illegible] 122

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Qy        123 [illegible] 182

Db      22117 [illegible] 22176

Qy        183 [illegible] 204

Db      22177 [illegible] 22198


RESULT 11
US-09-096-776B-3/c
; Sequence 3, Application US/09096776B
; Patent No. 6270964
; GENERAL INFORMATION:
;  APPLICANT:  Miyazono, Kohei
;  APPLICANT:  Kawabata, Masahiro
;  TITLE OF INVENTION:   SMAD6 AND USES THEREOF
;  FILE REFERENCE:   10461/7038
;  CURRENT APPLICATION NUMBER:  US/09/096,776B
;  CURRENT FILING DATE:  1998-06-12
;  PRIOR APPLICATION NUMBER:   US 60/049,[illegible]
;  PRIOR FILING DATE:   1997-06-13
;  PRIOR APPLICATION NUMBER:   US 60/053,040
;  PRIOR FILING DATE:   1997-07-18
;  PRIOR APPLICATION NUMBER:   US 60/066,173
;  PRIOR FILING DATE:   1997-11-18
;  NUMBER OF SEQ ID NOS:   10
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1488
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-096-776B-3

  Query Match             3.1%;  Score 43.4;  DB 4;  Length 1488;
  Best Local Similarity   52.5%;  Pred. No. 0.[illegible];
  Matches   95;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy          5 [illegible] 64

Db        [illegible]

Qy         65 [illegible] 124

Db        [illegible]

Qy        125 [illegible] 184

Db        [illegible]

Qy        185 C 185

Db        [illegible]


RESULT 12
US-09-096-776B-1/c
; Sequence 1, Application US/09096776B
; Patent No. 6270964
; GENERAL INFORMATION:
;  APPLICANT:  Miyazono, Kohei
;  APPLICANT:  Kawabata, Masahiro
;  TITLE OF INVENTION:   SMAD6 AND USES THEREOF
;  FILE REFERENCE:   10461/7038
;  CURRENT APPLICATION NUMBER: US/09/096,776B
;  CURRENT FILING DATE:  1998-06-12
;  PRIOR APPLICATION NUMBER:   US 60/049,[illegible]
;  PRIOR FILING DATE:   1997-06-13
;  PRIOR APPLICATION NUMBER:   US 60/053,040
;  PRIOR FILING DATE:   1997-07-18
;  PRIOR APPLICATION NUMBER:   US 60/066,173
;  PRIOR FILING DATE:   1997-11-18
;  NUMBER OF SEQ ID NOS:   10
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 2534
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (751)..(2265)
US-09-096-776B-1

  Query Match             3.1%;  Score 43.4;  DB 4;  Length 2534;
  Best Local Similarity   52.5%;  Pred. No. 0.24;
  Matches   95;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy          5 [illegible] 64

Db        [illegible]

Qy         65 [illegible] 124

Db        [illegible]

Qy        125 [illegible] 184

Db        [illegible]

Qy        185 C 185

Db        869 C 869


RESULT 13
US-09-083-351-1/c
; Sequence 1, Application US/09083351
; Patent No. 6067[illegible]
;  GENERAL INFORMATION:
;     APPLICANT:  Sheffield, Val C.
;     APPLICANT: Alward, Wallace L.M.
;     APPLICANT: Stone, Edwin M.
;     APPLICANT: Nishimura, Darryl
;     APPLICANT: Patil, Shiva
;     TITLE OF INVENTION: THERAPEUTICS AND DIAGNOSTICS F
;     TITLE OF INVENTION: [illegible] HEART DISEASE BASED ON A NOVEL HUMAN
;     TITLE OF INVENTION: TRANSCRIPTION FACTOR
;     NUMBER OF SEQUENCES: [illegible]
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: [illegible]LEY, HOAG & ELIOT LLP
;       STREET: One Post Office Square
;       CITY: Boston
;       STATE: MA
;       COUNTRY: USA
;       ZIP: [illegible]
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.[illegible]
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: [illegible]
;       FILING DATE: [illegible] MAY [illegible]
;       CLASSIFICATION: 514
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Arnold, Beth E.
;       REGISTRATION NUMBER: [illegible]
;       REFERENCE/DOCKET NUMBER: UIA-[illegible]
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: [illegible]
;       TELEFAX: [illegible]
;   INFORMATION FOR SEQ ID NO: [illegible]:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: [illegible] base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: cDNA
;     FEATURE:
;       NAME/KEY: CDS
;       LOCATION: 4[illegible]..[illegible]
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; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
;   GENERAL INFORMATION:
;     APPLICANT: Sheffield, Val C.
;     APPLICANT: Alward, Wallace L.M.
;     APPLICANT: Stone, Edwin M.
;     APPLICANT: Nishimura, Darryl
;     APPLICANT: Patil, Shiva
;     TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
;     TITLE OF INVENTION: BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
;     NUMBER OF SEQUENCES: [illegible]
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;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: [illegible]LEY, HOAG & ELIOT LLP
;       STREET: One Post Office Square
;       CITY: Boston
;       STATE: MA
;       COUNTRY: USA
;       ZIP: [illegible]
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/[illegible]
;       FILING DATE: [illegible] MAY [illegible]
;       CLASSIFICATION: 514
;     ATTORNEY/AGENT INFORMATION:
;       NAME: Arnold, Beth E.
;       REGISTRATION NUMBER: [illegible]
;       REFERENCE/DOCKET NUMBER: UIA-[illegible]
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE: [illegible]
;       TELEFAX: [illegible]
;   INFORMATION FOR SEQ ID NO: [illegible]:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: [illegible] base pairs
;       TYPE: nucleic acid
;       STRANDEDNESS: single
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;       LOCATION: 4[illegible]..[illegible]
US-[illegible]

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; Sequence 1, Application US/[illegible]
; Patent No. [illegible]
;   GENERAL INFORMATION:
;     APPLICANT: SUTHERLAND, Grant R
;     APPLICANT: RICHARDS, Robert I
;     APPLICANT: SCHLESSINGER, David
;     APPLICANT: NA[illegible], [illegible]
;     APPLICANT: KREMER, Eric J
;     APPLICANT: YU, Sui
;     APPLICANT: BAKER, Elizabeth
;     APPLICANT: MULLEY, John C
;     APPLICANT: MANDEL, Jean Louis
;     APPLICANT: PRITCHARD, Melanie April
;     APPLICANT: LYNCH, Michael
;     TITLE OF INVENTION: DNA SEQUENCES RELATED [illegible]
;     TITLE OF INVENTION: FRAGILE X SYNDROME
;     NUMBER OF SEQUENCES: 1[illegible]
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
;       STREET:  P.O. Box 1404
;       CITY:  Alexandria
;       STATE:  Virginia
;       COUNTRY:  United States
;       ZIP:  22313-1404
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
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;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/118,200
;       FILING DATE:  09-SEP-1993
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/802,650
;       FILING DATE:  05-DEC-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/672,232
;       FILING DATE:  20-MAR-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/638,518
;       FILING DATE:  04-JAN-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/966,517
;       FILING DATE:  23-DEC-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Crane Feary, Sharon E
;       REGISTRATION NUMBER:  36,113
;       REFERENCE/DOCKET NUMBER:  020160-164
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703) 836-6620
;       TELEFAX:  (703) 836-2021
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1028 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-118-200-1

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Db        421 GCCGCCGCCGCCACCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 362

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Search completed: February 23, 2003, 09:27:29
Job time : 246 secs
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OM nucleic - nucleic search, using sw model

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Perfect score:  1380
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       442[illegible]8 seqs, 28[illegible] residues

Total number of hits satisfying chosen parameters:      884236

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Database :       Published_Applications_NA:*
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    and is derived by analysis of the total score distribution.

                              SUMMARIES
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   28     42.2     3.1  42999 9   US-09-799-462A-17               Sequence 17, Appl
   29     42.2     3.1  42999 9   US-10-12[illegible]-767-17       Sequence 17, Appl
   30     42.2     3.1  42999 9   US-[illegible]-83[illegible]-911A-17   Sequence 17, Appl
c  31     41.4     3.0  12733 9   US-10-032-393-47                Sequence 47, Appl
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c  33     41.2     3.0    18[illegible] 9   US-10-0[illegible]4-717-59   Sequence 59, Appl
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c  36     40.4     2.9    477 10  US-09-804-761-14662             Sequence 14662, A
   37     40.4     2.9   1058 10  US-09-917-800A-1479             Sequence 1479, Ap
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                              ALIGNMENTS

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; Sequence 3, Application US/09866987
; Patent No. US20020[illegible]7[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible]MAN, [illegible]
;  APPLICANT: HASTINGS, [illegible]ARD
;  APPLICANT: [illegible], DAVID
;  APPLICANT: MANNING, GERARD
;  APPLICANT: [illegible], [illegible]
;  APPLICANT: [illegible]N
;  APPLICANT: HILL, RON
;  APPLICANT: FLANAGAN, PETER
;  TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
;  FILE REFERENCE: 038602/1180
;  CURRENT APPLICATION NUMBER: US/09/866,987
;  CURRENT FILING DATE: 2001-[illegible]
;  PRIOR APPLICATION NUMBER: 60/208,[illegible]
;  PRIOR FILING DATE: 2000-05-30
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1380
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: phosphatase nucleotide
US-09-866-987-3

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; GENERAL INFORMATION:
;  APPLICANT: Algate, Paul A.
;  APPLICANT: Jones, Robert
;  APPLICANT: Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/867,701
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2968
;   LENGTH: 547
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-867-701-2968

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RESULT 3
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; Sequence 1714, Application US/[illegible]A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547
;  CURRENT APPLICATION NUMBER: [illegible]A
;  CURRENT FILING DATE:  2001-07-31
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
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; Patent No. US2002[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547C[illegible]
;  CURRENT APPLICATION NUMBER: US/10/[illegible]
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1714
;   LENGTH: 5791
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-[illegible]-1714

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Db   [illegible]


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; Patent No. [illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: A[illegible] A.
;  APPLICANT: [illegible] Robert
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO [illegible]
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;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)...([illegible])
;  OTHER INFORMATION: [illegible]
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; Sequence [illegible], Application US/[illegible]
; Patent No. US20[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;                      THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR
;                      DISEASE
;  NUMBER OF SEQUENCES: [illegible]
;  CORRESPONDENCE ADDRESS:
;   ADDRESSEE: PENNIE & EDMONDS LLP
;   STREET: 1155 Avenue of the Americas
;   CITY: New York
;   STATE: NY
;   COUNTRY: USA
;   ZIP: [illegible]
;  COMPUTER READABLE FORM:
;   MEDIUM TYPE: Diskette
;   COMPUTER: IBM Compatible
;   OPERATING SYSTEM: DOS
;   SOFTWARE: FastSEQ Version [illegible]
;  CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/[illegible]
;   FILING DATE: [illegible] Apr 2001
;   CLASSIFICATION: <Unknown>
;  PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/[illegible]
;   FILING DATE: 03 MAR 1998
;   APPLICATION NUMBER: 08/8[illegible]
;   FILING DATE: [illegible]
;   APPLICATION NUMBER: 08/[illegible]
;   FILING DATE: 1[illegible] FEB 1997
;   APPLICATION NUMBER: [illegible]
;   FILING DATE: [illegible] FEB-1996
;   APPLICATION NUMBER: 08/[illegible],654
;   FILING DATE: 09 FEB-1996
;   APPLICATION NUMBER: [illegible]
;   FILING DATE: [illegible]
;   APPLICATION NUMBER: 08/[illegible],841
;   FILING DATE: 1[illegible] FEB 199[illegible]
;  ATTORNEY/AGENT INFORMATION:
;   NAME: [illegible] A
;   REGISTRATION NUMBER: [illegible]
;   REFERENCE/DOCKET NUMBER: [illegible]
;  TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (212)[illegible]
;   TELEFAX: (212)869[illegible]
;   TELEX: [illegible] PENNIE
; INFORMATION FOR SEQ ID NO: [illegible]:
;  SEQUENCE CHARACTERISTICS:
;   LENGTH: [illegible] base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: both
;   TOPOLOGY: unknown
;  MOLECULE TYPE: DNA
;  SEQUENCE DESCRIPTION: SEQ ID NO: [illegible]:
US-[illegible]-924-4[illegible]

  Query Match [illegible] Score [illegible] DB [illegible] Length [illegible]
  Best Local Similarity [illegible] Pred. No. [illegible]
  Matches [illegible] Conservative [illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]

Qy   [illegible]
Db   456 [illegible]

Qy   [illegible]
Db   396 [illegible]
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Qy        125 [illegible] 184
Db        [illegible] [illegible] 277

Qy        185 [illegible] 185

Db        278 [illegible] 278


RESULT 7
US-09-996-140-94
; Sequence 94, Application US/09996140
; Patent No. US20020157136A1
; GENERAL INFORMATION:
;  APPLICANT: Thomashow, Michael
;  APPLICANT:  Stockinger, Eric
;  APPLICANT:  Jaglo-Ottosen, Kirsten
;  APPLICANT:  Gilmour, Sarah
;  APPLICANT:  Zarka, Daniel
;  APPLICANT:  Jiang, Cai-Zhong
;  TITLE OF INVENTION: PLANT [illegible]
;  TITLE OF INVENTION:  STRESS TOLERANCE
;  FILE REFERENCE: MSU-[illegible]
;  CURRENT APPLICATION NUMBER: US/09/996,140
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: 09/706,270
;  PRIOR FILING DATE: 1996-09-04
;  PRIOR APPLICATION NUMBER: 09/018,2[illegible]
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/017,816
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,235
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/017,575
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/019,227
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,234
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/198,119
;  PRIOR FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: PCT/US99/01895
;  PRIOR FILING DATE: 1999-01-28
;  NUMBER OF SEQ ID NOS: 25[illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94
;   LENGTH: 349
;   TYPE: DNA
;   ORGANISM: Zea maize
US-09-996-140-94

  Query Match              3.4%;  Score 47;  DB [illegible];  Length 349;
  Best Local Similarity   55.1%;  Pred. No. 0.014;
  Matches   92;  Conservative    0;  Mismatches   7[illegible];  Indels    0;  Gaps    0;

Qy         19 [illegible] 78

Db        1[illegible] [illegible] 1[illegible]

Qy         79 AGCCCCGTGCCCTACCGACGGCCCCGCTTCCTTCGCGGCTCCAGCTCCAGCCCCGCGCCG 138

Db        162 [illegible] 221

Qy        139 GCCGACGCCTGCGGCCGCCCAGACTCCCGCCCCCTGCGCAGCCCCGC 185

Db        222 [illegible] 268


RESULT 8
US-09-954-456-292/c
; Sequence 292, Application US/09954456
; Patent No. US2002011505?A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/236,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/[illegible]
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/[illegible]
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/[illegible]
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/[illegible]
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 292
;   LENGTH: 40658
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-292

  Query Match              3.4%;  Score 46.8;  DB 10;  Length 40658;
  Best Local Similarity   51.7%;  Pred. No. [illegible];
  Matches   93;  Conservative    [illegible];  Mismatches   77;  Indels    [illegible];  Gaps    [illegible];

Qy         18 [illegible] 77

Db      25721 [illegible] [illegible]

Qy         78 [illegible] [illegible]

Db      [illegible] [illegible] [illegible]

Qy        138 [illegible] [illegible]

Db      25601 [illegible] [illegible]


RESULT 9
US-09-954-456-529/c
; Sequence 529, Application US/09954456
; Patent No. US2002011[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/236,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US/60/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US/60/[illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
[illegible]

  Query Match [illegible]  Score [illegible]  DB [illegible]  Length [illegible]
  Best Local Similarity [illegible]  Pred. No. [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]


RESULT [illegible]
[illegible]
; Sequence [illegible], Application [illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible] Joseph [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: GenBank Accession No. [illegible]
[illegible]

  Query Match [illegible]  Score [illegible]  DB [illegible]  Length [illegible]
  Best Local Similarity [illegible]  Pred. No. [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]
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Qy [illegible]
Db 256[illegible]


RESULT [illegible]
US-09-925-[illegible]-474
; Sequence 474, Application US/09925[illegible]
; Patent No. US20[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible] et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA[illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US00/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 1604
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: [illegible]
;   OTHER INFORMATION: [illegible]
US-09-925-[illegible]-474

  Query Match [illegible]  Score [illegible]  DB [illegible]  Length [illegible]
  Best Local Similarity [illegible]  Pred. No. [illegible],044;
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

Qy [illegible]
Db 126[illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible] AA[illegible]
Db 1508 AA[illegible] 1531


RESULT [illegible]
US-09-976-[illegible]
; Sequence [illegible], Application US/09976[illegible]
; Publication No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT: Lees, Robert S.
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/976,[illegible]
;  CURRENT FILING DATE: 2001-10-12
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-09-976-740-48

  Query Match             8.2%;  Score 44.4;  DB 9;  Length 2561;
  Best Local Similarity   55.9%;  Pred. No. 0.14;
  Matches  104;  Conservative    0;  Mismatches   81;  Indels    1;  Gaps    1;

Qy     11 [illegible]
Db    620 [illegible]

Qy     71 [illegible] 129
Db    680 [illegible] 739

Qy    130 [illegible]
Db    740 [illegible] 799

Qy    190 GGACGC 195
Db    800 [illegible]


RESULT 13
US-10-023-529-48
; Sequence 48, Application US/10023529
; Patent No. US20020129388A1
; GENERAL INFORMATION:
;  APPLICANT: Loos, Ann M.
;  APPLICANT:  Loos, Robert S.
;  APPLICANT:  Law, Simon W.
;  APPLICANT:  Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION:  PROTEINS AND THEIR USE IN DIAGNOSING AND  TREATING
;  TITLE OF INVENTION:  ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/10/023,529
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: 09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-10-023-529-48

  Query Match             8.2%;  Score 44.4;  DB 12;  Length 2561;
  Best Local Similarity   55.9%;  Pred. No. 0.13;
  Matches  104;  Conservative    0;  Mismatches   81;  Indels    1;  Gaps    1;

Qy     11 [illegible]
Db    620 [illegible]

Qy     71 [illegible]
Db    680 [illegible]

Qy    130 [illegible]
Db    740 [illegible]

Qy    190 GGACGC 195
Db    800 [illegible]


RESULT 14
US-10-023-523-48
; Sequence 48, Application US/[illegible]
; Patent No. US2002015248[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Loos, Ann M.
;  APPLICANT:  Loos, Robert S.
;  APPLICANT:  Law, Simon W.
;  APPLICANT:  Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION:  PROTEINS AND THEIR USE IN DIAGNOSING AND  TREATING
;  TITLE OF INVENTION:  ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-[illegible]
;  CURRENT APPLICATION NUMBER: US/10/[illegible]
;  CURRENT FILING DATE:  [illegible]
;  PRIOR APPLICATION NUMBER: US/09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-10-023-523-48

  Query Match             8.2%;  Score 44.4;  DB 12;  Length 2561;
  Best Local Similarity   55.9%;  Pred. No. 0.13;
  Matches  104;  Conservative    0;  Mismatches   81;  Indels    1;  Gaps    1;

Qy     11 [illegible]
Db    620 [illegible]

Qy     71 [illegible]
Db    680 [illegible]

Qy    130 [illegible]
Db    740 [illegible]
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[illegible]
  Sequence [illegible], Application US/[illegible]
  Patent No. US[illegible]
  GENERAL INFORMATION:
   APPLICANT: [illegible]
   TITLE OF INVENTION: [illegible]
   FILE REFERENCE: [illegible]
   CURRENT APPLICATION NUMBER: [illegible]
   CURRENT FILING DATE: [illegible]
   NUMBER OF SEQ ID NOS: [illegible]
   SOFTWARE: [illegible]
  SEQ ID NO [illegible]
    LENGTH: [illegible]
    TYPE: DNA
    ORGANISM: [illegible]
    FEATURE:
    NAME/KEY: [illegible]
    LOCATION: [illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible]
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                         GenCore version 5.1.3
              Copyright (c) 1993 - 2003 Compugen Ltd.

 OM nucleic - nucleic search, using sw model

Run on:          February 23, 2003, 04:45:59 ; Search time 3784 Seconds
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Title:           US-09-866-987-3
Perfect score:   1389
Sequence:        1 atgtccgccggctgattccg.........aagaagagaggtgacaacga 1389

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2054640 seqs, 11551452874 residues

Total number of hits satisfying chosen parameters:        4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :         GenEmbl:*
                 1:  gb_ba:*
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                 3:  gb_in:*
                 4:  gb_om:*
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                 7:  gb_ph:*
                 8:  gb_pl:*
                 9:  gb_pr:*
                 10:  gb_ro:*
                 11:  gb_sts:*
                 12:  gb_sy:*
                 13:  gb_un:*
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                 18:  em_in:*
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                 20:  em_om:*
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                 35:  em_htg_rod:*
                 36:  em_htg_mam:*
                 37:  em_htg_vrt:*
                 38:  em_sy:*
                 39:  em_htgo_hum:*
                 40:  em_htgo_mus:*
                 41:  em_htgo_other:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                   %
Result           Query
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     2   1369     99.[illegible] [illegible] 6  AX2[illegible]  AX2[illegible] Sequence
     3 1076.4     78.0    2121  9  AK096681                  AK096681 Homo sapi
     4   1049     7[illegible]  21[illegible]  9  HSM[illegible]  A[illegible] Homo sapi
     5 1014.4     73.5    242[illegible]  9  AK0[illegible]  AK0[illegible] Homo sapi
     6    783     56.7    1820  9  BC009644                  BC009644 Homo sapi
     7  281.8     20.4    [illegible]  9  AK0[illegible]     AK0[illegible] Homo sapi
     8  281.8     20.4    [illegible]  9  BC0[illegible]     BC0[illegible] Homo sapi
     9  2[illegible].8  19.2  25[illegible]  6  AX41[illegible]  AX41[illegible] Sequence
    10  264.8     19.2    25[illegible]  9  HSM801407        AL1[illegible]41 Homo sapi
    11  264.4     19.2    [illegible]  6  AX41[illegible]     AX41[illegible] Sequence
    12  2[illegible]  1[illegible]  [illegible]  6  AX1[illegible]  AX1[illegible] Sequence
c   13  260.2     18.9   82098  9  AC006252                  AC006252 Homo sapi
c   14  260.2     18.9  17[illegible]  9  A[illegible]       A[illegible] Homo sapi
    15  260.2     18.9  214[illegible]  9  A[illegible]      A[illegible] Homo sapi
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    17  243.4     17.6    57[illegible]  6  AX397459         AX397459 Sequence
    18  243.1     17.[illegible]  [illegible]  9  AB[illegible]  AB[illegible] Homo sapi
    19  242.4     17.6    [illegible]  9  AK0[illegible]     AK0[illegible] Homo sapi
    20  167.4     12.1     657  9  HSA336006                 AJ336006 Homo sapi
    21  16[illegible].6  11.[illegible]  [illegible]  9  HSA[illegible]  AJ[illegible] Homo sapi
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    23    157     11.4     372  9  HSNL3004R                 X83[illegible] H.sapiens
    24  154.4     11.2  [illegible]  2  AC044892             AC04489[illegible] Homo sapi
    25  12[illegible].2  9.4  [illegible]  9  HSA[illegible]  AJ[illegible] Homo sapi
    26  101.2      7.3    26[illegible]  3  AY07[illegible]  AY07[illegible] Drosophil
    27  101.2      7.3   187[illegible]  2  AC017949         AC017949 Drosophil
c   28  101.2      7.3  144746  3  AC1[illegible]            AC1[illegible] Drosophil
    29  101.2      7.3  17[illegible]  3  AC1[illegible]4515  AC1[illegible]4515 Drosophil
c   30  101.2      7.3  206845  2  AC011760                  AC011760 Drosophil
c   31  101.2      7.3  274[illegible]  3  AE00[illegible]574  AE00[illegible]574 Drosophil
c   32   68.6      5.0  125[illegible]  9  AF4293[illegible]  AF4293[illegible] Homo sapi
    33   66.2      4.8  125[illegible]  9  AF429315          AF429315 Homo sapi
c   34   64.8      4.7  15734[illegible]  2  AC11540[illegible]  AC11540[illegible] Rattus no
c   35   62.6      4.5   446[illegible]  9  AF04[illegible]  AF04[illegible] [illegible]
c   36   61.2      4.4  135733  2  AC128114                  AC128114 Rattus no
    37   58.6      4.2  141747  2  AC129004                  AC129004 Rattus no
c   38   58.2      4.2  12[illegible]  2  AC12798[illegible]  AC12798[illegible] Rattus no
    39   58.2      4.2  1[illegible]  2  AC121433              AC121433 Rattus no
c   40   58.2      4.2  2084[illegible]  2  AC094216          AC094216 Rattus no
    41   58.2      4.2  277[illegible]  2  AC0994[illegible]  AC0994[illegible] Rattus no
c   42     58      4.2  16125[illegible]  2  AC1[illegible]  AC1[illegible] Rattus no
c   43     58      4.2  1528[illegible]  2  AC1[illegible]38  AC1[illegible] Rattus no
c   44   57.8      4.2  [illegible]  2  AC09[illegible]44     AC09[illegible]44 Rattus no
    45   5[illegible]  4.2  214[illegible]  2  AC1[illegible]  AC1[illegible] Rattus no

                              ALIGNMENTS

RESULT 1
AX352514
LOCUS       AX352514                1389 bp    DNA     linear   PAT [illegible]-FEB-2002
DEFINITION  Sequence 3 from Patent WO0164[illegible].
ACCESSION   AX352514
VERSION     AX352514.1  GI:[illegible]
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Plowman,G.D., Whyte,D., Sudarsanam,S., Manning,G., Caenepeel,S.,
            Martinez,R., Hill,R.J. and [illegible]
  TITLE     Mammalian protein phosphatases
  JOURNAL   Patent: WO [illegible]-A [illegible]
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                    [illegible] Inc. (US)
FEATURES            Location/Qualifiers
     source         1..1897
                    /organism="synthetic construct"
                    /db_xref="taxon:[illegible]"
                    /note="[illegible] phosphatase [illegible]"
BASE COUNT [illegible]
ORIGIN

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  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 [illegible] 60
Db          1 [illegible] 60

Qy         61 [illegible] 120
Db         61 [illegible] 120

Qy        121 [illegible] 180
Db        121 [illegible] 180

Qy        181 [illegible] 240
Db        181 [illegible] 240

Qy        241 [illegible] 300
Db        241 [illegible] 300

Qy        301 [illegible] 360
Db        301 [illegible] 360

Qy        361 [illegible] 420
Db        361 [illegible] 420

Qy        421 [illegible] 480
Db        421 [illegible] 480

Qy        481 [illegible] 540
Db        481 [illegible] 540

Qy        541 [illegible] 600
Db        541 [illegible] 600

Qy        601 [illegible] 660
Db        601 [illegible] 660

Qy        661 [illegible] 720
Db        661 [illegible] 720

Qy        721 [illegible] 780
Db        721 [illegible] 780

Qy        781 [illegible] 840
Db        781 [illegible] 840

Qy        841 [illegible] 900
Db        841 [illegible] 900

Qy        901 [illegible] 960
Db        901 [illegible] 960

Qy        961 [illegible] 1020
Db        961 [illegible] 1020

Qy       1021 [illegible] 1080
Db       1021 [illegible] 1080

Qy       1081 [illegible] 1140
Db       1081 [illegible] 1140

Qy       1141 [illegible] 1200
Db       1141 [illegible] 1200

Qy       1201 [illegible] 1260
Db       1201 [illegible] 1260

Qy       1261 [illegible] 1320
Db       1261 [illegible] 1320

Qy       1321 [illegible] 1380
Db       1321 [illegible] 1380

RESULT 2
AX202234
LOCUS       AX[illegible]                1897 bp    DNA     linear   PAT [illegible]
DEFINITION  Sequence [illegible] from Patent WO[illegible].
ACCESSION   AX202234
VERSION     AX202234.1  GI:[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1897)
  AUTHORS   Bandman,O., Tang,Y.T., Azimzai,Y., Yue,H., Baughn,M.R.,
            Hillman,J.L., Lal,P., [illegible], [illegible], [illegible] and
            [illegible]
  TITLE     Phosphatases
  JOURNAL   Patent: WO [illegible]-A [illegible] 2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1897
                     /organism="Homo sapiens"
                     /db_xref="taxon:[illegible]"
                     /note="Incyte ID No: [illegible]"
BASE COUNT     [illegible]
ORIGIN

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  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy          1 [illegible] 60
Db          1 [illegible] 60

Qy         61 [illegible] 120
Db         61 [illegible] 120

Qy        121 [illegible] 180
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Db        121 A[illegible] 1[illegible]

Qy        181 [illegible]AATGAGAG 240
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Db        181 [illegible]AATGAGAG 24[illegible]

Qy        241 AAA[illegible]ATGTGAG [illegible]
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Db        241 AAA[illegible]GATGTGAG 300

Qy        [illegible] [illegible]ATTAC [illegible]
              [illegible]
Db        [illegible] [illegible]ATTAC [illegible]

Qy        [illegible] [illegible] 420
              [illegible]
Db        [illegible] [illegible] 42[illegible]

Qy        421 [illegible] 4[illegible]
              [illegible]
Db        421 [illegible] [illegible]

Qy        481 [illegible]AAAAC [illegible]
              [illegible]
Db        481 [illegible]AAAAC [illegible]

Qy        541 [illegible] [illegible]
              [illegible]
Db        541 [illegible] [illegible]

Qy        601 [illegible] 66[illegible]
              [illegible]
Db        601 [illegible] [illegible]

Qy        661 GCTGTGTCCTTGCAGGGAAAGCTGTACATGGCCAATGCTGGGGATAGCAGGGCCATCTTC 720
              [illegible]
Db        661 [illegible]TGCAGGGAAA[illegible] 72[illegible]

Qy        721 [illegible] 7[illegible]
              [illegible]
Db        721 [illegible] 780

Qy        781 [illegible] 840
              [illegible]
Db        781 [illegible] [illegible]

Qy        841 [illegible] [illegible]
              [illegible]
Db        841 [illegible] 9[illegible]

Qy        901 [illegible] 960
              [illegible]
Db        901 [illegible] [illegible]

Qy        961 [illegible] 1020
              [illegible]
Db        961 [illegible] [illegible]

Qy        1021 [illegible] 10[illegible]
               [illegible]
Db        1021 [illegible] 10[illegible]

Qy        10[illegible] [illegible] 11[illegible]
               [illegible]
Db        10[illegible] [illegible] 11[illegible]

Qy        1141 [illegible] 12[illegible]
               [illegible]
Db        1141 [illegible] 1[illegible]

Qy        12[illegible] [illegible] 12[illegible]
               [illegible]
Db        1201 [illegible] 1260

Qy        12[illegible] GATA[illegible] 1[illegible]
               [illegible]
Db        1261 GATACACAG[illegible] 1[illegible]

Qy        1[illegible] [illegible]
               [illegible]
Db        13[illegible] [illegible]

Qy        1380 A 1380
               |
Db        1381 A 1381


RESULT 3
AK096681
LOCUS       AK096681               2121 bp    mRNA    linear   [illegible]
DEFINITION  Homo sapiens cDNA FLJ3[illegible] fis, clone PEBLM2[illegible], weakly similar
            to PROTEIN PHOSPHATASE 2C HOMOLOG [illegible] (EC [illegible]).
ACCESSION   AK096681
VERSION     AK096681.1  GI:21756[illegible]
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens peripheral blood mononuclear cells (HPB[illegible]) cDNA to
            mRNA, clone_lib:PEBLM2 clone:PEBLM2[illegible].
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible];
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   [illegible]shima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K.,
            Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
            Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
            Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
            Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
            Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B.,
            Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and
            Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2121)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); [illegible]
            Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:[illegible], Tel:[illegible], Fax:[illegible])
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="PEBLM2[illegible]"
                     /cell_type="peripheral blood mononuclear cells
                     (HPBMC[illegible])"
                     /clone_lib="PEBLM2"
                     /note="cloning vector: pME18SFL3 primary culture,
                     peripheral blood mononuclear cells"
     CDS             4[illegible]..[illegible]
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="BAC048[illegible].1"
                     /db_xref="GI:2175[illegible]"
                     /translation="MH[illegible]
                     [illegible]
                     [illegible]"
BASE COUNT      457 a   [illegible] c   [illegible] g   [illegible] t
ORIGIN
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[illegible]

RESULT 4
[illegible]
LOCUS       [illegible]    mRNA    linear   [illegible]
DEFINITION  Homo sapiens mRNA; cDNA DKFZp[illegible] (from clone DKFZp[illegible]).
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2184)
  AUTHORS   [illegible] Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) [illegible] Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by DKFZ (German Cancer Research Center,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp[illegible]) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg [illegible]
            Berlin [illegible], GERMANY; Email: [illegible] Further
            information about the clone and the sequencing project is available
            at http://mips.gsf.de/proj/cDNA/.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /tissue_type="[illegible]"
                     [illegible]
                     [illegible]
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     polyA_signal    [illegible]
     polyA_site      [illegible]
BASE COUNT      [illegible] a   [illegible] c   [illegible] g   [illegible] t
ORIGIN

  Query Match             [illegible]
  Best Local Similarity   [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

[illegible]
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Db        128 [illegible] 187

Qy        345 [illegible] 404
Db        188 [illegible] 247

Qy        405 [illegible] 464
Db        248 [illegible] 307

Qy        465 [illegible] 524
Db        308 [illegible] 367

Qy        525 [illegible] 584
Db        368 [illegible] 427

Qy        585 [illegible] 644
Db        428 [illegible] 487

Qy        645 [illegible] 704
Db        488 [illegible] 547

Qy        705 [illegible] 764
Db        548 [illegible] 607

Qy        765 AGAGATTGAGG[illegible]CAGCAGCT------------------------------- 794
Db        608 [illegible] 667

Qy        795 ------------------------------------------------------------ 794
Db        668 [illegible] 727

Qy        795 ----[illegible] 847
Db        728 [illegible] 787

Qy        848 [illegible] 907
Db        788 [illegible] 847

Qy        908 [illegible] 967
Db        848 [illegible] 907

Qy        968 [illegible] 1027
Db        908 [illegible] 967

Qy       1028 [illegible] 1087
Db        968 [illegible] 1027

Qy       1088 [illegible] 1147
Db       1028 [illegible] 1087

Qy       1148 [illegible] 1207
Db       1088 [illegible] 1147

Qy       1208 [illegible] 1267
Db       1148 [illegible] 1207

Qy       1268 [illegible] 1327
Db       1208 [illegible] 1267

Qy       1328 [illegible] 1390
Db       1268 [illegible]


RESULT [illegible]
AK056894
LOCUS       AK056894                2429 bp    mRNA    linear   PRI [illegible]
DEFINITION  Homo sapiens cDNA FLJ32332 fis, clone PROST2005121, weakly similar
            to PROBABLE PROTEIN PHOSPHATASE 2C [illegible].
ACCESSION   AK056894
VERSION     AK056894.1  GI:16552415
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens prostate cDNA to mRNA, clone_lib:PROST2
            clone:PROST2005121.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ishibashi,T., Kimchori,K., Yosida,M., Watanabe,S., Ishida,S.,
            Ono,Y., [illegible], [illegible], Murakawa,K., Takahashi,S.,
            Kunam,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
            Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
            Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
            Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y.,
            [illegible]
            Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2429)
  AUTHORS   Isogai,T., Otsuki,T. and Sugiyama,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:[illegible]@hri.co.jp, Tel:81-438-52-[illegible], Fax:81-438-52-[illegible])
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: RAB and
            HRI.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="PROST2005121"
                     /tissue_type="prostate"
                     /clone_lib="PROST2"
                     /note="cloning vector: pME18SFL3"
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                     /protein_id="BAB71[illegible].1"
                     /db_xref="GI:16552416"
                     /translation="[illegible]
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                     VRAI[illegible]ASSKEK"
BASE COUNT      [illegible] a   [illegible] c   [illegible] g   558 t
ORIGIN

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length 2429;
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches 1615;  Conservative    [illegible];  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy         22 [illegible]
Db        145 [illegible]
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[illegible]

RESULT [illegible]
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LOCUS       BC0[illegible]11          1820 bp    mRNA    linear   PRI [illegible]
DEFINITION  Homo sapiens, clone MGC:[illegible] IMAGE:[illegible], mRNA, complete cds.
ACCESSION   BC0[illegible]11
VERSION     BC0[illegible]11.1  GI:[illegible]
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1820)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site: http://www-shgc.stanford.edu
            Contact: (Dickson, Mark) mrd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 14 Row: p Column: 20.
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                     /clone_lib="NIH_MGC_71"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             [illegible]
                     /codon_start=1
                     /product="Unknown (protein for MGC:[illegible])"
                     /protein_id="AAH[illegible]44.1"
                     /db_xref="GI:[illegible]"
                     /translation="M[illegible]
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                     [illegible]
                     [illegible]VVVMA[illegible]
                     [illegible]VSYDEVSVEVIFLHSQGQESSDH"
BASE COUNT      4[illegible] a    46[illegible] c    515 g    3[illegible] t
ORIGIN

  Query Match             [illegible]%;  Score 785;  DB 9;  Length 1820;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-144;
  Matches  785;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

[illegible]
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Qy        [illegible] 957
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Db         529 [illegible]

Qy         958 [illegible]
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Db         585 [illegible] 644

Qy        1018 [illegible] 1077
              [illegible]
Db         645 [illegible]

Qy        1078 [illegible]
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Db         705 [illegible]

Qy        1138 [illegible]
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Db         765 [illegible] 824

Qy        1198 [illegible]
              [illegible]
Db        [illegible]

Qy        1258 [illegible]
              [illegible]
Db        [illegible]

Qy        [illegible]
              [illegible]
Db         945 [illegible]

Qy        1378 TGA [illegible]
              [illegible]
Db        [illegible] TGA [illegible]


RESULT [illegible]
AK[illegible]
LOCUS       AK[illegible]             1687 bp    mRNA    linear   PRI 19-[illegible]
DEFINITION  Homo sapiens cDNA FLJ[illegible] fis, clone TESTI2012104, weakly similar
            to PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16).
ACCESSION   AK[illegible]
VERSION     AK093270.1  GI:21752092
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens testis cDNA to mRNA, clone_lib:TESTI2
            clone:TESTI2012104.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ishibashi,T., Kanehori,K., Yoshida,M., Watanabe,S., Ishida,S.,
            [illegible]
            Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
            [illegible]
            Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai Hio,Y.,
            Saito,K., Nishikawa,T., [illegible]
            [illegible] Takahashi Fujii,A.,
            Oshima,A., Sugiyama,A., Kawakami,B., [illegible]
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1687)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology [illegible]
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.), 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
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Db         [illegible]

Qy         [illegible]
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Qy         [illegible]
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Qy         535 [illegible]
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Qy         [illegible]
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RESULT [illegible]
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DEFINITION  Homo sapiens, Similar to RIKEN cDNA [illegible] gene, clone
            MGC:[illegible] IMAGE:[illegible], mRNA, complete cds.
ACCESSION   [illegible]
VERSION     [illegible]  GI:[illegible]
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible] 2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, [illegible] Center Drive, Room [illegible], Bethesda, MD [illegible],
            USA
  REMARK    NIH-MGC Project URL: http://[illegible]
COMMENT     Contact: MGC help desk
            Email: [illegible]
            Tissue Procurement: [illegible]
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://[illegible]/
            Contact: [illegible]
            Cherukuri,Y., [illegible]
            Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
            [illegible], Maduro,Q.L., Masiello,C.A., Maskeri,B., McDowell,J.C.,
            [illegible]
            Thomson,P.E., Touchman,J.W., Sturgeon,[illegible], Vogt,J.L., Walker,M.A.,
            Zhang,L.-H. and Green,E.D.

            To see distribution and MGC clone distribution information, [illegible]
            the web the I.M.A.G.E. Consortium/LLNL at: http://image.[illegible]
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Db        [illegible]

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Qy        [illegible]
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Qy        772 [illegible] 831

Db        864 [illegible] 923

Qy        832 [illegible] 891

Db        924 [illegible] 983

Qy        892 [illegible] 951

Db        984 [illegible] 1043

Qy        952 [illegible] 1011

Db       1044 [illegible] 1103

Qy       1012 [illegible] 1071

Db       1104 [illegible] 1163

Qy       1072 [illegible] 1131

Db       1164 [illegible] 1223

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Qy       1249 [illegible]

Db       [illegible]

Qy       1297 [illegible]

Db       1404 [illegible]

Qy       1357 [illegible] 1359
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Db       1464 [illegible] 1466


RESULT 9
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DEFINITION  Sequence 3 from Patent WO0218565.
ACCESSION   AX419118
VERSION     AX419118.1  GI:[illegible]
KEYWORDS    .
SOURCE      human.
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human protein phosphatase IIc-like enzyme
  JOURNAL   Patent: WO 0218565-A 3 07-MAR-2002;
            Bayer AKTIENGESELLSCHAFT (DE)
FEATURES             Location/Qualifiers
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Qy       1165 [illegible]

Db       2088 [illegible] 2147
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DEFINITION  [illegible] cDNA [illegible] DKFZp[illegible]
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ACCESSION   AL[illegible]
VERSION     AL[illegible]
KEYWORDS    .
SOURCE      [illegible]
  ORGANISM  [illegible]
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   [illegible]
  AUTHORS   [illegible], Mewes,H.W., [illegible] and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) MIPS, Am Klopferspitz [illegible]
            Martinsried, GERMANY
COMMENT     [illegible] S. Wiemann, [illegible] Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by BMFZ (Biomedical Research Center at the Charite,
            Berlin/Germany) within the cDNA sequencing consortium of the German
            Genome Project.
            [illegible] (DKFZp[illegible]) is available at the RZPD [illegible]
            [illegible] Ressourcenzentrum, Heubnerweg [illegible]
            Berlin-Charlottenburg, GERMANY; Email: [illegible] Further
            [illegible] the clone and the sequencing project is available
            at http://www.[illegible]/cDNA/.
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     [illegible]
[illegible]

  [illegible]   Score [illegible]   Length [illegible]
  [illegible]
  [illegible]

[illegible]

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DEFINITION  Sequence [illegible] from Patent WO[illegible]
ACCESSION   AX4[illegible]
VERSION     AX4[illegible]
KEYWORDS    .
SOURCE      human.
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human protein phosphatase IIc like enzyme
  JOURNAL   Patent: WO 0219[illegible] A 1 [illegible] MAR-2002;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
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Db       157 [illegible] 216
Qy        70[illegible] [illegible] 762
Db       217 [illegible] 27[illegible]
Qy        76[illegible] [illegible] 8[illegible]
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Qy       82[illegible] [illegible] 882
Db       [illegible]7 AGTGAAT[illegible] 396
Qy       88[illegible] [illegible] 942
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Db       6[illegible] [illegible]
Qy      11[illegible] [illegible]
Db       697 [illegible] 7[illegible]
Qy      12[illegible] [illegible]
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DEFINITION  Sequence [illegible] from Patent WO [illegible]
ACCESSION   AX4[illegible]71
VERSION     AX400071.1  GI:21[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tang,[illegible], [illegible], Xue,A.J., [illegible], Zhang,[illegible]
            Wang,[illegible], Zhao,[illegible], Wang,[illegible], Liu,[illegible], Drmanac,[illegible] and [illegible]
  TITLE     Nucleic acids and polypeptides
  JOURNAL   Patent: WO [illegible] A [illegible] MAR 2002;
            HYSEQ, INC. (US)
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ORIGIN

  Query Match             [illegible]%;  Score 2[illegible];  DB 6;  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
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Qy       [illegible] [illegible]
Db       [illegible] [illegible]
Qy       [illegible] [illegible]
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Qy       6[illegible] [illegible]
Db       [illegible] [illegible]
Qy       716 [illegible]
Db       [illegible] [illegible]
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[illegible]
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AC[illegible]
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DEFINITION  Homo sapiens [illegible] BAC [illegible] (Roswell Park Cancer
            Institute Human BAC Library) complete sequence.
ACCESSION   A[illegible]
VERSION     A[illegible]  GI:[illegible]
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   M[illegible], A[illegible], [illegible]
            [illegible]
            [illegible]
            [illegible] Hernandez,[illegible], K[illegible], [illegible]
            [illegible] Martinez,[illegible]
            M[illegible], Nguyen,N., [illegible], P[illegible], [illegible]
            P[illegible], R[illegible], [illegible], Shen,H.,
            [illegible], V[illegible], Wei,Y., Williamson,A.[illegible], Worley,K., Zhou,X.,
            N[illegible] and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to [illegible])
  AUTHORS   Worley,K.[illegible]
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) Molecular and Human Genetics, Baylor
            College of Medicine, One Baylor Plaza, Houston, TX [illegible], USA
REFERENCE   3  (bases 1 to 8[illegible])
  AUTHORS   Worley,K.[illegible]
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible] FEB [illegible]) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX [illegible], USA
COMMENT     On Mar [illegible] this sequence version replaced gi:[illegible].
            INFORMATION: http://[illegible] Email:
            [illegible]

            INSERT LENGTH: This sequence does not necessarily represent the
            entire insert of this clone. Overlapping regions of clones are only
            sequenced and submitted once, so the sequence for the remainder of
            the insert may be found in the record for the adjacent clone.
            Overlapping clones are noted at the beginning and end of the
            Features listing.

            ANNOTATION OF FEATURES:
               STSs are identified using ePCR (Genome Res. 7:541-550) searches
            of a local database that includes entries from dbSTS, GDB, and
            local mapping efforts.
               Repeats are identified using RepeatMasker (A. Smit and P. Green,
            unpublished) for human and Mouse sequences.
               Genes and regions of sequence similarity are identified by BLAST
            (Nat. Genet. 3:266-272) similarity (expect < 1e-4) to the
            EST and cDNA sequences. Genes demonstrate at least two exons
            flanked by consensus splice sites that maintained sequence
            continuity across the splice junctions. Sequences that are not
            identical matches are annotated as similar.

            SEQUENCING READ COVERAGE:Sequencing is completed to a minimum
            standard of double strand coverage with a minimum of 2 clones and 2
            reads with no ambiguities or 2 chemistries with a minimum of 2
            clones and 3 reads with no ambiguities. If the sequence quality for
            a region does not meet this standard, it will be indicated in the
            annotation as low coverage.

            QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality
            standards - estimated error rate less than 1 per 10,000 bases.
            Reports of lowest quality individual bases and measures of base
            quality are listed below. Description of the metrics can be found
            at URL: http://[illegible]/quality.info/[illegible]
            [illegible]

            QUALSTAT REPORT


                              Summary Statistics
            Total Length:                                           8[illegible]
            Phrap values in estimate:                               8[illegible]
            Average error rate (BCM Phrap estimate):                [illegible]
            Fraction of Phrap values less than 40 :                 [illegible]
            Number of consensus changing edits:                     [illegible]
            Number of N's in consensus :                            [illegible]


                           Consensus changing edits
            Position        Original Context          Edited Context
            [illegible]     [illegible](n)[illegible]      [illegible](t)[illegible]
            [illegible]     [illegible](n)[illegible]      [illegible](a)[illegible]
            [illegible]     [illegible](n)[illegible]      [illegible](a)[illegible]
            4[illegible]    [illegible](n)[illegible]      [illegible](a)[illegible]
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            6[illegible]    gcctcccagg(n)tcacaccatt      gcctcccagg(t)tcacaccatt


                   Distribution of quality < 40 bases

                                                                          *
                                                                          *
                                                                          *
            #                                                             *
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                   [illegible]                                             4
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            Version [illegible]
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                     /note="Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
                     Eutheria; Primates; Catarrhini; Hominidae; Homo."
     repeat_region   1..69
                     /rpt_family="Alu"
     repeat_region   78..[illegible]
                     /rpt_family="AluSx"
     gene            complement(join(588..1542,1865..2013,2124..2237,
                     2487..2550,2734..2853))
                     /note="UniGene cluster containing AI[illegible], [illegible],
                     AA227593, [illegible], AA728[illegible], R[illegible], and AA[illegible]."
     STS             647..783
                     /standard_name="stSG4882"
                     /db_xref="GDB:4[illegible]425"
     STS             695..860
                     /standard_name="[illegible]"
                     /db_xref="dbSTS:32797"
     misc_feature    5021..5285
                     /note="Region: Similar to H.sapiens genomic DNA, X87[illegible]."
     repeat_region   5178..5285
                     /rpt_family="GC_rich"
     repeat_region   5290..5532
                     /rpt_family="GC_rich"
     misc_feature    5533..5640
                     /note="Region: Similar to H.sapiens genomic DNA, X87528."
     repeat_region   6319..6652
                     /rpt_family="AluSx"
     repeat_region   complement(7672..7745)
                     /rpt_family="L1M4"
     repeat_region   complement(7747..7929)
                     /rpt_family="AluSp"
     repeat_region   8106..8173
                     /rpt_family="MER4A2"
     repeat_region   complement(8207..8491)
                     /rpt_family="AluSx"
     repeat_region   complement(8542..8591)
                     /rpt_family="AluSp"
     repeat_region   9144..9289
                     /rpt_family="MER4[illegible]"
     repeat_region   complement(9421..9582)
                     /rpt_family="FRAM"
     repeat_region   complement(9586..9631)
                     /rpt_family="(TAGA)n"
     repeat_region   complement(9665..9894)
                     /rpt_family="AluJo"
     repeat_region   9935..10052
                     /rpt_family="MIR"
     repeat_region   complement(10124..10260)
                     /rpt_family="L2"
     repeat_region   11050..11126
                     /rpt_family="L2"
     repeat_region   11143..11427
                     /rpt_family="AluSp"
     repeat_region   11960..12050
                     /rpt_family="GC_rich"
     gene            join(12104..12195,16081..16158,19[illegible]65..19[illegible],19[illegible]..[illegible],
                     20192..20[illegible]7,21117..21267,21405..21526,21986..22575)
                     /note="UniGene cluster containing AI[illegible], AA77[illegible],
                     W9[illegible]722, [illegible], AA[illegible], [illegible], and AA298126."
     repeat_region   complement(14197..14295)
                     /rpt_family="MIR"
     repeat_region   complement(14866..15168)
                     /rpt_family="AluSq"
     repeat_region   complement(15623..15726)
                     /rpt_family="(CA)n"
     repeat_region   complement(17254..17544)
                     /rpt_family="AluY"
     repeat_region   complement(18160..18451)
                     /rpt_family="AluSp"
     STS             [illegible]
                     /standard_name="[illegible]"
                     /db_xref="dbSTS:7608"
     STS             22820..22[illegible]
                     /standard_name="[illegible]"
                     /db_xref="[illegible]"
     repeat_region   complement(228[illegible]..23[illegible])
                     /rpt_family="MER[illegible]"
     repeat_region   complement(24[illegible]..24[illegible])
                     /rpt_family="L2"
     repeat_region   complement(25824..26124)
                     /rpt_family="AluSp"
     repeat_region   complement([illegible])
                     /rpt_family="([illegible])n"

  Query Match             18.9%;  Score 260.2;  DB 9;  Length 82098;
  Best Local Similarity   98.[illegible]%;  Pred. No. 1.8e-41;
  Matches  262;  Conservative    [illegible];  Mismatches    3;  Indels    [illegible];  Gaps    [illegible];

Qy        [illegible]
Db     4222 [illegible]

Qy        [illegible]
Db     4162 [illegible]

Qy      454 [illegible]
Db     4102 [illegible]

Qy      514 AGTGACCTCATTTGTTGAGGAAAAGGGCATTAGGGCAGAAGACTTATGATGGTTCA [illegible]
              ||||||||||||||||||||||||||||||||||||||||| |||| ||||||||||||
Db     4042 [illegible]

Qy      574 TTGGAGAGTGCTTTCAGGAATGTG 598
              |||||||||||||||| |||||||
Db     3982 TTGGAGATGCCTTTCAGGAATGTG 3958


RESULT 14
AC092045/c
LOCUS       AC092045               17[illegible] bp    DNA     linear   [illegible]
DEFINITION  Homo sapiens chromosome [illegible] clone RP11-[illegible], complete sequence.
ACCESSION   AC092045 AC024148
VERSION     AC092045.2  GI:15[illegible]257
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171[illegible])
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C. and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 171[illegible])
  AUTHORS   Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J., Levy,R.[illegible] and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (1[illegible]-JUN-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 171[illegible])
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C. and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (2[illegible]-[illegible]-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
COMMENT     On Aug 2[illegible], 2001 this sequence version replaced gi:1[illegible].
            [illegible] Genome Center
                Center: University of Washington Genome Center
                Center code: UWGC
                Web site: http://www.genome.washington.edu
```

[illegible]
Finishing Center: BCM
Project Information
Center project name: [illegible]
Center clone name: RP11-[illegible] ([illegible])
Summary Statistics
Sequencing vector: M13; [illegible]; [illegible]% of reads
Sequencing vector: plasmid; [illegible]; [illegible]% of reads
Chemistry: Dye-terminator [illegible]; [illegible] of reads
Chemistry: Dye-primer [illegible]; [illegible] of reads
Chemistry: Dye-terminator [illegible]; [illegible]% of reads
Assembly program: Phrap; version [illegible]
Consensus quality: [illegible] bases at least Q40
Consensus quality: [illegible] bases at least Q30
Consensus quality: [illegible] bases at least Q20
Insert size: [illegible]; [illegible] error; agarose-fp
Insert size: [illegible]; sum of contigs
Quality coverage: [illegible] in Q20 bases; agarose-fp
Quality coverage: [illegible] in Q20 bases; sum of contigs

Overlapping Sequences:
5': RP11-[illegible] ([illegible]) AC[illegible]
3': RP11-758M[illegible] ([illegible]) AC[illegible]

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest Fingerprinting. Comparison of the experimentally derived digest fragments with sequence predicted fragments is given below. The predicted fragments from the finished sequence consist of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately [illegible] bp) are not resolved on the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

BglII		EcoRI		HindIII	
SeqPredMap	FingPrint	SeqPredMap	FingPrint	SeqPredMap	FingPrint
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
3598	3563	1567	4662	1010	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
2644	2725	6125	6141	4985	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
17110	17042	1490	1430	11873	11554
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	5268	5277	17479	17922
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	27557	26855	8945	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]				
[illegible]	[illegible]				
[illegible]	[illegible]				
[illegible]	[illegible]				
[illegible]	[illegible]				
[illegible]	[illegible]				
[illegible]	[illegible]				

FEATURES Location/Qualifiers

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                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /chromosome "3"
                     /clone "RP11-168J18"
                     /clone_lib "RPCI human BAC library 11"
BASE COUNT     39231 a  46165 c  45178 g  40769 t
ORIGIN

  Query Match             18.9%;  Score 260.2;  DB 9;  Length 171343;
  Best Local Similarity   95.9%;  Pred. No. 1.2e-41;
  Matches  262;  Conservative    0;  Mismatches    [illegible];  Indels    0;  Gaps    0;

Qy        334 [illegible] 393
              [illegible]
Db     165894 [illegible] 165835

Qy        394 GCAGGCAGCTGGGCTGGCAAGACCCTGGACTCCTGCTTGCCTGGGCAGCTGGAGGCCCGTG 453
              [illegible]
Db     165834 [illegible] 165775

Qy        454 [illegible] 513
              [illegible]
Db     165774 [illegible] 165715

Qy        514 [illegible] 573
              [illegible]
Db     165714 AGTGACCCTCAGTTTGTGGAGGAAAAGGGATGCAGGGAGAAAGACTGGTGATCGGGCA 165655

Qy        574 TTGGAGACCTCTTTTCAGGAAGGTG 598
              [illegible]
Db     165654 TTGGAGAGTCCTTTTCAGGAAGGTG 165630


RESULT 15
AC094021
LOCUS       AC094021               214160 bp    DNA     linear   PRI 27 MAR 2002
DEFINITION  Homo sapiens chromosome 3 clone RP11-804L18, complete sequence.
ACCESSION   AC094021 AC069253
VERSION     AC094021.2  GI:19745[illegible]
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Raymond,C., Loudenmilch,J. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-2002) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
COMMENT     On Mar 27, 2002 this sequence version replaced gi:15504[illegible].
                  ------ Genome Center
                Center: University of Washington Genome Center
                Center Code: UWGC
                Web site: http://www.genome.washington.edu
                Contact: rwgcinfo@u.washington.edu
                Mapping Center: BCM
            -------------- Project Information
                Center project name: [illegible]
                Center clone name: RP11-804L18 ([illegible])
                   ---- Summary Statistics
                Sequencing vector: M13; 108821; 49% of reads
                Sequencing vector: plasmid; 51% of reads
                Chemistry: Dye-terminator ET; 83% of reads
                Chemistry: Dye-primer Bodipy; 11% of reads
                Chemistry: Dye-terminator Big Dye; 5% of reads
                Assembly program: Phrap; version [illegible]
                Consensus quality: 213971 bases at least Q40
                Consensus quality: 214139 bases at least Q30
                Consensus quality: 214157 bases at least Q20
                Insert size: 214160; sum-of-contigs
                Quality coverage: [illegible].8x in Q20 bases; sum-of-contigs
            ---------------.
            Overlapping Sequences:
                5': Mapping in progress
                3': RP11-[illegible] (CWW[illegible] 7-8) AC[illegible]
            ---------------.
            Sequence Quality Assessment:
             This entry has been annotated with sequence quality
             estimates computed by the Phrap assembly program.
             All manually edited bases have been reduced to quality zero.
             quality levels above 40 are expected to have less than
             1 error in 10,000 bp.
             Base-by-base quality values are not generally included in the
             GenBank flat file format but are available as part
             of this entry's ASN.1 file.

            This sequence was finished as follows unless otherwise noted:
            all regions were either double-stranded or sequenced with an
            alternate chemistry or covered by high quality data (i.e., Phred
            quality [illegible] 30); an attempt was made to resolve all sequencing
            problems, such as compressions and repeats; all regions were
            covered by at least one plasmid subclone or more than one M13
            subclone; and the assembly was confirmed by restriction digest.
            ---------------.
            Sequence Validation:
             This sequence has been validated by Multiple Complete Digest
             Fingerprinting. Comparison of the experimentally derived digest
             fragments with sequence predicted fragments is given below.
             The electronically-digested sequence consists of both insert and
             vector, in order to accurately represent the entire circular BAC.
             Small fragments below a variable cutoff (approximately [illegible])
             are not resolved in the fingerprint and hence do not appear
             in the table. There are no significant remaining discrepancies
             between the experimental and predicted values. Unique [illegible]
             fragments are separated by dashed lines.
                    BglII                    EcoRI                   HindIII
                  -----                 ---------                 -------
            SeqDerMap  FingPrint    SeqDerMap  FingPrint    SeqDerMap  FingPrint
            ---------  ---------    ---------  ---------    ---------  ---------


                 8254       [illegible]        [illegible]       8724       4[illegible]       [illegible]
                                   ------
                 [illegible]       [illegible]        [illegible]       [illegible]       [illegible]       [illegible]
                                   ------
                10268      10181        4872       4941        512        [illegible]
                                   -------
                14177      14184        7562       7539        11[illegible]      [illegible]
                                   -------
                 [illegible]       [illegible]        1[illegible]       1647       [illegible]       [illegible]
                                   -----
                 [illegible]       [illegible]        14[illegible]       1413       [illegible]       14[illegible]
                                   -----
                 1606       1[illegible]        4966       4941       [illegible]       [illegible]
                                   ----
                 1601       1579        5291       5277       41[illegible]       4167
                                   -------                -
                 4213       [illegible]        [illegible]       6041       [illegible]       [illegible]
                  ---               -- ---               ---
                 14[illegible]       [illegible]        8[illegible]       8[illegible]       [illegible]       [illegible]

                 1[illegible]       [illegible]        [illegible]       [illegible]       [illegible]       [illegible]
                                   ---              ---
                 5502       [illegible]        8244       8387       [illegible]       [illegible]
```

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[illegible]

              / [illegible] "[illegible] Human BAC library [illegible]"
BASE COUNT [illegible]
ORIGIN

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  Best Local Similarity [illegible]  Pred. No. [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Search completed: February [illegible]
Total time: [illegible] seconds
```

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                    GenCore version 5.1.[illegible]
          Copyright (c) 1993 - 2003 Compugen Ltd.

 [illegible] nucleic search, using sw model

Run on:          February 23, 2003, 06:41:39 ; Search time [illegible] Seconds
                                      (without alignments)
                                      [illegible] Million cell updates/sec

Title:           US-[illegible]
Perfect score:   [illegible]
Sequence:        1 [illegible]............[illegible] 138

Scoring table:   IDENTITY_NUC
                 Gapop [illegible] , Gapext [illegible]

Searched:        [illegible] seqs, [illegible] residues

Total number of hits satisfying chosen parameters:      [illegible]

Minimum DB seq length: [illegible]
Maximum DB seq length: [illegible]

Post-processing: Minimum Match [illegible]
                 Maximum Match [illegible]
                 Listing first 45 summaries

Database :       N_Geneseq_101002:*
                 1:  [illegible]*
                 2:  [illegible]*
                 3:  [illegible]*
                 4:  [illegible]*
                 5:  [illegible]*
                 6:  [illegible]*
                 7:  [illegible]*
                 8:  [illegible]*
                 9:  [illegible]*
                 10: [illegible]*
                 11: [illegible]*
                 12: [illegible]*
                 13: [illegible]*
                 14: [illegible]*
                 15: [illegible]*
                 16: [illegible]*
                 17: [illegible]*
                 18: [illegible]*
                 19: [illegible]*
                 20: [illegible]*
                 21: [illegible]*
                 22: [illegible]*
                 23: [illegible]*
                 24: [illegible]*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES

Result          Query
  No.   Score  Match Length DB  ID                    Description
----------------------------------------------------------------------------
    1   [illegible]   99.2   1837  22  AAH22961       Human phosphatase
    2   [illegible]   [illegible]    [illegible]  24  ABA94429       Human protein phos
    3   [illegible]   38.8    547  24  ABL7[illegible]       Human ovarian canc
    4   [illegible]   [illegible]   [illegible]  24  ABK47452       DNA encoding human
    5   [illegible]   [illegible]   4262  17  AAT[illegible]       Rat petrin cDNA cl
    6   [illegible]   [illegible]   [illegible]  17  AAT[illegible]       Rat petrin cDNA.
    7   24[illegible]  17.6   1617  23  AAS93640       DNA encoding novel
    8   2[illegible].4  17.6   1887  22  AAI58166       Human polynucleoti
    9   2[illegible]   17.[illegible]   [illegible]  [illegible]  ABK[illegible]       cDNA encoding [illegible]
   10   242.4  17.6   [illegible]  22  AAH17958       Human cDNA sequenc
   11   [illegible]   [illegible]   [illegible]  17  AAT[illegible]       Rat petrin cDNA [illegible]
   12   1[illegible].2   [illegible]   [illegible]  2[illegible]  AAA[illegible]       Human [illegible]
   13   [illegible]   7.[illegible]   [illegible]  2[illegible]  AAT[illegible]       Human gene express
   14   1[illegible]   7.4   [illegible]  2[illegible]  AAX[illegible]       Human [illegible]
   15   101.2   7.[illegible]   [illegible]  2[illegible]  ABL2[illegible]       Drosophila melan [illegible]
   16   101.2   7.[illegible]   [illegible]  2[illegible]  ABL2[illegible]       Drosophila melan [illegible]
   17   [illegible]   [illegible]   [illegible]  24  ABL[illegible]       Human ovarian canc
   18   [illegible]   [illegible]   [illegible]  2[illegible]  AAX[illegible]       Human [illegible]
   19   87.[illegible]   [illegible]   [illegible]  21  AAA[illegible]       Human [illegible]
   20   8[illegible]   [illegible]   [illegible]  21  AAA[illegible]       Human [illegible]
   21   81.2   [illegible]   [illegible]  2[illegible]  ABV22[illegible]       Human prostate exp
   22   81.2   [illegible]   [illegible]  2[illegible]  ABV2[illegible]       Human prostate exp
   23   81.2   [illegible]   [illegible]  2[illegible]  ABV2[illegible]       Human prostate exp
   24   81.2   [illegible]   [illegible]  2[illegible]  ABV2[illegible]       Human prostate exp
   25   81.2   [illegible]   [illegible]  2[illegible]  ABV2[illegible]       Human prostate exp
c  26   [illegible]   [illegible]   [illegible]  22  AAH[illegible]       Human cDNA [illegible]
   27   [illegible]   4.[illegible]   [illegible]  17  AAT[illegible]       Rat petrin cDNA [illegible]
   28   [illegible]   [illegible]   [illegible]  2[illegible]  AAF[illegible]       [illegible]
c  29   4[illegible]   [illegible]   [illegible]  21  AAZ[illegible]       Nucleotide sequence
c  30   4[illegible]   [illegible]   [illegible]  21  AAZ[illegible]       Nucleotide sequence
c  31   4[illegible]   [illegible]   [illegible]  21  AAZ[illegible]       Nucleotide sequence
c  32   4[illegible]   [illegible]   [illegible]  22  AAK[illegible]       Human immune/haema
   33   4[illegible]   [illegible]   [illegible]  2[illegible]  AAI[illegible]       Human p[illegible]
c  34   4[illegible]   [illegible]   [illegible]  24  ABK4[illegible]       Protein phosphatase
c  35   48.[illegible]   [illegible]   [illegible]  24  ABQ68452       Listeria monocytog
c  36   48.2   [illegible]   [illegible]  2[illegible]  AAX[illegible]147       Nucleotide sequence
c  37   48.2   [illegible]   288[illegible]  24  AAD36162       Human Smad[illegible] cDNA.
c  38   48   [illegible]   [illegible]  24  ABQ37614       Oligonucleotide to
   39   48   [illegible]   [illegible]  24  ABQ37015       Oligonucleotide to
   40   47.[illegible]   [illegible]   [illegible]  12  AAZ11247       PPV 38K gene. Pse
c  41   47.[illegible]   [illegible]   [illegible]  [illegible]  [illegible]       [illegible]
   42   47   [illegible]   [illegible]  [illegible]  AAZ23504       Z. mays CBF homolo
c  43   4[illegible]   [illegible]   [illegible]  21  ABN97155       Gene #[illegible] used to
c  44   4[illegible]   [illegible]   [illegible]  21  ABL64932       Lung cancer relate
c  45   4[illegible]   [illegible]   [illegible]  21  ABL65219       Lung cancer relate

                              ALIGNMENTS

RESULT 1
AAH22961
ID   AAH22961 standard; DNA; 1837 BP.
XX
AC   AAH22961;
XX
DT   17 SEP 2001  (first entry)
XX
DE   Human phosphatase (II) [illegible] cDNA (clone ID 172[illegible]).
XX
KW   Phosphatase; PI; Alzheimer's disease; Huntington's disease; [illegible]
KW   immune disorder; cancer; [illegible]; immunomodulatory; cytostatic;
KW   neuroprotective; anti[illegible].
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             [illegible]
FT                   /*tag= a
FT                   /product= "phosphatase"
XX
PN   W[illegible]-A[illegible].
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US[illegible].
XX
PR   21-JAN-2000; 2000US-[illegible].
PR   28-JAN-2000; 2000US-[illegible].
PR   25-FEB-2000; 2000US-[illegible].
PR   17-MAR-2000; 2000US-[illegible].
XX
```

```
PA   (INCY ) INCYTE GENOMICS INC.
XX
PI   Bandman O,  Tang YT,  Azimzai Y,  Yue H,  Baughn MR,  Hafalia AJA;
PI   Lal P,  Wang E,  Gandhi AR,  Policky JL,  Mathur P;
XX
DR   WPI; 2001-[illegible]05/18.
DR   P-PSDB; [illegible].
XX
PT   Novel phosphatases useful for treating diseases associated with
PT   decreased expression of functional phosphatases, e.g., Alzheimer's
PT   disease, Huntington's disease, immune disorders, and cancers
XX
PS   Claim 5; Page 100; 108pp; English.
XX
CC   The invention provides human phosphatases (PP) and polynucleotides
CC   encoding the phosphatases. The polypeptides can be expressed by standard
CC   recombinant methodology. The PP are useful for treating a disease or
CC   condition associated with decreased expression of functional
CC   phosphatases. Compositions containing agonists or antagonists of PP may
CC   be used to treat a disease associated with decreased expression or
CC   overexpression of PP, respectively. Such diseases may include
CC   Alzheimer's disease, Huntington's disease, immune disorders, and
CC   cancers. The present sequence represents a human phosphatase encoding
CC   cDNA
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; 0 other;

  Query Match             [illegible];  Score [illegible];  DB 22;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative    0;  Mismatches    [illegible];  Indels    1;  Gaps    1;

Qy          1 [illegible] 60
              [illegible]
Db          1 [illegible] 60

Qy         61 [illegible] 120
              [illegible]
Db         61 [illegible] 120

Qy        121 [illegible] 180
              [illegible]
Db        121 [illegible] 180

Qy        181 [illegible] 240
              [illegible]
Db        181 [illegible] 240

Qy        241 [illegible] 300
              [illegible]
Db        241 [illegible] 300

Qy        301 [illegible] 360
              [illegible]
Db        301 [illegible] 360

Qy        361 [illegible] 420
              [illegible]
Db        361 [illegible] 420

Qy        421 [illegible] 480
              [illegible]
Db        421 [illegible] 480

Qy        481 [illegible] 540
              [illegible]
Db        481 [illegible] 540

Qy        541 [illegible] 600
              [illegible]
Db        541 [illegible]

Qy        601 [illegible]
              [illegible]

Db        601 [illegible] 660

Qy        661 [illegible] 720
              [illegible]
Db        661 [illegible] 720

Qy        721 GTGCGGAGAGATGAGATACGGCCACTGAGCTTGAGTTCACCCAGAGACTGAGCGGCAG 780
              [illegible]
Db        721 [illegible] 780

Qy        781 CGGATCCAGCAGCTGGCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCGACTG 840
              [illegible]
Db        781 CGGATCCAGCAGCTGGCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCGACTG 840

Qy        841 GAGTTCCCTCGGCGGCTGAAGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCAC 900
              [illegible]
Db        841 GAGTTCCCTCGGCGGCTGAAGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCAC 900

Qy        901 CACATGAGTGGCTGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATC 960
              [illegible]
Db        901 CACATGAGTGGCTGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATC 960

Qy        961 [illegible] 1020
              [illegible]
Db        961 [illegible] 1020

Qy       1021 [illegible] 1080
              [illegible]
Db       1021 [illegible] 1080

Qy       1081 [illegible] 1140
              [illegible]
Db       1081 [illegible] 1140

Qy       1141 ATGGCAACTGATGGACTTGGAGATGTACTGTTCAAGGACCAGGTGGCATGGCTGGTGCGG 1200
              [illegible]
Db       1141 ATGGCAACTGATGGACTTGGAGATGTACTGTTCAAGGACCAGGTGGCATGGCTGGTGCGG 1200

Qy       1201 AGCTTCCTCCCTGGGAACCAAGAGG-ACCCACACAGGTTCTCAAAGCTGGCCCAGATGCT 1259
              [illegible]
Db       1201 AGCTTCCTCCCTGGGAACCAAGAGGAACCCACACAGGTTCTCAAAGCTGGCCCAGATGCT 1260

Qy       1260 GATACACAGCACACAGGGAAAGGAAGACAGTCTCACAGAGGAAGGGCAGGTGTCCTACGA 1319
              [illegible]
Db       1261 GATACACAGCACACAGGGAAAGGAAGACAGTCTCACAGAGGAAGGGCAGGTGTCCTACGA 1320

Qy       1320 TGACGTCTCTGTGGTCGTGATTCCCTTGCACAGTCAGGGCCAAGAGAGCAGTGACCACTG 1379
              [illegible]
Db       1321 [illegible] 1380

Qy       1380 A 1380
              |
Db       1381 A 1381


RESULT 2
ABA94426
ID   ABA94426 standard; cDNA; 917 BP.
XX
AC   ABA94426;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human protein phosphatase SGP050 encoding cDNA.
XX
KW   Protein phosphatase; serine threonine phosphatase; PTP; STP; SGP050;
KW   cytostatic; immunosuppressive; vasotropic; analgesic; hypertensive;
KW   hypotensive; nootropic; neuroprotective; virucide; antibacterial; human;
KW   fungicide; ophthalmological; antiinflammatory; cardiant; antimigraine;
KW   antiarthritic; muscular; antiasthmatic; osteopathic; antipsoriatic;
KW   antiarteriosclerotic; antiallergic; antidiabetic; tranquilizer; cancer;
KW   neuroleptic; antiparkinsonian; anorectic; gene therapy; ss.
XX
```

```
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..917
FT                   /*tag= a
FT                   /product= "[illegible]"
FT                   /note= "Sequence coding for approximately another 174
FT                          amino acid residues in the corresponding protein
FT                          is not printed in the specification."
XX
PN   W[illegible]-A2.
XX
PD   [illegible]
XX
PF   30-MAY-2001; 2001WO-US17[illegible].
XX
PR   [illegible]-MAY-[illegible]; [illegible]US-208[illegible]P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   [illegible], Whyte D, Sudarsanam S, Manning G, Caenepeel S;
PI   Martinez R, Hill RJ, Flanagan P;
XX
DR   WPI; [illegible]
DR   P-PSDB; ABB07334.
XX
PT   New phosphatase polypeptides for treating e.g., cancers, immune-related
PT   diseases and disorders, cardiovascular diseases, or brain or
PT   neuronal-associated diseases -
XX
PS   Claim 28; Fig 1A; 161pp; English.
XX
CC   The invention relates to human protein phosphatase polypeptides and
CC   polynucleotides. The phosphatase polypeptides are useful for diagnosing
CC   and treating various phosphatase-related diseases and conditions, such as
CC   cancers, immune-related diseases and [illegible]
CC   (e.g., reperfusion restenosis), brain or neuronal-associated diseases,
CC   metabolic disorders (e.g., diabetes or obesity), central or peripheral
CC   nervous system diseases and conditions (e.g., pain, migraine, mood
CC   disorders, hypotension, or hypertension), psychotic and neurological
CC   disorders (e.g., anxiety, schizophrenia), neurodegenerative diseases
CC   (e.g., Alzheimer's or Parkinson's disease), infections caused by viral
CC   (e.g., human immunodeficiency virus (HIV)), bacterial, fungal or prion
CC   agents, ocular diseases, macular degeneration, and inflammatory disorders
CC   (e.g., rheumatoid arthritis, multiple sclerosis, osteoarthritis). The
CC   polypeptides may also be used for screening for small molecule compounds
CC   that inhibit the catalytic activity of the encoded protein phosphatase
CC   with potential use for treating the above mentioned diseases, for
CC   generating antibodies or hybridomas, and as a diagnostic tool for
CC   detecting a disease or disorder. Genetic sequences of phosphatases are
CC   useful in gene therapy. The present sequence represents a cDNA encoding
CC   a novel human serine threonine phosphatase (STP) like phosphatase
CC   polypeptide SGP050.
XX
SQ   Sequence 917 BP; 181 A; 276 C; [illegible] G; 17[illegible] T; 0 other;

  Query Match             66.4%;  Score 917;  DB 24;  Length 917;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-203;
  Matches  917;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 [illegible]
Db          1 [illegible] 60

Qy         61 [illegible] 120
Db         61 [illegible] 120

Qy        121 [illegible] 180
Db        121 [illegible] 180

Qy        181 [illegible]
Db        181 [illegible]

Qy        241 [illegible]
Db        241 [illegible]

Qy        301 [illegible]
Db        301 [illegible]

Qy        361 [illegible]
Db        361 [illegible]

Qy        421 [illegible]
Db        421 [illegible]

Qy        481 [illegible]
Db        481 [illegible]

Qy        541 [illegible]
Db        541 [illegible]

Qy        601 [illegible]
Db        601 [illegible]

Qy        661 [illegible]
Db        661 [illegible]

Qy        721 [illegible]
Db        721 [illegible]

Qy        781 [illegible]
Db        781 [illegible]

Qy        841 [illegible]
Db        841 [illegible]

Qy        901 CACATGAGTGGTGGAG 917
              ||||||||||||||||
Db        901 CACATGAGTGGTGGAG 917


RESULT 3
ABL79990
ID   ABL79990 standard; cDNA; 917 BP.
XX
AC   ABL79990;
XX
DT   17-MAY-2002  (first entry)
XX
DE   Human ovarian cancer-related cDNA clone SEQ ID NO: [illegible].
XX
KW   Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192[illegible]-A2.
XX
PD   [illegible]-DEC-2001.
XX
PF   29-MAY-2001; 2001WO-US17[illegible].
XX
PR   2[illegible]-MAY-2000; 2000US-0[illegible].
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XX
PA   [illegible]
XX
PI   [illegible]
XX
DR   [illegible]
XX
PT   [illegible] therapy and diagnosis of ovarian cancer [illegible]
PT   polypeptide [illegible] ovarian tumor polypeptides [illegible]
PT   polypeptide [illegible] polypeptide [illegible]
PT   polypeptide
XX
PS   Claim [illegible]; SEQ ID [illegible]; [illegible]pp; English.
XX
CC   The present invention describes a composition (I) comprising [illegible]
CC   [illegible] polypeptide (II) [illegible]
CC   polypeptide encoded by a polynucleotide (III) having a cDNA sequence
CC   (S1) from the [illegible] nucleotide sequences as given in ABK[illegible]
CC   ABK[illegible]. (III) encoding (II) having a sequence (S2), a T cell
CC   population of (II), or antigen presenting cells that express (II).
CC   [illegible] activity. An oligonucleotide (IV) that hybridises to
CC   (III) can be used to detect ovarian cancer in a patient's [illegible]
CC   sample preferably serum or ovarian tissue. The method comprises
CC   contacting a biological sample from a patient with (IV), detecting the
CC   amount of polynucleotide hybridising to (IV) and comparing the amount to
CC   a predetermined cut-off value and thereby detecting ovarian cancer in the
CC   patient, where the amount of polynucleotide hybridising to (IV) is
CC   detected preferably by polymerase chain reaction (PCR). (I) comprising
CC   (II) and/or (III) is useful for stimulating and/or expanding T cells
CC   specific for an ovarian tumour protein comprising contacting T cells
CC   with (II) or (III). (III) is useful in design and preparation of
CC   [illegible] molecules for inhibiting expression of the tumour polypeptides
CC   and proteins in tumour cells and [illegible] full length genes from a
CC   suitable [illegible] cDNA library using well known
CC   techniques.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; 0 other;

  Query Match             [illegible]  Score [illegible]  DB [illegible]  Length [illegible];
  Best Local Similarity   [illegible]  Pred. No. [illegible];
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible] GTTTGA [illegible]
            |||||||
Db   [illegible] GTTTGA [illegible]


RESULT 4
ABK474[illegible]2
ID   ABK474[illegible] standard; DNA; [illegible] BP.
XX
AC   ABK474[illegible];
XX
DT   18-JUN-2002  (first entry)
XX
DE   DNA encoding human protein phosphatase IIC like (PPIIC) enzyme.
XX
KW   Protein phosphatase IIC like; agonist; antagonist; apoptosis; AIDS;
KW   Acquired Immunodeficiency virus; genetic immunodeficiency; HIV;
KW   neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW   retinitis pigmentosa; amyotropic lateral sclerosis; myelodysplasia;
KW   aplastic anaemia; ischaemic injury; myocardial infarction; stroke;
KW   reperfusion injury; toxin induced disease; cirrhosis; wasting disease;
KW   cachexia; viral infection; hepatitis; osteoporosis; cancer; diabetes;
KW   central nervous system disorder; CNS disorder; cardiovascular disorder;
KW   inflammatory disorder; chronic obstructive pulmonary disease; [illegible]
KW   gene; ds; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             [illegible]
FT                   /*tag=  a
FT                   /product= "PPIIC"
FT                   /note= "Protein phosphatase IIC like enzyme.
FT                          Specifically claimed in claim [illegible]"
FT   misc_binding    [illegible]
FT                   /*tag=  b
FT                   /note= "Bound by the antisense oligonucleotide shown
FT                          in ABK47461"
XX
PN   WO[illegible]A1.
XX
PD   [illegible]-MAR-2002.
XX
PF   [illegible]-AUG-2001; 2001WO-EP09558.
XX
PR   [illegible]-AUG-[illegible]; [illegible].
PR   [illegible]-APR-[illegible]; [illegible].
XX
PA   (FARB ) BAYER AG.
XX
PI   Xiao Y;
XX
DR   WPI; [illegible].
DR   P-PSDB; AAU[illegible].
XX
PT   New protein phosphatase IIC like enzyme and polynucleotide, useful for
PT   treating a disease associated with an increase or decrease in
PT   apoptosis e.g. neurodegenerative diseases, viral infection,
PT   myelodysplasia, cancer, diabetes
XX
PS   Disclosure; Fig [illegible]; [illegible]pp; English.
XX
CC   The invention describes an isolated polynucleotide (I) which encodes a
CC   protein phosphatase IIC (PPIIC) like enzyme (II). (I) and (II) can be
CC   used in diagnostic assays for detecting diseases and abnormalities or
CC   susceptibility to diseases and abnormalities related to the presence of
CC   mutations in the nucleic acid sequences encoding the enzyme. (I) and (II)
CC   or its antagonists, agonists, or modulators are useful for treating a
CC   disease or disorder associated with an increase in apoptosis such as AIDS
CC   or other infections or genetic immunodeficiencies, neurodegenerative
CC   diseases (e.g. Alzheimer's disease or Parkinson's disease, retinitis
CC   pigmentosa, or amyotrophic lateral sclerosis), myelodysplasia (e.g.
CC   aplastic anaemia), ischaemic injuries (e.g. myocardial infarction, stroke
CC   or reperfusion injury), toxin induced diseases (e.g. alcohol induced
CC   liver damage or cirrhosis), wasting diseases (e.g. cachexia), viral
CC   infections (e.g. hepatitis B or C), and osteoporosis; or a decrease in
CC   apoptosis such as cancer, diabetes, CNS disorders, cardiovascular
CC   disorders, chronic obstructive pulmonary disease (COPD), and inflammatory
CC   disorders. Regulation of human PP2C-like enzyme can be used to treat
CC   disorders such as diabetes, CNS disorders, cardiovascular disorders,
CC   COPD, and cancers (e.g. leukaemia, lymphoma, or cancers of the organs).
CC   This sequence encodes the novel human protein phosphatase 2C-like enzyme
CC   described in the invention.
XX
SQ   Sequence 2518 BP; 507 A; 768 C; 759 G; 484 T; 0 other;

  Query Match             19.2%;  Score 264.6;  DB 24;  Length 2518;
  Best Local Similarity   57.7%;  Pred. No. 7.8e-52;
  Matches  537;  Conservative    0;  Mismatches  377;  Indels   16;  Gaps    [illegible];

Qy        445 [illegible] 504
Db       1369 [illegible] 1428

Qy        505 [illegible] 564
Db       1429 [illegible] 1487

Qy        565 [illegible] 624
Db       1488 [illegible] 1547

Qy        625 [illegible] 684
Db       1548 [illegible] 1607

Qy        685 [illegible] 744
Db       1608 [illegible] 1667

Qy        745 [illegible] 804
Db       1668 [illegible] 1727

Qy        805 [illegible] 864
Db       1728 [illegible] 1787

Qy        865 [illegible] 924
Db       1788 [illegible] 1847

Qy        925 [illegible] 984
Db       1848 [illegible] 1907

Qy        985 [illegible] 1044
Db       1908 [illegible] 1967

Qy       1045 [illegible] 1104
Db       1968 [illegible] 2027

Qy       1105 [illegible] 1164
Db       2028 [illegible] 2087

Qy       1165 [illegible] 1221
Db       2088 [illegible] 2147

Qy       1222 [illegible]
Db       2148 [illegible]

Qy       1280 [illegible]
Db       2208 [illegible]

Qy       1330 [illegible] 1359
Db       2268 [illegible] 2297


RESULT 5
AAT38484
ID   AAT38484 standard; cDNA; 4262 BP.
XX
AC   AAT38484;
XX
DT   16-JAN-1997  (first entry)
XX
DE   Rat petrin cDNA clone D1.
XX
KW   Petrin; neurite outgrowth associated protein; CNS;
KW   central nervous system; myelin; protein phosphatase 2C; stroke;
KW   neurodegeneration; gene therapy; ss.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 3825
FT                   /*tag= a
FT                   /note= "base 3825 is given as N in the
FT                          specification"
XX
PN   WO96[illegible] A1.
XX
PD   17-OCT-1996.
XX
PF   12-APR-1996;   [illegible].
XX
PR   13-APR-1995;   95US-[illegible].
XX
PA   [illegible]
XX
PI   [illegible]
XX
DR   WPI; 1996-477127/47.
DR   P-PSDB; AAW[illegible].
XX
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, Petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 2; Page [illegible]; [illegible]pp; English.
XX
CC   A cDNA sequence (AAT38484) codes for petrin (AAW[illegible]), a protein
CC   involved in modulating neurite growth inhibition. It was deduced
CC   from fragments of clone D1 (see also AAT38483) isolated from an
CC   adult rat brain cDNA library in lambda gt11 by screening with
CC   a monoclonal antibody that blocks the effect on neurons in culture
CC   of CNS myelin inhibitors. The petrin gene is expressed in neurons
CC   in brain tissue, particularly cerebellum Purkinje cells. It can be
CC   used to produce petrin protein and to prepare probes. Antisense
CC   sequences (see also AAT38485) can be used in gene therapy to enhance
CC   axonal regeneration.
XX
SQ   Sequence 4262 BP; [illegible] A; 1164 C; [illegible] G; [illegible] T; 0 other;

  Query Match             [illegible];  Score 262.1;  DB 17;  Length 4262;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
```

```
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible]

[illegible]
AA[illegible]
ID   AA[illegible] standard; cDNA; [illegible]
XX
AC   AA[illegible];
XX
DT   [illegible] (first entry)
XX
DE   [illegible] cDNA.
XX
KW   [illegible]
KW   central nervous system; [illegible] protein phosphatase [illegible] stroke;
KW   [illegible] degeneration; gene therapy; [illegible]
XX
OS   [illegible]
XX
FH   [illegible]
FT   [illegible]
```

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FT                   /*tag= [illegible]
FT                   /product= petrin
FT   misc_difference [illegible]
FT                   /*tag= [illegible]
FT                   /note= "Base [illegible] is given as [illegible] in the
FT                          specification"
XX
PN   W[illegible]-A1.
XX
PD   17-OCT-1996.
XX
PF   [illegible]-APR-1996; [illegible]
XX
PR   13-APR-1995; [illegible]
XX
PA   (M[illegible]) M[illegible] SINAI H[illegible]
XX
PI   Labes M, Lozano A, Roach A, Roder J;
XX
DR   WPI; [illegible]
DR   P-PSDB; AAW[illegible].
XX
PT   Assay for substances that modulate response of neuronal cells [illegible]
PT   [illegible] isolated protein, petrin, useful in [illegible]
PT   involving nerve damage resulting from traumatic injury, stroke [illegible]
PT   CNS degenerative disorders
XX
PS   Claim 4; [illegible]; English.
XX
CC   A nucleotide sequence (AA[illegible]) codes for petrin (AAW[illegible]), a protein
CC   involved in modulating neurite growth inhibition. It was isolated
CC   from an adult rat brain cDNA library in lambda gt11 by screening
CC   with probes based on partial petrin clones (see also AA[illegible]).
CC   The human petrin locus was localised to chromosome 12. The gene
CC   is expressed in neurons in brain tissue, partic. in cerebellum
CC   Purkinje cells. It can be used to produce petrin protein and to
CC   prepare probes. Antisense sequences (see also AA[illegible]) can be used
CC   in gene therapy to enhance axonal regeneration.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible]; Score [illegible]; DB 17; Length [illegible];
  Best Local Similarity   [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible]
```

```
Qy        918 [illegible] 977

Db       1511 [illegible] 157[illegible]

Qy        978 GGCTCGGTTACTAGGAACACTGGCTGCTCCCGGGGCCTGGGAGACCATCAGCTCAGAGT 1037

Db       1571 [illegible] 16[illegible]

Qy       1038 GCTGGACACAAACATCCAGCTCAAGCCCTTCTTGCTCTCTGTGCCACAGGTGACTGTGCT 1097

Db       1631 [illegible]

Qy       1[illegible] [illegible] 11[illegible]

Db       16[illegible] [illegible] 17[illegible]

Qy       11[illegible] [illegible] 121[illegible]

Db       1751 [illegible]

Qy       1215 [illegible] 12[illegible]

Db       1811 [illegible] 1[illegible]


RESULT 7
AAS93640
ID   AAS93640 standard; DNA; 1[illegible]17 BP.
XX
AC   AAS93640;
XX
DT   1[illegible]-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #29444.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO2001[illegible] A2.
XX
PD   [illegible]-2001.
XX
PF   [illegible]-MAR-2001; 2001WO-[illegible].
XX
PR   [illegible]
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT, Liu C, Tang YT;
XX
DR   WPI; 200[illegible]/73.
DR   P-PSDB; ABG2945[illegible].
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 1; SEQ ID No 29444; 10[illegible]pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy, to help
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS[illegible] AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp://ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1[illegible] BP; [illegible] A; 44[illegible] C; 4[illegible] G; [illegible] T; 0 other;

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length 1[illegible];
  Best Local Similarity   [illegible].9%;  Pred. No. 6.5e-47;
  Matches  45[illegible];  Conservative    [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy          [illegible]

Db        7[illegible] [illegible]

Qy        5[illegible] [illegible]

Db        7[illegible] [illegible]

Qy        620 [illegible]

Db        8[illegible] [illegible]

Qy        6[illegible] [illegible]

Db        911 [illegible]

Qy        74[illegible] [illegible]

Db        971 [illegible]

Qy        80[illegible] [illegible]

Db       10[illegible] [illegible]

Qy        86[illegible] [illegible]

Db       1[illegible] [illegible]

Qy        92[illegible] [illegible]

Db       1151 [illegible] 121[illegible]

Qy        980 [illegible]

Db       1211 [illegible] 12[illegible]

Qy       1040 [illegible]

Db       1271 [illegible]

Qy       1100 [illegible] 115[illegible]

Db       1[illegible] [illegible]

Qy       1[illegible] [illegible] 12[illegible]

Db       1[illegible] [illegible] 145[illegible]

Qy       1217 [illegible] 127[illegible]

Db       1[illegible] [illegible] 151[illegible]

Qy       127[illegible] [illegible] 127[illegible]

Db       1511 G 1511
```

```
[illegible]
[illegible]
ID   [illegible] NA [illegible]
XX
AC   [illegible]
XX
DT   [illegible] (first entry)
XX
DE   [illegible] polypeptide [illegible] N [illegible]
XX
KW   [illegible] immunosuppressant; cytostatic; gene therapy; [illegible]
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   [illegible] disease; [illegible]
KW   [illegible] lateral sclerosis; Shy Drager syndrome; chemotaxis;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   [illegible]
XX
OS   Homo sapiens.
XX
PN   W[illegible]
XX
PD   [illegible]
XX
PF   [illegible] W[illegible]
XX
PR   [illegible] JAN [illegible]
PR   [illegible] APR [illegible]
PR   [illegible] 2000; 2000US [illegible]
PR   16-JUN-2000; 2000US 0620312.
PR   [illegible] AUG 2000; 2000US [illegible]
PR   11-SEP-2000; 2000US [illegible]
PR   19-OCT-2000; 2000US 0693036.
PR   [illegible] NOV 2000; 2000US [illegible]
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang Y, [illegible] Asundi V, [illegible]
PI   Wang [illegible] Wang Z, Wehrman T, Xu C, Xue A, Yang Y, Zhang [illegible]
PI   [illegible] Goodrich R, Drmanac RT;
XX
DR   WPI; [illegible]
DR   [illegible] AAM[illegible]
XX
PT   [illegible] acids and polypeptides [illegible] treat [illegible]
PT   [illegible] central nervous system disorders
XX
PS   [illegible] N [illegible] English.
XX
CC   The invention relates to human nucleic acids (AA[illegible] AA[illegible]) and
CC   the encoded polypeptides (AAM[illegible] AAM[illegible]) with neotropic,
CC   [illegible] suppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   [illegible] neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy Drager Syndrome. Other uses include the
CC   [illegible]
CC   A[illegible] chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   [illegible] receptor activity, arthritis and inflammation, leukaemias and
CC   CNS disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] other;

  [illegible]
  [illegible]
  Matches [illegible] Conservative [illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]
```

```
Qy   [illegible]
Db   677 [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   740 [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   920 [illegible]
Db   1097 [illegible]

Qy   980 [illegible]
Db   1157 [illegible]

Qy   1040 [illegible]
Db   1217 [illegible]

Qy   1100 [illegible]
Db   1277 [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   1457 G 1457


RESULT [illegible]
ABK46[illegible]
ID   ABK46[illegible] standard; cDNA; [illegible] BP.
XX
AC   ABK46[illegible];
XX
DT   [illegible] (first entry)
XX
DE   cDNA encoding [illegible] protein, SEQ ID NO 1714.
XX
KW   Human; [illegible] cancer; immuno[illegible]
KW   immunotherapy; [illegible]
XX
OS   Homo sapiens.
XX
PN   W[illegible] A[illegible]
```

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XX
PD   14-FEB-2002.
XX
PF   [illegible] JUL-2001; 2001WO-US21218.
XX
PR   [illegible]
PR   2[illegible] MAR-2001; 2001US-279763P.
PR   29-JUN-2001; 2001US-302051P.
XX
PA   (C[illegible] ) C[illegible]IXA CORP.
XX
PI   King GP, Meagher M[illegible]
XX
DR   WPI; 2002-[illegible]
XX
PT   New colon cancer polypeptides and polynucleotides, useful as vaccines
PT   for diagnosing, preventing, and treating colon cancer, and as markers
PT   for the progression of cancer
XX
PS   Claim 1; SEQ ID NO 1714; 147pp; English.
XX
CC   The invention relates to polynucleotides encoding colon tumour proteins.
CC   The polynucleotides and encoded polypeptides are useful in pharmaceutical
CC   compositions, such as vaccines, for the diagnosis, prevention, and
CC   treatment of colon cancer. Polynucleotide sequences may be used as
CC   hybridisation probes or primers, and in the design and preparation of
CC   ribozyme molecules for inhibiting expression of tumour polypeptides and
CC   proteins in tumour cells. The compositions are useful for stimulating an
CC   immune response against cancer, particularly for the immunotherapy of
CC   colon cancer, and as markers for the progression of cancer.
CC   ABK11450-ABK46237 represent coding sequences of human colon tumour
CC   proteins of the invention.
CC   Note: With the exception of SEQ ID No 1 and 2, the sequence data
CC   for this patent did not form part of the printed specification but was
CC   supplied by the European Patent Office.
XX
SQ   Sequence 5791 BP; 1436 A; 1312 C; 1395 G; 1648 T; 0 other;

  Query Match             17.6%;  Score 243.4;  DB 24;  Length 5791;
  Best Local Similarity   57.9%;  Pred. No. [illegible];
  Matches  452;  Conservative    0;  Mismatches  [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy        500 GCTGCAT[illegible] 559

Db        401 GCTCCCCCAGCACGCCCCCCACAGGCTTCTTTACCGAGAAGAAGATTCCCCATCACTCCC 460

Qy        560 TGGTGATCGGGCATTGGAGAGTGCCTTTCAGGAATCTCATCACCTCATCCCCCCCAGC 619

Db        461 TGGTCAT[illegible] 520

Qy        620 TGGAGGCCTCAGCCCAGATGGCGGCTGCACAGCCCTGGTGGCTGTGTCCCTGCAGGGAA 679

Db        521 GGACTTCATATAATATATCTGGTGGCTGCATGGCCCTCATTGTGATTTGCCTTTTGGGGA 580

Qy        680 [illegible] 739

Db        581 [illegible] 640

Qy        740 [illegible] 799

Db        641 TCCCCA[illegible] 700

Qy        800 TTGTCTATCTTGAGCTTCTGGCTGGTGAGTTCACCGGACTGGAGTTCCTCGGGCGGCTGA 859

Db        701 [illegible] 760

Qy        860 AGGGGGAT[illegible] 919

Db        761 [illegible] 820

Qy        920 [illegible] 979

Db        821 [illegible] 880

Qy        980 [illegible] 1039

Db        881 [illegible] 940

Qy       1040 [illegible] 1099

Db        941 ATGAC[illegible] 1000

Qy       1100 [illegible] 1159

Db       1001 [illegible] 1060

Qy       1160 [illegible] 1216

Db       1061 [illegible] 1120

Qy       1217 [illegible] 1276

Db       1121 ATCCAGATGAT[illegible] 1180

Qy       1277 G 1277
              |
Db       1181 G 1181


RESULT 10
AAH17958
ID   AAH17958 standard; cDNA; 1903 BP.
XX
AC   AAH17958;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:17737.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 8; SEQ ID 17737; 2537pp; CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5' end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3' end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5' end sequence/3' end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full length cDNAs. The primers allow obtaining of the full length
CC   cDNAs easily, without any specialised methods. AAH0[illegible] to AAH1[illegible] and
CC   AAH1[illegible] to AAH18[illegible] represent human cDNA sequences; AAB9[illegible] to
CC   AAB[illegible] represent human amino acid sequences; and AAH1[illegible] to AAH1[illegible]
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 19[illegible] BP; 4[illegible] A; [illegible] C; [illegible] G; [illegible] T; 0 other;

  Query Match             1[illegible]%;  Score 2[illegible];  DB 22;  Length 19[illegible];
  Best Local Similarity   5[illegible]%;  Pred. No. [illegible];
  Matches  4[illegible];  Conservative    [illegible];  Mismatches  3[illegible];  Indels    [illegible];  Gaps    [illegible];

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]
```

```
RESULT 11
AAI38482
ID   AAI38482 standard; cDNA; 479 BP.
XX
AC   AAI38482;
XX
DT   16-JAN-1997  (first entry)
XX
DE   Rat petrin cDNA clone BI 413.
XX
KW   Petrin; neurite outgrowth associated protein; CNS;
KW   central nervous system; myelin; protein phosphatase 2C; stroke;
KW   neurodegeneration; gene therapy; ss.
XX
OS   Rattus sp.
XX
PN   WO9632476-A1.
XX
PD   17-OCT-1996.
XX
PF   12-APR-1996;   96WO-CA00214.
XX
PR   13-APR-1995;   95US-0421701.
XX
PA   ([illegible]) [illegible] HOSPITAL CORP.
XX
PI   [illegible] M,  Lozano A,  Roach A,  Roder J;
XX
DR   WPI; 1996-[illegible]/47.
XX
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, Petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 2; Page 49; 119pp; English.
XX
CC   A cDNA clone (AAI38482), designated BI 413, is a fragment of clone
CC   BI (see also AAI38479-81 and AAI38483) that codes for petrin (AAW04027),
CC   a protein involved in modulating neurite growth inhibition. It
CC   was isolated from an adult rat brain cDNA library by screening with
CC   a monoclonal antibody capable of neutralising the inhibition of
CC   neurite growth by several neuronal types on CNS myelin substrates.
CC   The gene is expressed in neurons in brain tissue, partic. in
CC   cerebellum Purkinje cells.  It can be used to produce petrin
CC   protein and to prepare probes.  Antisense sequences (see also
CC   AAI38484) can be used in gene therapy to enhance axonal regeneration.
XX
SQ   Sequence 479 BP; 140 A; 105 C; 127 G; 107 T; 0 other;

  Query Match             12.9%;  Score 178;  DB 17;  Length 479;
  Best Local Similarity   63.1%;  Pred. No. 7.5e-32;
  Matches  274;  Conservative    0;  Mismatches  160;  Indels    0;  Gaps    0;

Qy       [illegible]
Db        27 [illegible] 86

Qy       [illegible]
Db       [illegible] 146

Qy       [illegible]
Db       147 [illegible] 206

Qy       [illegible]
Db       207 [illegible]

Qy       [illegible]
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Db        267 [illegible] 326

Qy       1054 [illegible]
Db        327 [illegible]

Qy       1114 [illegible]
Db        387 [illegible] 446

Qy       1174 AA[illegible] 1187
Db        447 AA[illegible] 460


RESULT 12
AAA02811
ID   AAA02811 standard; cDNA; 729 BP.
XX
AC   AAA02811;
XX
DT   14-MAY-2000  (first entry)
XX
DE   Human colon cancer cell line polynucleotide sequence SEQ ID NO:2802.
XX
KW   Human; colon cancer; tumour; diagnosis; gene expression product;
KW   probe; detection; cancerous state; metastasis; identification;
KW   breast cancer; oestrogen receptor-positive breast cancer; therapy;
KW   oestrogen receptor negative breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9958675-A2.
XX
PD   18-NOV-1999.
XX
PF   14-MAY-1999;   99WO-US10602.
XX
PR   14-MAY-1998;   98US-0085426.
PR   15-MAY-1998;   98US-0085537.
PR   15-MAY-1998;   98US-[illegible].
PR   21-OCT-1998;   98US-0105234.
PR   27-OCT-1998;   98US-0105877.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE ) HYSEQ INC.
XX
PI   Williams LT,  Escobedo J,  Innis MA,  Garcia PD,  Sudduth-Klinger J;
PI   Reinhard C,  Giese K,  Randazzo F,  Kennedy GC,  Pot D,  Kassam A,
PI   Lamson G,  Drmanac R,  Crkvenjakov R,  Dickson M,  Drmanac S,  Labat I,
PI   Leshkowitz D,  Kita D,  Garcia V,  Jones LW,  Stache-Crain B;
XX
DR   WPI; 2000-126359/11.
XX
PT   Polynucleotide library used to determine cancerous states of mammalian
PT   cells -
XX
PS   Claim 1; Page 905; 1097pp; English.
XX
CC   AAA0[illegible] to AAA0[illegible]716 represent polynucleotides isolated from cDNA
CC   libraries constructed from human colon cancer cell lines. The present
CC   invention also describes a method of detecting differentially expressed
CC   genes correlated with a cancerous state of a mammalian cell, comprising
CC   detecting at least one differentially expressed gene product in a test
CC   sample derived from a cell suspected of being cancerous, where detection
CC   of the differentially expressed gene product is correlated with a
CC   cancerous state of the cell from which the test sample was derived.
CC   The polynucleotides sequences can be used in a method for detecting
CC   differentially expressed genes correlated with a cancerous state of a
CC   mammalian cell. The polynucleotides can also be used as probes for
CC   detecting and mapping related genes. They can be used in diagnosis and
CC   prognosis of diseases and disorders (e.g. identification of
CC   pre-metastatic or metastatic cancerous states, stages of cancer, or
CC   responsiveness of cancer to therapy). This is particularly for breast
CC   cancer, oestrogen receptor-positive breast cancer, oestrogen receptor
CC   negative breast cancer, lung cancer, and colon cancer.
XX
SQ   Sequence 729 BP; 180 A; 198 C; 185 G; 161 T; 5 other;

  Query Match             [illegible];  Score [illegible];  DB 21;  Length [illegible];
  Best Local Similarity   55.0%;  Pred. No. 8.2e-16;
  Matches  266;  Conservative    0;  Mismatches  203;  Indels   [illegible];  Gaps    [illegible];

Qy        891 [illegible]
Db         2[illegible] [illegible]

Qy        951 [illegible]
Db         85 [illegible]

Qy       1011 [illegible]
Db        145 [illegible]

Qy       1071 [illegible]
Db        205 [illegible]

Qy       1131 [illegible]
Db        265 [illegible]

Qy       1191 [illegible] 1247
Db        325 [illegible]

Qy       1248 [illegible] 1295
Db        381 [illegible] 441

Qy       1296 AGA[illegible] 1355
Db        442 [illegible]

Qy       1356 GGG 1359
Db        505 AGG 508


RESULT 13
AAZ12841
ID   AAZ12841 standard; cDNA; 300 BP.
XX
AC   AAZ12841;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Human gene expression product cDNA sequence SEQ ID NO:[illegible].
XX
KW   Human; gene; gene expression product; diagnosis; therapy; probe;
KW   detection; mapping; tissue typing; profiling; forensic analysis;
KW   genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9938972-A2.
XX
PD   05-AUG-1999.
XX
PF   23-JAN-1999;   99WO-US01619.
XX
PR   03-APR-1998;   98US-[illegible].
PR   23-JAN-1998;   98US-[illegible].
PR   21-FEB-1998;   98US-0075954.
PR   [illegible] MAY-1999; [illegible]
PR   [illegible] NOV-1999; [illegible]
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
PI   Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
PI   Jones LW, Kassam A, Kennedy GC, Kita D, Labat I;
PI   Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
PI   Stache-Crain B, Sudduth Klinger J, Williams LT;
XX
DR   WPI; [illegible]/[illegible].
XX
PT   Novel human genes and their expression products which are
PT   differentially expressed in different cell types
XX
PS   Claim 1; Page [illegible]; [illegible]pp; English.
XX
CC   The present invention describes a library of human polynucleotides
CC   comprising the sequences given in AAZ[illegible] to AAZ[illegible]. Also described is
CC   a method of detecting differentially expressed genes associated with the
CC   cancerous state of a mammalian cell, comprising detecting at least one
CC   differentially expressed gene product in a test sample from a cell
CC   suspected of being cancerous, where the gene product is encoded by one
CC   of the [illegible] polynucleotide sequences given in AAZ[illegible] to AAZ[illegible]. The
CC   polynucleotides can be used as a source of primers and probes, which can
CC   be used for a variety of purposes, e.g. detection of expression levels,
CC   mapping, tissue typing or profiling, forensics, genetic analysis and
CC   detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC   can be used for raising antibodies for experimental, diagnostic and
CC   therapeutic purposes. The polynucleotides may also be used to construct
CC   arrays for diagnostics (which may be used to determine function of an
CC   encoded protein); and to detect differences in expression levels between
CC   two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC   identify a genetic predisposition or susceptibility to a disease such as
CC   cancer). The polynucleotides of the invention are especially used in the
CC   diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC   and lung cancer. The polynucleotides can also be used to screen for
CC   peptide agonists and antagonists.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy   [illegible]
Db   [illegible] 60

Qy   [illegible]
Db   [illegible] 120

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible] 240

Qy   [illegible]
Db   [illegible]


RESULT [illegible]
AAX[illegible]
ID   AAX[illegible] standard; cDNA; [illegible] BP.
XX
AC   AAX[illegible];
XX
DT   [illegible] 1999 (first entry)
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DE   Human validated cancer cell derived cDNA #[illegible].
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KW   Cancer; tumour; colon; breast; lung; transmembrane receptor; A[illegible];
KW   integral membrane protein; aspartyl protease; GATA family; wnt family;
KW   transcription factor; G protein alpha subunit; protein phosphatase;
KW   phosphodiesterase binding protein; diacylglycerol binding protein; trypsin;
KW   protein kinase; tyrosine phosphatase; developmental signalling protein;
KW   WW/rsp5/WWP domain; therapy; forensic; genetic mapping; diagnostic;
KW   detection; treatment; cervical; melanoma; colorectal adenocarcinoma;
KW   Wilm's tumour; retinoblastoma; sarcoma; myosarcoma; lung carcinoma;
KW   leukemia; lymphoma; dysplasia; hyperplasia; endometrium; adrenal;
KW   prostate; ss.
XX
OS   Homo sapiens.
XX
PN   W[illegible]-A1.
XX
PD   08-JUN-2000.
XX
PF   2[illegible] DEC-1999; [illegible]WO-US[illegible].
XX
PR   21-DEC-1998;   98US-0[illegible].
PR   23-DEC-1998;   [illegible].
PR   [illegible] APR-1999;   [illegible].
PR   21-OCT-1998;   98US-0[illegible].
PR   27-OCT-1998;   98US-0[illegible].
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;
PI   Escobedo J, Garcia PD, Garcia V, Giese K, Innis MA;
PI   Jones LW, Kassam A, Kennedy GC, Kita D, Labat I;
PI   Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;
PI   Stache-Crain B, Sudduth Klinger J, Williams LT;
XX
DR   WPI; [illegible]/[illegible].
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PT   New isolated human polynucleotides
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PS   Claim 1; Page [illegible]; [illegible]pp; English.
XX
CC   This invention describes novel isolated human polynucleotides obtained
CC   by screening for differential expression in colon cancer, breast cancer
CC   and lung cancer cell lines. The polynucleotides of the invention are
CC   represented in AAX[illegible] [illegible] and encode polypeptides of protein
CC   families selected from 4 transmembrane segments integral membrane
CC   proteins, 7 transmembrane receptors, ATPases associated with various
CC   cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of
CC   transcription factors, G protein alpha subunit, phosphodiesterases or
CC   diacylglycerol binding proteins, protein kinase, protein phosphatase 2C,
CC   protein tyrosine phosphatase, trypsin, wnt family of developmental
CC   signalling proteins and WW/rsp5/WWP domain containing proteins. The
CC   encoded polypeptides may have a functional domain selected from Ank
CC   repeat, basic region plus leucine zipper transcription factors,
CC   bromodomain, EF hand, SH3 domain, WD domain/G beta repeats, zinc finger
CC   (C2H2 type), zinc finger (C3HC4 class), and zinc binding metalloprotease
CC   domain. The polynucleotides encode polypeptides with similarity to known
CC   protein families and are predicted to have similar properties. The novel
CC   polynucleotides can be used to develop products for use as therapeutic
CC   agents and in diagnostics, genetic analysis, mapping and diagnostic
CC   applications. In particular, the product can be used for the detection
CC   and management of cancers. They can be used for treating e.g. cervical
CC   cancers, melanomas, colorectal adenocarcinomas, Wilm's tumour, sarcomas,
CC   retinoblastoma, myosarcomas, lung carcinomas, leukemias such as chronic
CC   myelogenous leukemia, promyelocytic leukemia, monocytic leukemia and
CC   myeloid leukemia, and lymphomas such as histiocytic lymphoma, anhydrotic
CC   hereditary ectodermal dysplasia, congenital alveolar dysplasia,
CC   epithelial dysplasia of the cervix, fibrous dysplasia of bone and
CC   mammary dysplasia, hyperplasias, e.g. endometrial, adrenal, breast,
CC   prostate or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of
CC   the skin.
XX
SQ   Sequence 750 BP; 170 A; 203 C; 182 G; 180 T; 15 other;

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  Best Local Similarity   54.4%;  Pred. No. 2.5e-14;
  Matches  257;  Conservative    0;  Mismatches  199;  Indels   16;  Gaps    2;

Qy        904 ATGAGTGGCTGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATCCAT 963
              | || |||||| |||||||    | |||     |||||||| ||  || ||| ||  |
Db         58 [illegible] 117

Qy        964 GGACAGGGTAGGCAGGCTCGGTTACTAGGAACACTGGCTGTCTCCGGGGGCTGGGAGAC 1023
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Db        118 [illegible] 177

Qy       1024 [illegible] 1083
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Db        178 [illegible] 237

Qy       1084 CAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATC 1143
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Db        238 [illegible] 297

Qy       1144 [illegible] 1199
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Qy       1200 [illegible] 1259
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Db        358 [illegible] 417

Qy       1260 [illegible] 1307
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Db        418 GGTCCTGGGGGCCCGGGGTA[illegible] 477

Qy       1308 GGTGTCCTACCGATGACCGTCTCTGTGTTCCTGATTCCC[illegible] 1379
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Db        478 [illegible]


RESULT 15
ABL25549
ID   ABL25549 standard; DNA, 2087 BP.
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AC   ABL25549;
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DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID No 28120.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   [illegible]
XX
PD   27-[illegible]
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions
XX
PS   Claim 1; SEQ ID No 28120; 21pp; Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences ([illegible]-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2087 BP; 510 A; 582 C; 594 G; 401 T; 0 other;

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  Best Local Similarity   50.9%;  Pred. No. 7.9e-14;
  Matches  287;  Conservative    0;  Mismatches  253;  Indels   24;  Gaps    [illegible];

Qy        741 [illegible] 800
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Db       1112 [illegible] 1171

Qy        801 [illegible] 860
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Db       1172 [illegible] 1231

Qy        861 [illegible] 920
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Db       1232 [illegible] 1291

Qy        921 [illegible] 980
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Db       1292 CAAAACTTTGATCATGCAAGACTTCTCCATCCCCGTGGTCAATGCCCACGCAAAGAGAAG 1351

Qy        981 [illegible] 1040
              |||  || ||  || ||  |||  ||| | || ||| | || || |   ||||   | | |
Db       1352 TCGCTTGCTGGGTACGTTGGGGGTCACGCGGGCTTTGGCGATCACGAGCTGCTAGCCAT 1411

Qy       1041 [illegible] 1100
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Db       1412 [illegible] 1471

Qy       1101 [illegible] 1136
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Db       1472 [illegible] 1531

Qy       1137 [illegible] 1196
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Db       1532 [illegible] 1591

Qy       1197 GCGGAGCTTCCTCCTGGGAACTAAGAGGACCCACACAGGTTCTCAAAGCTGGCCCAGAT 1256
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Db       1592 [illegible] 1651

Qy       1257 [illegible] 1290
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Db       1652 GCTGGTGGCCCGTGCTCGTGGCAA 1675


Search completed: February 23, 2003, 01:34:03
Job time : 338 secs
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                         GenCore version 5.1.3
                 Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 23, 2003, 01:41:44 ; Search time 65 Seconds
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Title:           US-09-866-987-3
Perfect score:   1380
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                 Gapop 10.0 , Gapext 1.0

Searched:        441362 seqs, 15[illegible]8381 residues

Total number of hits satisfying chosen parameters:      882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
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                 6: [illegible]:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
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  No.     Score     Match Length DB  ID                            Description
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c   1     49.8      3.6   6714   4   US-09-299-141-6               Sequence 6, Appl
c   2     49.8      3.6   6924   4   US-09-299-141-9               Sequence 9, Appl
c   3     49.8      3.6   6924   4   US-09-299-141-10              Sequence 10, Appl
c   4     49.8      3.6   6924   4   US-09-299-141-11              Sequence 11, Appl
c   5     48.2      3.5   1491   4   US-09-082-092-9               Sequence 9, Appl
c   6     48.2      3.5   1817   4   US-09-288-292A-45             Sequence 45, Appl
    7     47        3.4    349   4   US-09-198-119C-94             Sequence 94, Appl
c   8     46.4      3.4    774   3   US-08-415-655-11              Sequence 11, Appl
c   9     45.2      3.3    645   4   US-09-535-008-30              Sequence 30, Appl
   10     43.6      3.2 152[illegible] 3 US-09-128-155-17          Sequence 17, Appl
c  11     43.4      3.1   1488   4   US-09-096-776B-3              Sequence 3, Appl
c  12     43.4      3.1   2534   4   US-09-357-776B-1              Sequence 1, Appl
c  13     43.2      3.1   3946   3   US-09-080-351-1               Sequence 1, Appl
c  14     43.2      3.1   3446   4   US-09-080-172-1               Sequence 1, Appl
c  15     43        3.1   1128   4   US-08-118-200-1               Sequence 1, Appl
c  16     43        3.1   1128   4   US-08-454-745-1               Sequence 1, Appl
   17     42.8      3.1   8460   1   US-08-409-005A-3              Sequence 3, Appl
   18     42.8      3.1   8519   4   US-09-261-907-1               Sequence 1, Appl
c  19     42.4      3.1    320   4   US-09-165-264-7               Sequence 7, Appl
c  20     42.4      3.1    320   4   US-09-165-264-13              Sequence 13, Appl
c  21     41.4      3.0    319   4   US-09-165-264-8               Sequence 8, Appl
   22     41.4      3.0   4252   2   US-08-475-844-4               Sequence 4, Appl
   23     41.4      3.0   4252   5   PCT-US95-08422-4              Sequence 4, Appl
   24     41.2      3.0   1413   4   US-08-984-709A-52             Sequence 52, Appl
   25     41.2      3.0   6454   1   US-08-866-918-14              Sequence 14, Appl
   26     41.2      3.0   6454   3   US-09-299-608-1               Sequence 1, Appl
   27     41.2      3.0    645   3   US-09-[illegible]             Sequence [illegible], Appl
   28     41.2      3.0  12011   1   US-08-458-508A-11             Sequence 11, Appl
c  29     40.8      3.0   3978   3   US-08-726-214-1               Sequence 1, Appl
c  30     40.8      3.0   4522   4   US-09-473-716-1               Sequence 1, Appl
c  31     40.4      2.9   3342   1   US-09-423-800-11              Sequence 11, Appl
c  32     40.2      2.9   8438   1   US-07-945-283-1               Sequence 1, Appl
c  33     40        2.9   1413   4   US-08-984-709A-52             Sequence 52, Appl
c  34     39.8      2.9    322   4   US-09-165-264-11              Sequence 11, Appl
c  35     39.6      2.9   7218   1   US-08-232-463-14              Sequence 14, Appl
c  36     39.4      2.9     70   4   US-09-236-097-7               Sequence 7, Appl
c  37     39.4      2.9   2502   1   US-08-07[illegible]-7         Sequence 7, Appl
c  38     39.4      2.9   2512   1   US-08-254-359A-7              Sequence 7, Appl
c  39     39.4      2.9   2502   1   US-08-483-043-7               Sequence 7, Appl
c  40     39.4      2.9   2512   1   US-08-481-238-7               Sequence 7, Appl
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c  42     39.4      2.9   2502   2   US-08-484-956-7               Sequence 7, Appl
c  43     39.4      2.9   2512   2   US-08-757-653-7               Sequence 7, Appl
c  44     39.4      2.9   2502   2   US-08-599-491-7               Sequence 7, Appl
c  45     39.4      2.9   2512   2   US-08-756-388-7               Sequence 7, Appl

                              ALIGNMENTS

RESULT 1
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; Sequence 6, Application US/09299141
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: FISHER, [illegible]
;  APPLICANT: SONG, [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO 6
;   LENGTH: 6714
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:[illegible]
;   OTHER INFORMATION: [illegible]
US-09-299-141-6

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  Best Local Similarity   51.7%;  Pred. No. [illegible];
  Matches   99;  Conservative   [illegible];  Mismatches   82;  Indels   [illegible];  Gaps   [illegible];

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Qy      [illegible]
Db      [illegible]


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; Sequence 9, Application US/09299141
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/[illegible]
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p[illegible]
US-[illegible]

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Db [illegible]

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Db [illegible]


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; Patent No. [illegible]
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;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/[illegible]
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p[illegible]
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Db [illegible]

Qy [illegible]
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Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]


RESULT [illegible]
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; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/[illegible]
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p[illegible]
US-[illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
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Db [illegible]

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Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]


RESULT [illegible]
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; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;     APPLICANT:  Nakao, Atsuhito
;     APPLICANT:  Moren, Anita
;     APPLICANT:  Heuchel, Rainer
;    APPLICANT:  Itoh, Susumu
;    APPLICANT:  Afrakhte, Morteza
;    APPLICANT:  Souchelnytskyi, Serhiy
;    APPLICANT:  Brodin, Greger
;    APPLICANT:  Landstrom, Marene
;    APPLICANT:  Heldin, Nils Erik
;    APPLICANT:  Heldin, Carl-Henrik
;    APPLICANT:  ten Dijke, Peter
;    TITLE OF INVENTION:  SMAD7 AND USES THEREOF
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.[illegible]
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/[illegible]
;      FILING DATE:  2[illegible] MAY 1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/047,221
;      FILING DATE:  20-MAY-1997
;      APPLICATION NUMBER:  60/060,465
;      FILING DATE:  30-SEP-1997
;      APPLICATION NUMBER:  60/075,94[illegible]
;      FILING DATE:  25-FEB-1998
;      APPLICATION NUMBER:  60/077,03[illegible]
;      FILING DATE:  06-MAR-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7032
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617 720-3500
;      TELEFAX:  617 720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-[illegible]-5

  Query Match             [illegible].5%;  Score 48.2;  DB 4;  Length 1491;
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Qy          5 [illegible] 64

Db        302 [illegible] 243

Qy         65 [illegible] 124

Db        242 [illegible] 183

Qy        125 [illegible] 184

Db        182 CGGACTTCGGAGCGG[illegible] 123

Qy        185 C 185
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Db        122 C 122
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RESULT 6
US-09-288-252A-45/c
; Sequence 45, Application US/09288252A
; Patent No. 6359194
; GENERAL INFORMATION:
;  APPLICANT: Dean A. Falk
;  APPLICANT:  Katherine Galvin
;  APPLICANT:  Michael Donovan
;  APPLICANT:  Dennis Huszar
;  APPLICANT:  Michael A. Gimbrone, Jr.
;  TITLE OF INVENTION: Compositions and Methods for the Treatment and Diagnosis of
;  TITLE OF INVENTION:  Cardiovascular Disease
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/288,252A
;  CURRENT FILING DATE:  1999-04-08
;  PRIOR APPLICATION NUMBER: 08/870,4[illegible]4
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: 08/[illegible]
;  PRIOR FILING DATE: 1997-02-1[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 199[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1995-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible],844
;  PRIOR FILING DATE: 1995-12-[illegible]
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
;   LENGTH: 1817
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-288-252A-45

  Query Match             [illegible];  Score 48.2;  DB 4;  Length 1817;
  Best Local Similarity   54.1%;  Pred. No. [illegible];
  Matches   98;  Conservative    [illegible];  Mismatches   83;  Indels    [illegible];  Gaps    [illegible];

Qy          5 [illegible] 64

Db        456 CCAGGCGGG[illegible]

Qy         65 [illegible] 124

Db        [illegible]

Qy        125 [illegible]

Db        [illegible]

Qy        185 C 185
              |
Db        276 C 276


RESULT 7
US-09-198-[illegible]-94
; Sequence 94, Application US/[illegible]
; Patent No. 6417428
; GENERAL INFORMATION:
;  APPLICANT:  Thomashow, Michael
;  APPLICANT:  Stockinger, Eric
;  APPLICANT:  Jaglo-Ottosen, Kirsten
;  APPLICANT:  Gilmour, Sarah
;  APPLICANT:  Zarka, Daniel
;  APPLICANT:  Jiang, Cai-Zhong
;  TITLE OF INVENTION:  Plant Having Altered Environmental Stress Tolerance
;  FILE REFERENCE:  19117.713 Seq List
;  CURRENT APPLICATION NUMBER: US/09/198,[illegible]
;  CURRENT FILING DATE:  1998-11-[illegible]
;  PRIOR APPLICATION NUMBER:  US 08/[illegible]
;  PRIOR FILING DATE:  1998-[illegible]
;  PRIOR APPLICATION NUMBER:  US [illegible]
;  PRIOR FILING DATE:  1998-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: [illegible]
;   FEATURE:
;   OTHER INFORMATION: [illegible]
[illegible]

  Query Match             [illegible]  Score [illegible]  DB [illegible]  Length [illegible]
  Best Local Similarity   [illegible]  Pred. No. [illegible]
  Matches  [illegible]  Conservative  [illegible]  Mismatches  [illegible]  Indels  [illegible]  Gaps  [illegible]

[illegible]


RESULT [illegible]
[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;    APPLICANT: [illegible]
;    APPLICANT: [illegible]
;    TITLE OF INVENTION: [illegible]
;    TITLE OF INVENTION: [illegible] KINASE INHIBITOR AND [illegible]
;    TITLE OF INVENTION: SAME
;    NUMBER OF SEQUENCES: [illegible]
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: [illegible]
;      STREET: 1185 Avenue of the Americas
;      CITY: New York
;      STATE: New York
;      COUNTRY: United States of America
;      ZIP: [illegible]
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.[illegible]
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: [illegible]
;      FILING DATE:
;      CLASSIFICATION: [illegible]
;    ATTORNEY/AGENT INFORMATION:
;      NAME: [illegible]
;      REGISTRATION NUMBER: [illegible]
;      REFERENCE/DOCKET NUMBER: [illegible]
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (212) 278-[illegible]
;      TELEFAX: (212) [illegible]
;  INFORMATION FOR SEQ ID NO: [illegible]
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: [illegible] base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;    MOLECULE TYPE: cDNA
;    HYPOTHETICAL: NO
;    ANTI-SENSE: NO
[illegible]

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  Best Local Similarity   [illegible]  Pred. No. [illegible]
  Matches  [illegible]  Conservative  [illegible]  Mismatches  61;  Indels  [illegible]  Gaps  [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      652 [illegible]AAGAGAGGC 613


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; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: Wong, Alexander K.C.
;  APPLICANT: Tavtigian, Sean V.
;  APPLICANT: Teng, David H.-F.
;  TITLE OF INVENTION: [illegible] TUMOR SUPPRESSOR THAT IS MUTATED IN [illegible]
;  TITLE OF INVENTION: AND OTHER CANCER TYPES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: U.S. [illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 77
;  SOFTWARE: PatentIn Ver. 2.[illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-[illegible]

  Query Match             [illegible]  Score 45.2;  DB 4;  Length [illegible]
  Best Local Similarity   52.7%;  Pred. No. 0.061;
  Matches  98;  Conservative  0;  Mismatches  88;  Indels  0;  Gaps  0;

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      410 [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]


RESULT [illegible]
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; Sequence [illegible], Application US/[illegible]
; Patent No. 6117654
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;   TITLE OF INVENTION: NOVEL MOLECULES OF TANG[illegible] RELATED PROTEIN FAMILY
;   TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 9404/[illegible]
;  CURRENT APPLICATION NUMBER: US/09/128,155
;  CURRENT FILING DATE: 1998-08-[illegible]
;  EARLIER APPLICATION NUMBER: US 60/091,650
;  EARLIER FILING DATE: 1998-07-02
;  EARLIER APPLICATION NUMBER: US 60/054,646
;  EARLIER FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
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;   LENGTH: 152381
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(152381)
;   OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

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Qy      123 CTCCAGCCC[illegible]GCCGCCCCCACCCCTCGCGCC[illegible]ACAC[illegible]CCCCAGCCC 182
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Qy      183 [illegible] 204
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Db    22177 [illegible] 22198


RESULT 11
US-09-096-776B-3/c
; Sequence 3, Application US/09096776B
; Patent No. 627[illegible]994
; GENERAL INFORMATION:
;  APPLICANT:  Miyamoto, Kohei
;  APPLICANT:  Kawabata, Masahiro
;  TITLE OF INVENTION:   SMAD6 AND USES THEREOF
;  FILE REFERENCE:   L0461/7038
;  CURRENT APPLICATION NUMBER:  [illegible]
;  CURRENT FILING DATE:   1998-06-12
;  PRIOR APPLICATION NUMBER:   US 60/[illegible]
;  PRIOR FILING DATE:   1997-06-1[illegible]
;  PRIOR APPLICATION NUMBER:   US 60/[illegible]
;  PRIOR FILING DATE:   1997-07-18
;  PRIOR APPLICATION NUMBER:   US 60/[illegible]
;  PRIOR FILING DATE:   1997-11-18
;  NUMBER OF SEQ ID NOS:   1[illegible]
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1488
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-096-776B-3

  Query Match             [illegible]%;  Score 43.4;  DB 4;  Length 1488;
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  Matches   95;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    [illegible]

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              [illegible]
Db      2[illegible] [illegible]

Qy       65 [illegible] 124
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Qy      125 [illegible] 184
              [illegible]
Db      1[illegible] [illegible]

Qy      185 C 185

Db      1[illegible] C 1[illegible]


RESULT 12
US-09-096-776B-1/c
; Sequence 1, Application US/[illegible]
; Patent No. 627[illegible]
; GENERAL INFORMATION:
;  APPLICANT:  Miyamoto, Kohei
;  APPLICANT:  Kawabata, Masahiro
;  TITLE OF INVENTION:   SMAD6 AND USES THEREOF
;  FILE REFERENCE:   L0461/7038
;  CURRENT APPLICATION NUMBER: US/09/096,776B
;  CURRENT FILING DATE:   1998-06-12
;  PRIOR APPLICATION NUMBER:   US 60/049,[illegible]
;  PRIOR FILING DATE:   1997-06-1[illegible]
;  PRIOR APPLICATION NUMBER:   US 60/053,04[illegible]
;  PRIOR FILING DATE:   1997-07-18
;  PRIOR APPLICATION NUMBER:   US 60/066,17[illegible]
;  PRIOR FILING DATE:   1997-11-18
;  NUMBER OF SEQ ID NOS:   [illegible]
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 2534
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (7[illegible]1)..(22[illegible])
US-09-096-776B-1

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  Matches   95;  Conservative    0;  Mismatches   86;  Indels    [illegible];  Gaps    [illegible];

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              [illegible]
Db     1049 [illegible]

Qy       65 [illegible] 124
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Db      [illegible]

Qy      125 [illegible] 184
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Db      [illegible]

Qy      185 C 185
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Db      869 C 869


RESULT 13
US-09-[illegible]/c
; Sequence 1, Application US/[illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;     APPLICANT:  Sheffield, Val C.
;     APPLICANT:  [illegible]
;     APPLICANT:  [illegible] Edwin M
;     APPLICANT:  Nishimura, Darryl
;     APPLICANT:  Patel, Shiva
;     TITLE OF INVENTION:  THERAPEUTICS AND DIAGNOSTICS FOR
;     TITLE OF INVENTION:  CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
;     TITLE OF INVENTION:  TRANSCRIPTION FACTOR
;     NUMBER OF SEQUENCES:  [illegible]
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;       STREET:  One Post Office Square
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  [illegible]
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/083,852
;       FILING DATE:  22-MAY-1998
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Arnold, Beth E.
;       REGISTRATION NUMBER:  [illegible]
;       REFERENCE/DOCKET NUMBER:  [illegible]
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-832-1000
;       TELEFAX:  617-832-7000
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  [illegible] base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
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;       NAME/KEY:  CDS
;       LOCATION:  [illegible]..2133
US-09-083-852-1

  Query Match             [illegible]%;  Score 43.2;  DB 4;  Length [illegible];
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Db        468 [illegible] 409

Qy        148 [illegible] 207
              [illegible]
Db        408 [illegible] 349

Qy        208 AA[illegible]
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Db        348 [illegible]


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;  GENERAL INFORMATION:
;     APPLICANT:  [illegible]
;     APPLICANT:  [illegible] Edwin M
;     APPLICANT:  Nishimura, Darryl
;     APPLICANT:  Patel, Shiva
;     TITLE OF INVENTION:  GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
;     TITLE OF INVENTION:  BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
;     NUMBER OF SEQUENCES:  [illegible]
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;       STREET:  One Post Office Square
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  [illegible]
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/083,852
;       FILING DATE:  22-MAY-1998
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Arnold, Beth E.
;       REGISTRATION NUMBER:  [illegible]
;       REFERENCE/DOCKET NUMBER:  [illegible]
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-832-1000
;       TELEFAX:  617-832-7000
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  [illegible] base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  [illegible]..2133
US-09-083-852-1

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Db        408 [illegible] 349

Qy        208 AA[illegible]
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Db        348 [illegible]


RESULT [illegible]
US-08-118-[illegible]
; Sequence 1, Application US/[illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;     APPLICANT:  SUTHERLAND, Grant R
;     APPLICANT:  RICHARDS, Robert I
;     APPLICANT:  SCHLESSINGER, David
;     APPLICANT:  NAGARAJA, Ramaiah
;     APPLICANT:  KREMER, Eric J
;     APPLICANT:  YU, Sui
;     APPLICANT:  BAKER, Elizabeth
;     APPLICANT:  MULLEY, John C
;     APPLICANT:  MANDEL, Jean Louis
;     APPLICANT:  PRITCHARD, Melanie April
;     APPLICANT:  LYNCH, Michael
;     TITLE OF INVENTION:  DNA SEQUENCES RELATED TO ISOLATED
;     TITLE OF INVENTION:  FRAGILE X SYNDROME
;     NUMBER OF SEQUENCES:  [illegible]
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;       STREET:  P.O. Box 1404
;       CITY:  Alexandria
;       STATE:  Virginia
;       COUNTRY:  United States
;       ZIP:  22313-1404
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/118,200
;       FILING DATE:  09-SEP-1993
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/802,650
;       FILING DATE:  05-DEC-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/672,232
;       FILING DATE:  20-MAR-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/638,518
;       FILING DATE:  04-JAN-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/966,517
;       FILING DATE:  23-DEC-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Crane Feury, Sharon E
;       REGISTRATION NUMBER:  36,113
;       REFERENCE/DOCKET NUMBER:  020160-164
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703) 836-6620
;       TELEFAX:  (703) 836-2021
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1028 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-118-200-1

  Query Match              3.1%;  Score 43;  DB 4;  Length 1028;
  Best Local Similarity   57.4%;  Pred. No. 0.23;
  Matches   97;  Conservative    0;  Mismatches   70;  Indels    2;  Gaps    1;

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              | |||  ||||  ||  |||||| ||||||    ||||    | ||| |    | |  ||
Db        479 CCGGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGC--CGCCGCCGCCGCCGCCGCC 422

Qy         95 GACGGCCCCGCTTCCTTCGCGGCTCCAGCTCCAGCCCCGGGCGGCCGACGCCTCGCGCC 154
              | || | ||||  ||  ||| ||  | ||  | ||| | |        |  |  |   ||||
Db        421 GCCGCCGCCGCCACCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 362

Qy        155 GCTCAGACTGCCGGCCCGTGCGCAGCTCGGCACGAGGATGCACGCTACC 203
              ||||    ||| | | | |  ||| ||||      ||||  || | | |||
Db        361 GCCCGCGCTCGCCGTCGGCCCGCCGCCCGCTCAGAGGCGGCCCTCCACC 313


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Job time : 254 secs
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                    GenCore version 5.1.4
              Copyright (c) 1993 - 2003 Compugen Ltd.

 OM nucleic - nucleic search, using sw model

Run on:          February 23, 2003, 03:29:02 ; Search time 64 Seconds
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Title:           US-09-866-987-3
Perfect score:   1380
Sequence:        1 atgtccgccgctgattccg............aaaggcagtgacgactga 1380

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 1:  [illegible]US07_PUBCOMB.seq:*
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                 4:  [illegible]
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                 13: [illegible]_NEW_PUB[illegible]
                 14: [illegible]

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES
                  %
Result           Query
   No.   Score   Match Length DB  ID                          Description
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     1    1380   100.0   1380 10  US-09-866-987-3             Sequence 3, Appli
     2     536    38.8    547 10  US-09-867-701-2466          Sequence 2466, Ap
     3   243.4    17.6   5791 10  US-09-920-[illegible]A-1714 Sequence 1714, Ap
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     5      98     7.1    551 10  US-09-867-701-5460          Sequence 5460, Ap
c    6    48.2     3.5   1817 10  US-09-924-417-[illegible]   Sequence [illegible], Appl
     7      47     3.4    349  9  US-09-996-140-94            Sequence 94, Appl
c    8    46.8     3.4  43058 10  US-09-954-456-292           Sequence 292, App
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    11    46.4     3.4   3209 10  US-09-925-301-474           Sequence 474, App
    12    44.4     3.2   2561  9  US-09-976-74[illegible]-48  Sequence 48, Appl
    13    44.4     3.2   2561 12  US-10-023-529-48            Sequence 48, Appl
    14    44.4     3.2   2561 12  US-10-023-528-48            Sequence 48, Appl
c   15    44.2     3.2   4286 10  US-09-899-[illegible]4A-1   Sequence 1, Appli
c   16    44.2     3.2   [illegible]  9  US-09-954-[illegible]A-14 Sequence 14, Appl
c   17    44.2     3.2   6148  9  US-09-954-483A-13           Sequence 13, Appl
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    22      43     3.1   1614  9  US-09-976-740-45            Sequence 45, Appl
    23      43     3.1   1614 12  US-10-023-529-45            Sequence 45, Appl
    24      43     3.1   1614 12  US-10-023-528-45            Sequence 45, Appl
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    26      43     3.1  12425 12  US-10-023-529-50            Sequence 50, Appl
    27      43     3.1  12425 12  US-10-023-528-50            Sequence 50, Appl
    28    42.2     3.1  42999  9  US-09-79[illegible]-462A-17 Sequence 17, Appl
    29    42.2     3.1  42999  9  US-10-125-767-17            Sequence 17, Appl
    30    42.2     3.1  42999  9  US-09-8[illegible]-911A-17  Sequence 17, Appl
c   31    41.4     3.0  12[illegible]  9  US-1[illegible]-47  Sequence 47, Appl
c   32    41.4     3.0  127[illegible]  9  US-10-[illegible]-6 Sequence 6, Appli
c   33    41.2     3.0    485  9  US-10-004-717-59            Sequence 59, Appl
c   34      41     3.0 1[illegible]  9  US-1[illegible]-026-188-6 Sequence 6, Appli
c   35    40.8     3.0   45[illegible]  9  US-10-175-158-1    Sequence 1, Appli
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    37    40.4     2.9   1[illegible]  1[illegible]  US-09-417-8[illegible]A-147[illegible] Sequence 147[illegible], Ap
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    40    40.4     2.9   1[illegible]  1[illegible]  US-09-814-777A-17  Sequence 17, Appl
c   41    40.4     2.9   [illegible]2 12  US-1[illegible]-864-1[illegible] Sequence 1[illegible], Appl
c   42    40.2     2.9   1157 10  US-09-778-844-166           Sequence 166, App
c   43    40.2     2.9   11[illegible]  1[illegible]  US-09-778-844-167  Sequence 167, App
    44      40     2.9   [illegible]  1[illegible]  US-[illegible]-7[illegible]8-1[illegible]2 Sequence [illegible], App
    45    39.8     2.9   8280 10  US-09-764-878-384           Sequence 384, App

                              ALIGNMENTS

RESULT 1
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; Sequence 3, Application US/09866987
; Patent No. US20[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible]AN, JEFFREY [illegible]
;  APPLICANT: MAL[illegible]NE[illegible], RICHARD
;  APPLICANT: WHITE, DAVID
;  APPLICANT: [illegible], GERARD
;  APPLICANT: SUBARYANAM, SUDHA
;  APPLICANT: [illegible]ENEFEEL, SEAN
;  APPLICANT: HILL, RON
;  APPLICANT: [illegible]MANN, PETER
;  TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
;  FILE REFERENCE: 038602/1180
;  CURRENT APPLICATION NUMBER: US/09/866,987
;  CURRENT FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: 60/208,2[illegible]1
;  PRIOR FILING DATE: 2000-[illegible]
;  NUMBER OF SEQ ID NOS: 1[illegible]
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1380
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: phosphatase nucleotide
US-09-866-987-3

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Qy         61 [illegible] 120
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; Sequence 2[illegible], Application US/[illegible]
; Patent No. US20020[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Algate, Paul A.
;  APPLICANT: Jones, Robert
;  APPLICANT: Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: 210121.497
;  CURRENT APPLICATION NUMBER: US/09/867,[illegible]
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 1091
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2[illegible]
;   LENGTH: 547
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-867-[illegible]

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  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

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Db        540 TTTGGTGA 547


RESULT 3
US-09-920-300A-1714
; Sequence 1714, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547
;  CURRENT APPLICATION NUMBER: US/09/920,300A
;  CURRENT FILING DATE:  2001-07-31
;  NUMBER OF SEQ ID NOS: 1789
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1714
;   LENGTH: 5791
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-920-300A-1714

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              [illegible]
Db        581 [illegible]

Qy        740 [illegible]
              [illegible]
Db        641 [illegible]

Qy        [illegible]
              [illegible]
Db        701 [illegible]

Qy        [illegible]
              [illegible]
Db        761 [illegible]

Qy        [illegible]
              [illegible]
Db        [illegible]

Qy        [illegible]
              [illegible]
Db        [illegible]

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Qy       [illegible]
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Db       1041 [illegible]

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Db       1061 [illegible]

Qy       1217 [illegible] 1276
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Db       1121 [illegible]

Qy       1277 G 1277
              |
Db       1181 G 1181


RESULT 4
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; Sequence 1714, Application US/10033528
; Patent No. US20020137471A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.54701
;  CURRENT APPLICATION NUMBER: US/10/033,528
;  CURRENT FILING DATE:  2001-12-28
;  NUMBER OF SEQ ID NOS: 1896
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1714
;   LENGTH: 5791
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-528-1714

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Db        [illegible]

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              [illegible]
Db        [illegible]

Qy        [illegible]
              [illegible]
Db        521 [illegible]

Qy        [illegible]
              [illegible]
Db        581 [illegible]

Qy        [illegible]
              [illegible]
Db        641 [illegible]

Qy        [illegible]
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Db        [illegible]

Qy        [illegible]
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Db        761 [illegible]

Qy        [illegible]
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Db        821 [illegible]
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Db [illegible]

Qy [illegible]
Db [illegible]

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Qy [illegible]
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Db [illegible]

Qy [illegible]

Db [illegible]


RESULT [illegible]
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; Sequence [illegible], Application [illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: Algate, Paul A
;  APPLICANT: [illegible], Robert
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: 2001-[illegible]
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;  SOFTWARE: FastSEQ for Windows Version [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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;     LOCATION: [illegible]
;     OTHER INFORMATION: [illegible]
US [illegible]

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Db [illegible]

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Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]

Qy [illegible]
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RESULT [illegible]
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; Sequence 64, Application US/09924417
; Patent No. [illegible]
;  GENERAL INFORMATION:
;        APPLICANT: [illegible], Dean
;        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;                             THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR
;                             DISEASE
;        NUMBER OF SEQUENCES: [illegible]
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: PENNIE & EDMONDS LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2711
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version 2.
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/924,417
;             FILING DATE: 07 Aug 2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/034,286
;             FILING DATE: 04 MAR 1998
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: [illegible] JUN 1997
;             APPLICATION NUMBER: [illegible]/799,910
;             FILING DATE: [illegible] FEB 1997
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: [illegible] FEB 1996
;             APPLICATION NUMBER: 08/599,654
;             FILING DATE: [illegible] FEB 1996
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: [illegible] JUN 1995
;             APPLICATION NUMBER: 08/386,844
;             FILING DATE: [illegible] FEB 1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: [illegible], Laura A
;             REGISTRATION NUMBER: [illegible]
;             REFERENCE/DOCKET NUMBER: [illegible]
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212)790[illegible]
;             TELEFAX: [illegible]
;             TELEX: [illegible] PENNIE
;   INFORMATION FOR SEQ ID NO: 64:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: [illegible] base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: both
;             TOPOLOGY: unknown
;        MOLECULE TYPE: DNA
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  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

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Db 456 [illegible]

Qy [illegible]
Db 396 [illegible]
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; GENERAL INFORMATION:
;  APPLICANT: Th[illegible]ow, Michael
;  APPLICANT:  St[illegible]ckinger, Eric
;  APPLICANT:  Ja[illegible] Ottosen, Kirsten
;  APPLICANT:  Gilmour, Sarah
;  APPLICANT:  Zarka, Daniel
;  APPLICANT:  Jiang, Cai-Zhong
;  TITLE OF INVENTION: PLANT HAVING ALTERED ENVIR[illegible]
;  TITLE OF INVENTION:  STRESS TOLERANCE
;  FILE REFERENCE: MBI[illegible]
;  CURRENT APPLICATION NUMBER: [illegible]/996,140
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-09-04
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: [illegible]/017,816
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,235
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;  PRIOR APPLICATION NUMBER: 09/017,525
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;  PRIOR APPLICATION NUMBER: 09/018,227
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,234
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/198,119
;  PRIOR FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: PCT/[illegible]1395
;  PRIOR FILING DATE: 1999-01-28
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Zea maize
US-[illegible]-94

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Qy         7[illegible] 138
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Db        162 [illegible] 221

Qy        139 [illegible] 185
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Db        222 [illegible] 268


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; Patent No. US2[illegible]115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti Cancer Therapeutic Agents Using C
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US/[illegible]17
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US/[illegible]52
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/[illegible]
;  PRIOR FILING DATE: 2000-09-25
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;  PRIOR APPLICATION NUMBER: US/[illegible]
;  PRIOR FILING DATE: [illegible]
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;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US/[illegible]720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/[illegible]840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/[illegible]
;  PRIOR FILING DATE: [illegible]27
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;  SOFTWARE: PatentIn version [illegible]
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;   LENGTH: 43058
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-292

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Db      25721 [illegible]

Qy         78 [illegible] 137
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Db      25661 [illegible]

Qy        138 [illegible]
              [illegible]
Db      25601 [illegible]


RESULT 9
US-09-954-456-529/c
; Sequence 529, Application US/[illegible]4456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti Cancer Therapeutic Agents Using C
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US/[illegible]17
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US/[illegible]/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/[illegible]
;  PRIOR FILING DATE: [illegible]
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;   ORGANISM: Homo sapiens
[illegible]

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  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

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Db [illegible]

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Db [illegible]

Qy [illegible]

Db [illegible]


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;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: Gene Expression [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: 2001-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. [illegible]
[illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]
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Qy [illegible]

Db [illegible]


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; Sequence 474, Application US/[illegible]
; Patent No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1[illegible])
;   OTHER INFORMATION: [illegible]
US-[illegible]-474

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  Best Local Similarity [illegible]; Pred. No. [illegible] 44;
  Matches 128; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

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Db       1268 [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]


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; Sequence [illegible], Application US/[illegible]
; Publication No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: NOVEL [illegible] PROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US [illegible]/[illegible],939
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US [illegible]/[illegible]48,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-[illegible]-476-741-48

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  Best Local Similarity   55.9%;  Pred. No. 0.13;
  Matches  104;  Conservative    0;  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

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              [illegible]
Db        620 [illegible] 679

Qy         71 [illegible] 129
              [illegible]
Db        680 GGGCGGGCGGCCCTGCGGGGCCGCGGCCGGCTGCCGCCACAGGCGCCGCCTCGCCCGG 739

Qy        130 [illegible]GACGGC[illegible]GCCCAGACT[illegible]GACA 189
              [illegible]
Db        740 [illegible]GCAGCGGGCCC[illegible]GCAGCGGGCCG[illegible]GGCCG[illegible] 799

Qy        190 GGACGC 195
              [illegible]
Db        800 G[illegible] 805


RESULT 13
US-10-023-529-48
; Sequence 48, Application US/10023529
; Patent No. US20020129388A1
; GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT:  Lees, Robert S.
;  APPLICANT:  Law, Simon W.
;  APPLICANT:  Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION:  PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION:  ATHEROSCLEROSIS
;  FILE REFERENCE: 1[illegible]797-004001
;  CURRENT APPLICATION NUMBER: US/10/023,529
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: 09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US [illegible]/[illegible]1,939
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US [illegible]/[illegible]48,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-10-023-529-48

  Query Match             3.2%;  Score 44.4;  DB 12;  Length 2561;
  Best Local Similarity   55.9%;  Pred. No. 0.19;
  Matches  104;  Conservative    0;  Mismatches   81;  Indels   [illegible];  Gaps   [illegible];

Qy         11 [illegible] 70
              [illegible]
Db        620 [illegible] 679

Qy         71 [illegible] 129
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Db        680 [illegible] 739

Qy        130 [illegible] 189
              [illegible]
Db        740 [illegible] 799

Qy        190 GGACGC 195
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Db        800 [illegible] 805


RESULT 14
US-10-023-523-48
; Sequence 48, Application US/10023523
; Patent No. US20020152485A1
; GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT:  Lees, Robert S.
;  APPLICANT:  Law, Simon W.
;  APPLICANT:  Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION:  PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION:  ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/10/02[illegible],523
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: US/09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US [illegible]/[illegible]1,939
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 6[illegible]/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.[illegible]
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-10-023-523-48

  Query Match             [illegible];  Score 44.4;  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  [illegible];  Conservative    [illegible];  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy         11 [illegible] 70
              [illegible]
Db        620 [illegible] 679

Qy         71 [illegible] 129
              [illegible]
Db        680 [illegible] 739

Qy        130 [illegible] 189
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Db        740 [illegible] 799
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[illegible]

[illegible]

[illegible]
[illegible]
[illegible] APPLICANT [illegible]
[illegible]
GENERAL INFORMATION:
APPLICANT: Thomas [illegible] Andreas [illegible] Reinhard K[illegible]
TITLE OF INVENTION: [illegible]AK and its uses
FILE REFERENCE: [illegible]
CURRENT APPLICATION NUMBER: US/[illegible]
CURRENT FILING DATE: [illegible]
NUMBER OF SEQ ID NOS: [illegible]
SOFTWARE: [illegible]
SEQ ID NO [illegible]
LENGTH: [illegible]
TYPE: DNA
ORGANISM: [illegible]
FEATURE:
NAME/KEY: [illegible]
LOCATION: [illegible]
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[illegible]

[illegible]

[illegible]
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          Copyright (c) [illegible]

OM nucleic - nucleic search, using sw model

Run on:          February 2[illegible], 2003, 0[illegible]:41:[illegible] ; Search time [illegible] Seconds
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Perfect score:   [illegible]
Sequence:        1 [illegible]

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters:      [illegible]582208

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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  Pred. No. is the number of results predicted by chance to have a
  score greater than or equal to the score of the result being printed,
  and is derived by analysis of the total score distribution.

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     9    127[illegible]   92.[illegible]   21[illegible]   [illegible]  US-09-76[illegible]-175-7[illegible]4    Sequence [illegible]4, App
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    18   [illegible]2   [illegible]         227                      Sequence 227, App
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ALIGNMENTS

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; Sequence [illegible], Application US/[illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible]WMAN, [illegible]
;  APPLICANT: MARTINEZ, RICARDO
;  APPLICANT: WHITE, DAVID
;  APPLICANT: MANNING, GERARD
;  APPLICANT: [illegible]ARANAM, [illegible]HA
;  APPLICANT: [illegible]ARNEFELT, SEAN
;  APPLICANT: HILL, RON
;  APPLICANT: FLANAGAN, PETER
;  TITLE OF INVENTION: MAMMALIAN PROTEIN [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: 2001-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO [illegible]
;  LENGTH: [illegible]
;  TYPE: DNA
;  ORGANISM: Artificial Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;  OTHER INFORMATION: phosphatase nucleotide
US-[illegible]

  Query Match            [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity  [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

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Db   [illegible]

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Qy   601 [illegible] 660
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Qy   721 [illegible] 780
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Qy   901 [illegible] 960
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Qy   961 [illegible] 1020
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Db  1201 [illegible]
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Db       1261 [illegible] 1320

Qy       1321 [illegible]
Db       1321 [illegible]


RESULT 2
PCT-US02-30474-316
; Sequence 316, Application PCT/US0230474
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: Zhang, Jie
;  APPLICANT: [illegible]
;  APPLICANT: Xue, Aidong J.
;  APPLICANT: [illegible] A.
;  APPLICANT: Wang, Jian-Rui
;  APPLICANT: Wehrman, Tom
;  APPLICANT: Zhou, Ping
;  APPLICANT: Ghosh, Malabika
;  APPLICANT: Wang, Dunrui
;  APPLICANT: [illegible]
;  APPLICANT: Asundi, Vinod
;  APPLICANT: [illegible]
;  APPLICANT: Wang, Gezhi
;  APPLICANT: Haley-Vicente, Dana
;  APPLICANT: Drmanac, Radoje T
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION: Polypeptides
;  FILE REFERENCE: 810CIP PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/30474
;  CURRENT FILING DATE: 2002-[illegible]-24
;  PRIOR APPLICATION NUMBER: US 60/324,631
;  PRIOR FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: US 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: PCT/US[illegible]/35017
;  PRIOR FILING DATE: [illegible]-12-22
;  PRIOR APPLICATION NUMBER: US [illegible]/491,404
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]2623
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]/4[illegible],914
;  PRIOR FILING DATE: 2000-02-[illegible]
;  PRIOR APPLICATION NUMBER: US 09/560,875
;  PRIOR FILING DATE: [illegible]-04-27
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;  PRIOR FILING DATE: 2001-02-0[illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]/515,126
;  PRIOR FILING DATE: [illegible]-02-[illegible]
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: [illegible]476
;  SOFTWARE: pt_FL_genes Version [illegible]
; SEQ ID NO [illegible]16
;   LENGTH: 2[illegible]54
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: ([illegible])..(15[illegible])
PCT-US02-30474-316

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  Matches 1380;  Conservative    0;  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy          1 [illegible]
Db        156 [illegible] 215

Qy         61 [illegible]
Db        216 [illegible]

Qy        121 [illegible]
Db        276 [illegible]

Qy        181 [illegible]
Db        336 [illegible]

Qy        241 [illegible]
Db        396 [illegible]

Qy        301 [illegible]
Db        456 [illegible]

Qy        361 [illegible]
Db        516 [illegible]

Qy        421 [illegible]
Db        576 [illegible]

Qy        481 [illegible]
Db        636 [illegible]

Qy        541 [illegible]
Db        696 [illegible] 755

Qy        601 [illegible]
Db        756 [illegible]

Qy        661 [illegible]
Db        816 [illegible]

Qy        721 [illegible]
Db        876 [illegible]

Qy        781 [illegible]
Db        936 [illegible]

Qy        841 [illegible]
Db        996 [illegible]

Qy        901 [illegible]
Db       1056 [illegible]

Qy        961 [illegible]
Db       1116 [illegible]

Qy       1021 [illegible]
Db       1176 [illegible]

Qy       1081 [illegible]
Db       1236 [illegible]
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Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

[illegible]
; Sequence [illegible], Application [illegible]
;  GENERAL INFORMATION:
;   APPLICANT: [illegible]
;   APPLICANT: [illegible]
;   APPLICANT: [illegible]
;   APPLICANT: Xu, Aidong [illegible]
;   APPLICANT: [illegible] A.
;   APPLICANT: Wang, [illegible]
;   APPLICANT: [illegible]
;   APPLICANT: Zhou, Ping
;   APPLICANT: Ghosh, Malabika
;   APPLICANT: [illegible]
;   APPLICANT: Ma, Yunqing
;   APPLICANT: [illegible]
;   APPLICANT: Wang, Zhiwei
;   APPLICANT: Wang, [illegible]
;   APPLICANT: [illegible], Vicente [illegible]
;   APPLICANT: [illegible]
;   TITLE OF INVENTION: Novel Nucleic Acids and
;   TITLE OF INVENTION: Polypeptides
;   FILE REFERENCE: [illegible]
;   CURRENT APPLICATION NUMBER: [illegible]
;   CURRENT FILING DATE: [illegible]
;   PRIOR APPLICATION NUMBER: [illegible]
;   PRIOR FILING DATE: [illegible]
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;   PRIOR FILING DATE: [illegible]
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;   PRIOR FILING DATE: 2000-[illegible]
;   PRIOR APPLICATION NUMBER: [illegible]
;   PRIOR FILING DATE: [illegible]
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;   PRIOR FILING DATE: 2000-[illegible]
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;   PRIOR FILING DATE: [illegible]
;   PRIOR APPLICATION NUMBER: [illegible]
;   PRIOR FILING DATE: [illegible]
;   PRIOR APPLICATION NUMBER: [illegible]
;   PRIOR FILING DATE: [illegible]
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;   PRIOR FILING DATE: 2000-[illegible]
;   PRIOR APPLICATION NUMBER: [illegible]
;   PRIOR FILING DATE: [illegible]
;   PRIOR APPLICATION NUMBER: US [illegible]
;   PRIOR FILING DATE: 2000-04-18
;   PRIOR APPLICATION NUMBER: US [illegible]
;   PRIOR FILING DATE: [illegible]
;   PRIOR APPLICATION NUMBER: [illegible]
;   PRIOR FILING DATE: 2001-04-18
;   PRIOR APPLICATION NUMBER: US [illegible],408
;   PRIOR FILING DATE: [illegible]
;   PRIOR APPLICATION NUMBER: [illegible]
;   PRIOR FILING DATE: [illegible]
;   NUMBER OF SEQ ID NOS: [illegible]
;   SOFTWARE: pt_FL_genes Version [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: [illegible]
US-[illegible]

  Query Match             100.0%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   100.0%;  Pred. No. [illegible];
  Matches [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy          1 [illegible]
Db        [illegible]

Qy         61 [illegible]
Db        [illegible]

Qy        121 [illegible]
Db        [illegible]

Qy        181 [illegible]
Db        [illegible]

Qy        241 [illegible]
Db        [illegible]

Qy        301 [illegible]
Db        [illegible]

Qy        361 [illegible]
Db        [illegible]

Qy        421 [illegible]
Db        [illegible]

Qy        481 [illegible]
Db        [illegible]

Qy        541 [illegible]
Db        [illegible]

Qy        601 [illegible]
Db        [illegible]

Qy        661 [illegible]
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Db      816 [illegible] 875

Qy      721 [illegible] 780

Db      876 [illegible] 935

Qy      781 [illegible] 840

Db      936 GGGATCCAGCAGCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCGGACTG 995

Qy      841 [illegible] 900

Db      996 GAGTTCCCTCGGCGGCTGAAGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCAC 1055

Qy      901 [illegible] 960

Db     1056 [illegible] 1115

Qy      961 [illegible] 1020

Db     1116 [illegible] 1175

Qy     1021 [illegible] 1080

Db     1176 [illegible] 1235

Qy     1081 [illegible] 1140

Db     1236 [illegible] 1295

Qy     1141 [illegible] 1200

Db     1296 [illegible] 1355

Qy     1201 [illegible] 1260

Db     1356 [illegible] 1415

Qy     1261 [illegible] 1320

Db     1416 [illegible] 1475

Qy     1321 [illegible] 1380

Db     1476 [illegible] 1535


RESULT 4
US-10-180-590-13
; Sequence 13, Application US/[illegible]
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  BANDMAN, Olga
;  APPLICANT:  MATHUR, Preete
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  AZIMZAI, Yalda
;  APPLICANT:  YUE, Henry
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  HILLMAN, Jennifer L.
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  WANG, Eureka
;  APPLICANT:  GANDHI, Ameena R.
;  APPLICANT:  POLICKY, Jennifer L.
;  TITLE OF INVENTION: PHOSPHATASES
;  FILE REFERENCE: PI-0018 PCT
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE:  2002-07-19
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-01-21; 2000-11-28; [illegible]
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PERL Program
; SEQ ID NO 13
;   LENGTH: 1867
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 1723447CB1
US-10-180-590-13

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   99.9%;  Pred. No. 6.30e-271;
  Matches 1380;  Conservative    0;  Mismatches    0;  Indels    [illegible];  Gaps    [illegible];

Qy        1 [illegible] 60

Db        1 [illegible] 60

Qy       61 [illegible] 120

Db       61 [illegible] 120

Qy      121 [illegible] 180

Db      121 [illegible] 180

Qy      181 [illegible] 240

Db      181 [illegible] 240

Qy      241 [illegible] 300

Db      241 [illegible] 300

Qy      301 [illegible] 360

Db      301 [illegible] 360

Qy      361 TGGGCACTGTTCGATGGGCACGGGGGTCCTGCAGCAGCCATCTTGGCTGCCAAGACCCTC 420

Db      361 [illegible] 420

Qy      421 [illegible] 480

Db      421 [illegible] 480

Qy      481 [illegible] 540

Db      481 [illegible] 540

Qy      541 [illegible] 600

Db      541 [illegible] 600

Qy      601 [illegible] 660

Db      601 [illegible] 660

Qy      661 [illegible] 720

Db      661 [illegible] 720

Qy      721 [illegible] 780

Db      721 [illegible] 780

Qy      781 [illegible] 840

Db      781 [illegible] 840

Qy      841 [illegible] 900

Db      841 [illegible] 900

Qy      901 [illegible] 960
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Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy   1141 [illegible]
Db   1141 [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible] A [illegible]
                      |
Db        [illegible] A [illegible]


RESULT [illegible]
[illegible]
[illegible] Application US/[illegible]
  GENERAL INFORMATION:
    APPLICANT: Yue, Henry
    APPLICANT: [illegible]
    APPLICANT: [illegible] Mariah R
    TITLE OF INVENTION: [illegible]
    FILE REFERENCE: [illegible]
    CURRENT APPLICATION NUMBER: US/[illegible]
    CURRENT FILING DATE: [illegible]
    NUMBER OF SEQ ID NOS: [illegible]
    SOFTWARE: PERL Program
  SEQ ID NO [illegible]
    LENGTH: [illegible]
    TYPE: DNA
    ORGANISM: Homo sapiens
    FEATURE:
    NAME/KEY: misc_feature
    OTHER INFORMATION: Incyte ID No: [illegible]
[illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db    181 [illegible]

Qy    241 [illegible]
Db    241 [illegible]

Qy    301 [illegible]
Db    301 [illegible]

Qy    361 [illegible]
Db    361 [illegible]

Qy    421 [illegible]
Db    421 [illegible]

Qy    481 [illegible]
Db    481 [illegible]

Qy    541 [illegible]
Db    541 [illegible]

Qy    601 [illegible]
Db    601 [illegible]

Qy    661 [illegible]
Db    661 [illegible]

Qy    721 [illegible]
Db    721 [illegible]

Qy    781 [illegible]
Db    781 [illegible]

Qy    841 [illegible]
Db    841 [illegible]

Qy    901 [illegible]
Db    901 [illegible]

Qy    961 [illegible]
Db    961 [illegible]

Qy   1021 [illegible]
Db   1021 [illegible]

Qy   1081 [illegible]
Db   1081 [illegible]

Qy   1141 [illegible]
Db   1141 [illegible]

Qy   1201 [illegible]
Db   1201 [illegible]
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Qy   [illegible] [illegible]
Db        1261 [illegible] 1320

Qy   [illegible] [illegible] 1379
Db        1321 [illegible] 1380

Qy        1380 A 1380

Db        1381 A 1381


RESULT 6
US-09-526-996-1047/c
; Sequence 1047, Application US/09526996
; GENERAL INFORMATION:
;  APPLICANT: Shyjan, Andrew W.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM
;  TITLE OF INVENTION: HUMAN PROSTATE AND BREAST LIBRARIES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/526,996
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: 60/125,469
;  EARLIER FILING DATE: 1999-03-22
;  EARLIER APPLICATION NUMBER: 60/125,566
;  EARLIER FILING DATE: 1999-03-22
;  NUMBER OF SEQ ID NOS: 1236
;  SOFTWARE: PatentIn for Windows Version 4.0
; SEQ ID NO 1047
;   LENGTH: 2110
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-526-996-1047

  Query Match             93.1%;  Score 1285;  DB 14;  Length 2110;
  Best Local Similarity   99.9%;  Pred. No. 1.2e-257;
  Matches 1296;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          85 [illegible] 144
Db        2110 [illegible] 2051

Qy         145 [illegible] 204
Db        2050 [illegible] 1991

Qy         205 [illegible] 263
Db        1990 [illegible] 1931

Qy         264 [illegible] 323
Db        1930 [illegible] 1871

Qy         324 [illegible] 383
Db        1870 [illegible] 1811

Qy         384 [illegible] 443
Db        1810 [illegible] 1751

Qy         444 [illegible] 503
Db        1750 [illegible] 1691

Qy         504 [illegible] 563
Db        1690 [illegible] 1631

Qy         564 [illegible] 623
Db        1630 [illegible] 1571

Qy         624 [illegible] 683
Db        1570 [illegible] 1511

Qy         684 [illegible] 743
Db        1510 [illegible] 1451

Qy         744 [illegible] 803
Db        1450 [illegible] 1391

Qy         804 [illegible] 863
Db        1390 [illegible] 1331

Qy         864 [illegible] 923
Db        1330 [illegible] 1271

Qy         924 [illegible] 983
Db        1270 [illegible] 1211

Qy         984 [illegible] 1043
Db        1210 [illegible] 1151

Qy        1044 [illegible] 1103
Db        1150 [illegible] 1091

Qy        1104 [illegible] 1163
Db        1090 [illegible] 1031

Qy        1164 [illegible] 1223
Db        1030 [illegible] 971

Qy        1224 [illegible] 1283
Db         970 [illegible] 911

Qy        1284 [illegible] 1343
Db         910 [illegible] 851

Qy        1344 [illegible]
Db         850 [illegible] 811


RESULT 7
US-09-546-216-1175/c
; Sequence 1175, Application US/09546216
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: Kingsbury, Gillian A.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM
;  TITLE OF INVENTION: HUMAN BONE MARROW AND T CELL LIBRARIES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/546,216
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: 60/126,971
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 1284
;  SOFTWARE: FastSEQ for Windows Version [illegible]
; SEQ ID NO 1175
;   LENGTH: 21[illegible]
;   TYPE: DNA
;  ORGANISM: Homo sapiens
[illegible]

  Query Match          [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative    [illegible];  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy        [illegible] 144
Db     [illegible] 2051

Qy      145 [illegible] 204
Db      [illegible]

Qy      205 [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible] 1811

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible] 1571

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Db      [illegible]

Qy     1104 [illegible]
Db     1090 [illegible]

Qy     1164 [illegible]
Db     1030 [illegible]

Qy     1224 GGAC[illegible]ACACAG[illegible]AAA[illegible]AGATG[illegible]GATACACAGCACACAGGGAAA[illegible]A 128[illegible]
Db      970 GGAC[illegible]ACACA[illegible]AAA[illegible]AGATG[illegible]GATACACAGCACACAGGGAAA[illegible]A [illegible]

Qy     1284 [illegible] 134[illegible]
Db      910 [illegible]

Qy     1344 [illegible] 13[illegible]
Db      850 [illegible]AAGAGAGCAG[illegible]ACCAC[illegible]A 814

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US-09-617-60[illegible]
; Sequence 1175, Application US/0961760[illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible] A.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM
;  TITLE OF INVENTION: HUMAN BONE MARROW AND T CELL LIBRARIES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 1284
;  SOFTWARE: FastSEQ for Windows Version [illegible]
; SEQ ID NO 1175
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-617-603-1175

  Query Match          [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    [illegible];

Qy       85 [illegible] 144
Db     2110 [illegible]

Qy      145 [illegible] 204
Db      [illegible]

Qy      205 [illegible]
Db     1990 [illegible]

Qy      264 [illegible]
Db     1930 [illegible]

Qy      324 [illegible]
Db     1870 [illegible]

Qy      384 [illegible]
Db      [illegible]

Qy      444 [illegible]
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Db       1750 [illegible] 1691

Qy        504 CATCTGGC[illegible]CAGTGAC[illegible]CAG[illegible]TTG[illegible]GAGGAAAAG[illegible] 563

Db       1690 [illegible] 1631

Qy        564 GA[illegible] 623

Db       1630 [illegible] 1571

Qy        624 GGC[illegible]CA[illegible] 683

Db       1570 GG[illegible]CA[illegible]CAGATGGGGG[illegible]CACAGGCC[illegible]A[illegible]GAAAG[illegible]T 1511

Qy        684 [illegible] 743

Db       1510 GT[illegible] 1451

Qy        744 A[illegible] 803

Db       1450 AC[illegible]CAG[illegible]CAG[illegible]CAGACACTGAGTGGCAGCTGATCCAGCAGCTGGCCTTTGT 1391

Qy        804 CTA[illegible]TGGA[illegible]GAAGGC 863

Db       1390 CTA[illegible]TGGA[illegible]TTGGCTGGTGAGTTCAGCCAGTGGA[illegible]GAAGGC 1331

Qy        864 GGATGACTTGGACAGAAGGTTTTGTTCAGGGATCAC[illegible]ATGA[illegible]GG[illegible]GAGCTACAA 923

Db       1330 GGATGACTTGGACAGAAGGTTTTGTTCAGGGATCAC[illegible]ATGA[illegible]GAGCTACAA 1271

Qy        924 ACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGACAGGGTAGGCAGGCTCG 983

Db       1270 ACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGACA[illegible]CCTAGGCAGGCTCG 1211

Qy        984 GTTACTAGGAACACTGGCTGT[illegible]GGGGGCCTGGGAGACCATCAG[illegible]CAGAGTCCTGGA 1043

Db       1210 GTTACTAGGAACACTGGCTGTCT[illegible]GGGGGCCTGGGAGACCATCAG[illegible]CAGAGTCCTGGA 1151

Qy       1044 CACAAACATCCAGCTCAAGCC[illegible]TTCTTGCTCTCTGTGCC[illegible]ACAGGTGACTGTGCTGGATGT 1103

Db       1150 CACAAACATCCAGCTCAAGCCCTTCTTGCTCTCTGTGCCACAGGTGACTGTGCTGGATGT 1091

Qy       1104 [illegible] 1163

Db       1090 GGACCAGGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGATGGACTCTGGGA 1031

Qy       1164 [illegible]GTACTGT[illegible]AA[illegible]CAAGA 1223

Db       1030 TGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTCCTCCCTGGAACCAAGA 971

Qy       1224 [illegible] 1283

Db        970 GGA[illegible]CACAGGTTCTCAAAGCTGGCCCAGATGCTGATACACAAACACAGGCAAAGGA 911

Qy       1284 AGACAGTCTCACAGAGGAAGGGCAGGTGTCCTACGATGAGGTCTCTGTGTTCGTGATTCC 1343

Db        910 AGACAGTCTCACAGAGGAAGGGCAGGTGTCCTACGATGAG[illegible]TCTGTGTTCGTGATTCC 851

Qy       1344 TTGCACATTCAGGG[illegible]AAGAGAGCAGTGACCACTGA 1380

Db        850 TTGCACATTCAGGGTAAGAGAGCAGTGACCACTGA 814


RESULT [illegible]
US-09-760-475-724
; Sequence 724, Application US/09760475
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PI249
;  CURRENT APPLICATION NUMBER: US/09/760,475
;  CURRENT FILING DATE: 2001-01-16
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 4122
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 724
;   LENGTH: 2156
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (65)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (78)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (83)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (2088)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-760-475-724

  Query Match             92.7%;  Score [illegible];  DB [illegible];  Length 2156;
  Best Local Similarity   [illegible];  Pred. No. 2e-[illegible];
  Matches 1301;  Conservative    0;  Mismatches    3;  Indels    2;  Gaps    2;

Qy         75 [illegible] 134

Db          1 TGCCAG[illegible]GTG[illegible]CAG[illegible] 60

Qy        135 GG[illegible]A[illegible]GA[illegible] 194

Db         61 GG[illegible]N[illegible]GA[illegible]N[illegible] 120

Qy        195 [illegible]AA 254

Db        121 [illegible]AATGAGAGAAA[illegible]AA 179

Qy        255 TGAGGATCAAG[illegible]AA[illegible]TGTG[illegible]GGAGATGTGAGTT[illegible]GCTGAAGA 314

Db        180 TGAGGATCAAG[illegible]GAAG[illegible]GAGATGTGAGTT[illegible]GAAGA 239

Qy        315 [illegible]GA 374

Db        240 AGAGTGG[illegible] 299

Qy        375 TGGGCAG[illegible] 434

Db        300 TGGGCAGG[illegible] 359

Qy        435 [illegible]AA 494

Db        360 CCGGCAGCTGGAGGCCGTGGTGGAAGCCTTGGTGGCCACTCAGCCCCCCATGGACTTCAA 419

Qy        495 [illegible]AGA 554

Db        420 [illegible]GAAAAAGG[illegible]AGA 479

Qy        555 A[illegible] 614

Db        480 A[illegible] 539

Qy        615 G[illegible]TGGA[illegible]A 674

Db        540 [illegible]A 599

Qy        675 [illegible]GATAGATGA 734

Db        600 GGAAAA[illegible]A 659

Qy        735 GATA[illegible] 794

Db        660 GATA[illegible] 719
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Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

RESULT [illegible]
[illegible]
; Sequence [illegible] Application [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: Wehrmann, [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: Mi, Yunqing
;  APPLICANT: [illegible] Vinod
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: [illegible]
;  TITLE OF INVENTION: [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US0[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 200[illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2000 02 03
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001 02 05
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: pt_FL_genes Version [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
[illegible]

  Query Match [illegible]
  Best Local Similarity [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       121 GCACGCTACCCTGGAATGCAGGCTACGCGATGCATTATCAATGCAGAGAAATCTGAATTC 180

Qy       [illegible]
Db       181 [illegible]

Qy       [illegible]
Db       241 [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       421 [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
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Db        [illegible] 72[illegible]

Qy        7[illegible] [illegible] 852
               [illegible]
Db        72[illegible] [illegible]

Qy        [illegible] [illegible] 912
               [illegible]
Db        781 [illegible] 84[illegible]

Qy        913 [illegible] 972
               [illegible]
Db        841 [illegible]

Qy        973 [illegible] 1032
               [illegible]
Db        901 [illegible] 96[illegible]

Qy        [illegible] [illegible] [illegible]
               [illegible]
Db        961 [illegible] [illegible]

Qy       1093 [illegible] 1152
               [illegible]
Db       1021 [illegible]

Qy       115[illegible] [illegible] 1212
               [illegible]
Db       1081 [illegible] 1140

Qy       1213 [illegible]---------------------------[illegible] 1247
               [illegible]
Db       1141 [illegible] 12[illegible]

Qy       1248 [illegible] 1[illegible]
               [illegible]
Db       12[illegible] [illegible] 12[illegible]

Qy       1[illegible] [illegible] [illegible]
               [illegible]
Db       1261 [illegible]

Qy       1[illegible] [illegible] 1[illegible]
               [illegible]
Db       1321 [illegible] 1[illegible]


RESULT 11
PCT-US02-30474-2218
; Sequence 2218, Application PC/US0230474
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: [illegible]
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  X[illegible], A[illegible]
;  APPLICANT:  Zh[illegible], [illegible] A.
;  APPLICANT:  Wang, [illegible]
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  [illegible]
;  APPLICANT:  Ghosh, Malabika
;  APPLICANT:  Wang, [illegible]
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Wang, [illegible]
;  APPLICANT:  Haley Vicente, Dana
;  APPLICANT:  [illegible], Radoje [illegible]
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE:  2002-09-24
;  PRIOR APPLICATION NUMBER: US [illegible]/221,[illegible]
;  PRIOR FILING DATE: 2[illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]/188,[illegible]
;  PRIOR FILING DATE: 2000-0[illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]/[illegible],[illegible]
;  PRIOR FILING DATE: 2[illegible]
;  PRIOR APPLICATION NUMBER: PCT/US[illegible]/[illegible]
;  PRIOR FILING DATE: 2[illegible]-12-12
;  PRIOR APPLICATION NUMBER: US [illegible]/[illegible],[illegible]
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: PCT/US01/02[illegible]
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US [illegible]/4[illegible],[illegible]
;  PRIOR FILING DATE: 2[illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]/[illegible],[illegible]
;  PRIOR FILING DATE: 200[illegible]-04-2[illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/03800
;  PRIOR FILING DATE: 2001-02-0[illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]/[illegible]
;  PRIOR FILING DATE: [illegible]
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: [illegible]476
;  SOFTWARE: pt_FL_genes Version [illegible]
; SEQ ID NO 2218
;   LENGTH: 2124
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US02-30474-2218

  Query Match             [illegible];  Score 12[illegible].4;  DB [illegible];  Length 21[illegible];
  Best Local Similarity   [illegible];  Pred. No. 2.7e-244;
  Matches [illegible];  Conservative    [illegible];  Mismatches    6;  Indels   [illegible];  Gaps    [illegible];

Qy         [illegible] [illegible]
               [illegible]
Db          1 [illegible]

Qy        1[illegible] [illegible]
               [illegible]
Db         [illegible] [illegible]

Qy        1[illegible] [illegible] 2[illegible]
               [illegible]
Db        121 [illegible]

Qy        2[illegible] [illegible]
               [illegible]
Db        181 [illegible]

Qy        [illegible] [illegible]
               [illegible]
Db        241 [illegible]

Qy        [illegible] [illegible]
               [illegible]
Db        [illegible] [illegible]

Qy        4[illegible] [illegible]
               [illegible]
Db        [illegible] [illegible]

Qy        4[illegible] [illegible]
               [illegible]
Db        421 [illegible]

Qy        5[illegible] [illegible]
               [illegible]
Db        481 [illegible]

Qy        6[illegible] [illegible]
               [illegible]
Db        [illegible] [illegible]

Qy        67[illegible] [illegible]
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RESULT [illegible]
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; GENERAL INFORMATION
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: [illegible]
;  TITLE OF INVENTION: [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
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;  EARLIER FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
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;  EARLIER FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: 1999-08-19
;  EARLIER APPLICATION NUMBER: US [illegible]
;  EARLIER FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER:
;  EARLIER FILING DATE: 1999-12-16
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: [illegible] Version [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (280)...(1804)
;   OTHER INFORMATION: similar to [illegible] in the [illegible]
;   OTHER INFORMATION: [illegible] with FASTXY [illegible] default parameters
[illegible]

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative   [illegible];  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy         75 [illegible] 134
Db          1 [illegible]
Db        601 [illegible] 660

Qy        733 [illegible] 792
Db        661 [illegible] 720

Qy        793 [illegible] 852
Db        721 [illegible] 780

Qy        853 [illegible] 912
Db        781 [illegible] 840

Qy        913 [illegible] 972
Db        841 [illegible] 900

Qy        973 [illegible] 1032
Db        901 [illegible] 960

Qy       1033 [illegible] 1092
Db        961 [illegible] 1020

Qy       1093 [illegible] 1152
Db       1021 [illegible] 1080

Qy       1153 [illegible] 1212
Db       1081 [illegible] 1140

Qy       1213 [illegible] 1247
Db       1141 [illegible] 1200

Qy       1248 [illegible] 1307
Db       1201 [illegible] 1260

Qy       1308 [illegible] 1367
Db       1261 [illegible] 1320

Qy       1368 CAGTGACTACTGA 1380
                ||||||||||||| 
Db       1321 CAGTGACTACTGA 1333


RESULT 14
US-60-324-631-2198
; Sequence 2198, Application US/60324631
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Ghosh, Malabika
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Weng, Gezhi
;  APPLICANT:  Daley Vicente, Dana
;  APPLICANT:  Drmanac, Radoje T
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 810
;  CURRENT APPLICATION NUMBER: US/60/324,631
;  CURRENT FILING DATE:  2001-09-24
;  PRIOR APPLICATION NUMBER: US 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: PCT/US00/35017
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: PCT/US01/02623
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 09/515,126
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: US 09/577,409
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: PCT/US01/04927
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 09/574,454
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 09/540,217
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 09/649,167
;  PRIOR FILING DATE: 2000-08-23
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 09/552,929
;  PRIOR FILING DATE: 2000-04-18
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2001-01-26
;  PRIOR APPLICATION NUMBER: PCT/US01/08656
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: US 09/577,408
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: PCT/US01/14827
;  PRIOR FILING DATE: 2001-05-16
;  NUMBER OF SEQ ID NOS: 3334
;  SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 2198
;   LENGTH: 2124
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-324-631-2198

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible]-244;
  Matches [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy         75 [illegible] 134
Db          1 [illegible] 60

Qy        135 [illegible] 194
Db         61 [illegible] 120

Qy        195 [illegible] 252
Db        121 [illegible] 180

Qy        253 [illegible]
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[illegible]

RESULT 11
US-[illegible]
; Sequence [illegible], Application US/[illegible]
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Xue, Aidong J.
; APPLICANT: [illegible], Qing A.
; APPLICANT: Wang, Jian Rui
; APPLICANT: Wehrman, Tom
; APPLICANT: [illegible], Tina
; APPLICANT: Ghosh, Malabika
; APPLICANT: Wang, Dunrui
; APPLICANT: Ma, Yunqing
; APPLICANT: Asundi, Vinod
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, [illegible]
; APPLICANT: Haley Vicente, Dana
; APPLICANT: Drmanac, Radoje T
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: [illegible]
; CURRENT APPLICATION NUMBER: US/[illegible]
; CURRENT FILING DATE: 2001-[illegible]-24
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,[illegible]
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/[illegible]/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/[illegible]
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
; PRIOR FILING DATE: [illegible]-25
; PRIOR APPLICATION NUMBER: US 09/[illegible]
; PRIOR FILING DATE: [illegible]
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: [illegible]-27
; PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/515,126
; PRIOR FILING DATE: [illegible]-28
; PRIOR APPLICATION NUMBER: US 09/[illegible]
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
; PRIOR FILING DATE: [illegible]
; PRIOR APPLICATION NUMBER: US 09/[illegible]
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: US 09/574,[illegible]
; PRIOR FILING DATE: [illegible]
; PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: US 09/[illegible]
; PRIOR FILING DATE: [illegible]
; PRIOR APPLICATION NUMBER: US 09/[illegible]
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
; PRIOR FILING DATE: [illegible]
; PRIOR APPLICATION NUMBER: US 09/[illegible]
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: US 09/[illegible]
; PRIOR FILING DATE: [illegible]
; PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
; PRIOR FILING DATE: [illegible]
; PRIOR APPLICATION NUMBER: US 09/[illegible]

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;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/14927
;  PRIOR FILING DATE: 2001-05-16
;  NUMBER OF SEQ ID NOS: 3334
;  SOFTWARE: [illegible] Version [illegible]
; SEQ ID NO 2109
;   LENGTH: 2124
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-324-631-2109

  Query Match             89.8%;  Score 1239.4;  DB 76;  Length 2124;
  Best Local Similarity   97.5%;  Pred. No. [illegible];
  Matches [illegible];  Conservative    0;  Mismatches    [illegible];  Indels   27;  Gaps    [illegible];

Qy         75 [illegible] 134
Db          1 [illegible] [illegible]

Qy        135 [illegible] 193
Db         61 [illegible] 120

Qy        194 [illegible] 252
Db        121 [illegible] [illegible]

Qy        253 [illegible] 312
Db        181 [illegible] 240

Qy        313 [illegible] [illegible]
Db        241 [illegible] [illegible]

Qy        373 [illegible] 432
Db        [illegible] [illegible] [illegible]

Qy        433 [illegible] 492
Db        361 [illegible] 420

Qy        493 [illegible] 552
Db        421 [illegible] [illegible]

Qy        553 [illegible] 612
Db        481 [illegible] 540

Qy        613 [illegible] [illegible]
Db        541 [illegible] [illegible]

Qy        673 [illegible] 732
Db        601 [illegible] [illegible]

Qy        733 [illegible] 792
Db        661 [illegible] [illegible]

Qy        793 [illegible] 852
Db        721 [illegible] [illegible]

Qy        853 [illegible] 912
Db        781 [illegible] 840

Qy        913 [illegible] 972
Db        841 [illegible] [illegible]

Qy        973 [illegible] [illegible]
Db        901 [illegible] [illegible]

Qy       1033 [illegible] [illegible]
Db        961 [illegible] [illegible]

Qy       1093 [illegible] [illegible]
Db       1021 [illegible] [illegible]

Qy       1153 [illegible] [illegible]
Db       1081 [illegible] [illegible]

Qy       1213 [illegible] [illegible]
Db       1141 [illegible] [illegible]

Qy       1248 [illegible] [illegible]
Db       1201 [illegible] [illegible]

Qy       1308 [illegible] [illegible]
Db       1261 [illegible] [illegible]

Qy       1368 [illegible] [illegible]
Db       1321 [illegible] [illegible]


RESULT 5
US-60-185-213-1400
; Sequence 1400, Application US/60185213
; GENERAL INFORMATION:
;  APPLICANT: Hodgson, David M.                    Jones, Anissa L.
;  APPLICANT: Lincoln, Stephen E.          Yu, Jimmy Y.
;  APPLICANT: Russo, Frank D.                       Greenawalt, [illegible]
;  APPLICANT: Spiro, Peter A.                       Panzer, Scott R.
;  APPLICANT: Banville, [illegible]        Roseberry, Ann M.
;  APPLICANT: Bratcher, Shawn R.           Wright, Rachel J.
;  APPLICANT: [illegible]                           Chen, Wensheng
;  APPLICANT: Cohen, Howard J.                      Lin, [illegible]
;  APPLICANT: Rosen, Bruce                 Yap, Pierre E.
;  APPLICANT: Shah, Purvi                           Stockdreher, Theresa K.
;  APPLICANT: Chalup, Michael S.           Amshey, Stefan
;  APPLICANT: Hillman, Jennifer L.                  Fong, Willy Tuen
;  TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
;  FILE REFERENCE: PF-[illegible] P
;  CURRENT APPLICATION NUMBER: US/60/185,213
;  CURRENT FILING DATE: [illegible]-24
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PERL Program
; SEQ ID NO 1400
;   LENGTH: 2084
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: [illegible]
US-60-185-213-1400

  Query Match             80.1%;  Score [illegible];  DB 62;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches 1156;  Conservative    0;  Mismatches    0;  Indels   26;  Gaps    2;

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Db        [illegible] [illegible] [illegible]
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Db        173 [illegible] 232

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Db        233 [illegible] 292

Qy        405 [illegible] 464
              [illegible]
Db        293 [illegible] 352

Qy        465 [illegible] 524
              [illegible]
Db        353 [illegible] 412

Qy        525 [illegible] 584
              [illegible]
Db        413 [illegible] 472

Qy        585 [illegible] 644
              [illegible]
Db        473 [illegible] 532

Qy        645 [illegible] 704
              [illegible]
Db        533 [illegible] 592

Qy        705 [illegible] 764
              [illegible]
Db        593 [illegible] 652

Qy        765 [illegible] 824
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Db        653 [illegible] 712

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Db        713 [illegible] 772

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Db        773 [illegible] 832

Qy        945 [illegible] 1004
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Db        833 [illegible] 892

Qy       1005 [illegible] 1064
              [illegible]
Db        893 [illegible] 952

Qy       1065 [illegible] 1124
              [illegible]
Db        953 [illegible] 1012

Qy       1125 [illegible] 1184
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Db       1013 [illegible] 1072

Qy       1185 [illegible] 1230
              [illegible]
Db       1073 [illegible] 1132

Qy       1231 [illegible] 1279
              [illegible]
Db       1133 [illegible] 1192

Qy       1280 [illegible] 1338
              [illegible]
Db       1193 [illegible] 1252

Qy       1339 [illegible] 1380
              [illegible]
Db       1253 [illegible] 1294

Search completed: February 23, 2003, 05:50:58
Job time : 3600 secs
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                       GenCore version 5.1.4
              Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 23, 2003, 03:39:46 ; Search time 2[illegible] Seconds
                                          (without alignments)
                                          7351.029 Million cell updates/sec

Title:           US-09-866-987-3
Perfect score:   1380
Sequence:        1 atgtccgaccagctgagttccg..........aaaatccagtgaccgctga 1380

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2850587 seqs, 777717511 residues

Total number of hits satisfying chosen parameters:      5761174

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Pending_Patents_NA_New:*
                 1: [illegible]_NEW_[illegible]:*
                 2: [illegible]_NEW_COMB.seq:*
                 3: [illegible]_NEW_COMB.seq:*
                 4: [illegible]_NEW_COMB.seq:*
                 5: [illegible]_NEW_COMB.seq:*
                 6: [illegible]_NEW_COMB.seq:*
                 7: [illegible]_NEW_COMB.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result             Query
   No.   Score  Match Length DB  ID                               Description
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     1    1346   97.5   2185  6  US-10-072-012-197                 Sequence 197, App
     2   843.6   61.1   1285  6  US-10-144-771-11494               Sequence 11494, A
     3     826   59.9   1930  6  US-10-072-012-199                 Sequence 199, App
     4   367.2   26.6    476  6  US-10-349-781-54107               Sequence 54107, A
     5   264.8   19.2   2513  6  US-10-342-887-312                 Sequence 312, App
     6   263.2   19.1   1480  1  PCT-US02-39126-65                 Sequence 65, App
     7   262.9   19.0   1691  6  US-10-144-771-12171               Sequence 12171, A
     8     259   18.8    271  6  US-10-349-781-22954               Sequence 22954, A
     9   252.6   18.3   2452  6  US-10-144-771-6858                Sequence 6858, Ap
    10     248   18.0   1481  1  PCT-US02-39126-63                 Sequence 63, App
    11   243.4   17.6   1887  5  US-09-620-312D-12                 Sequence 12, App
    12   233.6   16.9    241  6  US-10-349-781-23065               Sequence 23065, A
    13   164.6   11.9   1151  1  PCT-US02-39126-62                 Sequence 62, App
    14   168.8   12.2   1472  1  PCT-US02-39126-64                 Sequence 64, App
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    16    52.6    3.8    475  5  US-09-606-397A-167                Sequence 167, App
    17      51    3.7   1511  7  US-60-423-552-19                  Sequence 19, Appl
    18      51    3.7   1511  7  US-60-427-579-19                  Sequence 19, Appl
c   19    49.8    3.6   6714  6  US-10-267-117-6                   Sequence 6, Appl
c   20    49.8    3.6   6714  6  US-10-340-112-6                   Sequence 6, Appl
c   21    49.8    3.6   6924  6  US-10-267-117-9                   Sequence 9, Appl
c   22    49.8    3.6   6924  6  US-10-267-117-10                  Sequence 10, Appl
c   23    49.8    3.6   6924  6  US-10-267-117-11                  Sequence 11, Appl
c   24    49.8    3.6   6924  6  US-10-340-112-9                   Sequence 9, Appl
c   25    49.8    3.6   6924  6  US-10-340-112-10                  Sequence 10, Appl
c   26    49.8    3.6   6924  6  US-10-340-112-11                  Sequence 11, Appl
c   27    49.4    3.6   1477  5  US-09-724-676-19511               Sequence 19511, A
c   28    49.4    3.6   1477  5  US-09-724-676A-19511              Sequence 19511, A
c   29    49.4    3.6   1483  5  US-09-724-676-19546               Sequence 19546, A
c   30    49.4    3.6   1483  5  US-09-724-676A-19546              Sequence 19546, A
c   31    49.4    3.6   1505  5  US-09-724-676-19539               Sequence 19539, A
c   32    49.4    3.6   1505  5  US-09-724-676A-19539              Sequence 19539, A
c   33    49.4    3.6   1511  5  US-09-724-676-19543               Sequence 19543, A
c   34    49.4    3.6   1511  5  US-09-724-676A-19543              Sequence 19543, A
c   35    49.4    3.6   1512  5  US-09-724-676-19521               Sequence 19521, A
c   36    49.4    3.6   1512  5  US-09-724-676A-19521              Sequence 19521, A
c   37    49.4    3.6   1518  5  US-09-724-676-19525               Sequence 19525, A
c   38    49.4    3.6   1518  5  US-09-724-676A-19525              Sequence 19525, A
c   39    49.4    3.6   1525  5  US-09-724-676-19531               Sequence 19531, A
c   40    49.4    3.6   1525  5  US-09-724-676A-19531              Sequence 19531, A
c   41    49.4    3.6   1533  5  US-09-724-676-19535               Sequence 19535, A
c   42    49.4    3.6   1533  5  US-09-724-676A-19535              Sequence 19535, A
c   43    49.4    3.6   1650  5  US-09-724-676-19538               Sequence 19538, A
c   44    49.4    3.6   1650  5  US-09-724-676A-19538              Sequence 19538, A
c   45    49.4    3.6   1678  5  US-09-724-676-19542               Sequence 19542, A

                              ALIGNMENTS

RESULT 1
US-10-072-012-197
; Sequence 197, Application US/10072012
; GENERAL INFORMATION:
;  APPLICANT: Tchernev, Velizar
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Li, Li
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  [illegible]
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Taupier Jr, Raymond J.
;  APPLICANT:  Gusev, Vladimir Y.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Wolenc, Adam R.
;  APPLICANT:  Pena, Carol E. A
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Grosse, William M.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-278
;  CURRENT APPLICATION NUMBER: US/10/072,012
;  CURRENT FILING DATE: 2002-[illegible]
;  PRIOR APPLICATION NUMBER: 60/26[illegible]
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/265,514
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,517
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,412
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,395
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/266,406
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 60/266,737
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: 60/267,057
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/266,975
;  PRIOR FILING DATE: 2001-02-07
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Db  [illegible]
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RESULT 2
US-10-144-771-11494
; Sequence 11494, Application US/10144771
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: HUMAN [illegible] SYSTEM AND USES THEREOF
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/10/144,771
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
; SEQ ID NO 11494
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-144-771-11494

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  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches  962; Conservative    0; Mismatches  149; Indels    9; Gaps    [illegible];

Qy  [illegible]
Db  [illegible]
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Qy        45[illegible] [illegible] 51[illegible]

Db        353 [illegible] 412

Qy        519 [illegible] 578

Db        413 [illegible] 472

Qy        579 [illegible] 6[illegible]

Db        473 [illegible] 5[illegible]2

Qy        6[illegible] [illegible] 69[illegible]

Db        533 [illegible] 592

Qy        [illegible] [illegible] 75[illegible]

Db        593 [illegible] 6[illegible]2

Qy        759 [illegible] 818

Db        6[illegible] [illegible] 71[illegible]

Qy        819 [illegible] 878

Db        713 [illegible] 772

Qy        879 [illegible] [illegible]

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Qy        9[illegible] [illegible] [illegible]

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Db        95[illegible] [illegible] 1012

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Qy        1179 [illegible] 123[illegible]

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Qy        12[illegible] [illegible] 1[illegible]

Db        113[illegible] [illegible] 11[illegible]2

Qy        1296 [illegible] 1[illegible]

Db        1193 [illegible] 1232


RESULT 3
US 1[illegible]-072-012-139
; Sequence 1[illegible], Application US/10072012
; GENERAL INFORMATION:
;  APPLICANT: [illegible], Velizar
;  APPLICANT: Spytek, Kimberly
;  APPLICANT: Zerhusen, Bryan
;  APPLICANT: Patturajan, Meera
;  APPLICANT: Shimkets, Richard
;  APPLICANT: Li, Li
;  APPLICANT: Gangolli, Esha
;  APPLICANT: Padigaru, Muralidhara
;  APPLICANT: Anderson, David W.
;  APPLICANT: Rastelli, Luca
;  APPLICANT: Miller, Charles E.
;  APPLICANT: Gerlach, Valerie
;  APPLICANT: Taupier Jr, Raymond J.
;  APPLICANT: Gusev, Vladimir Y.
;  APPLICANT: Colman, Steven D.
;  APPLICANT: Wolenc, Adam R.
;  APPLICANT: Pena, Carol E. A
;  APPLICANT: Furtak, Katarzyna
;  APPLICANT: Grosse, William M.
;  APPLICANT: Alsobrook II, John P.
;  APPLICANT: Lepley, Denise M.
;  APPLICANT: Rieger, Daniel K.
;  APPLICANT: Burgess, Catherine E.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/10/072,012
;  CURRENT FILING DATE: 2002-02-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-01-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]/26[illegible],514
;  PRIOR FILING DATE: 2001-01-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: [illegible],412
;  PRIOR FILING DATE: 2001-01-[illegible]
;  PRIOR APPLICATION NUMBER: 60/265,[illegible]
;  PRIOR FILING DATE: 2001-01-[illegible]
;  PRIOR APPLICATION NUMBER: 6[illegible]/26[illegible],4[illegible]
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 60/266,767
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: 6[illegible]/267,057
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: [illegible]/26[illegible],[illegible]75
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/267,459
;  PRIOR FILING DATE: 2001-02-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US 10-072-012-139

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  Matches 112[illegible];  Conservative    0;  Mismatches    [illegible];  Indels  [illegible];  Gaps    [illegible];

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Db          1 [illegible]

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Qy        121 [illegible]

Db        121 [illegible]

Qy        181 [illegible]

Db        181 [illegible]

Qy        241 [illegible]

Db        241 [illegible]
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Qy   [illegible] 420
Db   [illegible] 412

Qy   [illegible] 480
Db   [illegible] 412

Qy   [illegible] 540
Db   [illegible] 412

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]
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Qy   [illegible] AAGAGA [illegible]
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Db   [illegible] AAGAGA [illegible]


RESULT 4
US [illegible]
; Sequence [illegible], Application US/[illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible]; [illegible], Angelo M.
;  APPLICANT: Stuart, Susan [illegible]; [illegible]
;  APPLICANT: [illegible], Sara [illegible]; Naughton, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIV
;  FILE REFERENCE: [illegible] 1028 [illegible] CON
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]/540,764
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible],838
;  PRIOR FILING DATE: 1996-12-13
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: 60/006,[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: 60/005,864
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: 60/008,794
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-12-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 61458
;  SOFTWARE: PERL Program
; SEQ ID NO [illegible]
;   LENGTH: 47[illegible]
;   TYPE: DNA
;   ORGANISM: [illegible]
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: [illegible]
US [illegible]

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  Best Local Similarity   [illegible];  Pred. No. [illegible];
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Qy   [illegible]
Db   [illegible]

Qy   [illegible]
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Db    405 TTTGTGGATGGAAAA[illegible] 464

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RESULT 5
US-10-342-887-312
; Sequence 312, Application US/10342887
; GENERAL INFORMATION:
;  APPLICANT: Dai, Hongyue
;  APPLICANT:  He, Yudong
;  APPLICANT:  Linsley, Peter S.
;  APPLICANT:  Mao, Mao
;  APPLICANT:  Roberts, Christopher J.
;  APPLICANT:  Van 't Veer, Laura Johanna
;  APPLICANT:  Van de Vijver, Marc J.
;  APPLICANT:  Bernards, Rene
;  TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;  FILE REFERENCE: 9301-188-999
;  CURRENT APPLICATION NUMBER: US/10/342,887
;  CURRENT FILING DATE: 2003-01-15
;  PRIOR APPLICATION NUMBER: 60/298,918
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: 60/380,710
;  PRIOR FILING DATE: 2002-05-14
;  PRIOR APPLICATION NUMBER: 10/172,118
;  PRIOR FILING DATE: 2002-06-14
;  NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 312
;   LENGTH: 2518
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-342-887-312

  Query Match             19.2%;  Score 264.8;  DB [illegible];  Length 2518;
  Best Local Similarity   57.7%;  Pred. No. 1.5e-50;
  Matches  5[illegible]7;  Conservative    0;  Mismatches  3[illegible]7;  Indels   16;  Gaps    [illegible];

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Qy    505 AT[illegible] 564
Db   1429 [illegible] 1487

Qy    565 A[illegible] 624
Db   1488 [illegible] 1547

Qy    625 [illegible] 684
Db   1548 [illegible] 1607

Qy    685 [illegible] 744
Db   1608 [illegible] 1667

Qy    745 [illegible] 804
Db   1668 [illegible] 1727

Qy    805 [illegible] 864
Db   1728 [illegible] 1787

Qy    865 GA[illegible] 924
Db   1788 AA[illegible] 1847

Qy    925 [illegible] 984
Db   1848 AAGAT[illegible] 1907

Qy    985 [illegible] 1044
Db   1908 [illegible] 1967

Qy   1045 ACAAA[illegible] 1104
Db   1968 [illegible] 2027

Qy   1105 [illegible] 1164
Db   2028 ACA[illegible] 2087

Qy   1165 [illegible] 1221
Db   2088 [illegible] 2147

Qy   1222 [illegible]
Db   [illegible] 2197

Qy   [illegible]
Db   [illegible] 2257

Qy   [illegible]
Db   2258 GTGTTCGTCAT[illegible]AGGG 2297


RESULT 6
PCT-US02-39126-65
; Sequence 65, Application PC/TUS0239126
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  KABLE, Amy E.
;  APPLICANT:  CHIEN, David
;  APPLICANT:  WILSON, Amy L.
;  APPLICANT:  GANDHAKAR, Anita
;  APPLICANT:  CORVAL, Ann E.
;  APPLICANT:  HAFALIA, April J.A.
;  APPLICANT:  EMERLING, Brooke M.
;  APPLICANT:  [illegible], Jayalaxmi
;  APPLICANT:  JIN, Pei
;  APPLICANT:  GRIFFIN, Jennifer A.
;  APPLICANT:  MARQUIS, Joseph P.
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  CHAWLA, Narinder K.
;  APPLICANT:  LEHR-MASON, Patricia M.
;  APPLICANT:  KHARE, Reena
;  APPLICANT:  LEE, Sally
;  APPLICANT:  HAWKINS, Phillip R.
;  APPLICANT:  BECHA, Shanya D.
;  APPLICANT:  LEE, Soo Yeun
;  APPLICANT:  SPRAGUE, William W.
;  APPLICANT:  ZEBARJADIAN, Yeganeh
;  TITLE OF INVENTION: KINASES AND PHOSPHATASES
;  FILE REFERENCE: PI-[illegible] PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/39126
;  CURRENT FILING DATE: 2002-12-[illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2001-12-07
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: 2001-12-[illegible]
;  PRIOR APPLICATION NUMBER: US 60/343,546
;  PRIOR FILING DATE: 2001-[illegible]-21
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2002-[illegible]-04
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2002-[illegible]
```

```
  NUMBER OF SEQ ID NOS: [illegible]
  SOFTWARE: [illegible]
SEQ ID NO [illegible]
  LENGTH: [illegible]
  TYPE: [illegible]NA
  ORGANISM: Homo sapiens
  FEATURE:
  NAME/KEY: [illegible]
  OTHER INFORMATION: [illegible]
[illegible]

  Query Match [illegible]
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]
Db [illegible]

[illegible]
  Sequence [illegible], Application US/[illegible]
  GENERAL INFORMATION:
  APPLICANT: [illegible]
  TITLE OF INVENTION: HUMAN [illegible]
  FILE REFERENCE: [illegible]
  CURRENT APPLICATION NUMBER: US/[illegible]
  CURRENT FILING DATE: 2002-[illegible]
```

```
; NUMBER OF SEQ ID NOS: [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: HUMAN
US-[illegible]

  Query Match [illegible]
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches 713; Conservative 0; Mismatches 517; Indels [illegible]; Gaps [illegible];

Qy [illegible]
Db [illegible]
Db       1121 [illegible] 1180

Qy       1046 [illegible] 1105

Db       1181 CTACTCTGTCATCAAGGCTTTGCTCTCCTGCTTCCTGAAGTACGAGTGTATGATCTGA 1240

Qy       1106 [illegible] 1165

Db       1241 [illegible] 1300

Qy       1166 T---ATTTTCAAGAGGA[illegible] 1221

Db       1301 [illegible]

Qy       1222 [illegible] 1279

Db       1361 ATGATCCCAGCAGGTATACAGCTCTGGCCCAAGCTCTGTCCTGGGGGCCCGGGAATC 1419

Qy       1280 ---------AGGAAGACAGTCTCACAGAGGAAG[illegible] 1329

Db       1420 [illegible] 1479

Qy       1330 GTGTTCTTGATTCCCTTGCACAGTCAGGGC 1359

Db       1480 [illegible] 1509


RESULT 8
US-10-349-781-22954
; Sequence 22954, Application US/10349781
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.; Delegeane, Angelo M.
;  APPLICANT: Stuart, Susan G.; Stuve, Laura L.
;  APPLICANT: Mullahy, Tara J.; Naughton, Rebecca B.
;  TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIVE S
;  FILE REFERENCE: PD-1028-2 CON
;  CURRENT APPLICATION NUMBER: US/10/349,781
;  CURRENT FILING DATE: 2003-01-21
;  PRIOR APPLICATION NUMBER: 09/540,764
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 08/992,868
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: 60/032,838
;  PRIOR FILING DATE: 1996-12-13
;  PRIOR APPLICATION NUMBER: 08/734,050
;  PRIOR FILING DATE: 1996-10-18
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1995-10-24
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-10-18
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-12-11
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1995-12-14
;  PRIOR APPLICATION NUMBER: 08/772,783
;  PRIOR FILING DATE: 1996-12-23
;  Remaining Prior Application data removed - See File Wrapper or PALM
;  NUMBER OF SEQ ID NOS: 61456
;  SOFTWARE: [illegible]
; SEQ ID NO 22954
;   LENGTH: 271
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: [illegible]
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: 132
;   OTHER INFORMATION: a, t, c, g, or other
US-10-349-781-22954

  Query Match             [illegible];  Score [illegible];  DB 6;  Length 271;
  Best Local Similarity   [illegible];  Pred. No. 1.6e-49;
  Matches  27[illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy       1051 [illegible]

Db          1 [illegible]

Qy       1111 [illegible]

Db         61 [illegible]

Qy       1171 [illegible]

Db        121 [illegible]

Qy       1231 [illegible]

Db        180 [illegible]

Qy       1291 [illegible] 1322

Db        240 [illegible] 271


RESULT 9
US-10-144-771-6858
; Sequence 6858, Application US/10144771
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/10/144,771
;  CURRENT FILING DATE: 2002-05-15
;  NUMBER OF SEQ ID NOS: 11245
; SEQ ID NO 6858
;   LENGTH: 2462
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-144-771-6858

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length 2462;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  [illegible];  Conservative [illegible];  Mismatches  [illegible];  Indels [illegible];  Gaps [illegible];

Qy        [illegible]

Db        [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible]

Db        686 [illegible]

Qy        [illegible]

Db        746 [illegible]

Qy        [illegible]

Db        806 [illegible]
```

```
RESULT [illegible]
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT: [illegible]
;  APPLICANT: KHARE, Reena
;  APPLICANT: LEE, [illegible]
;  APPLICANT: BAUGHN, Mariah R.
;  APPLICANT: RAMKUMAR, [illegible]
;  APPLICANT: LEE, [illegible] Yeun
;  TITLE OF INVENTION: KINASES AND PHOSPHATASES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: [illegible]
;  LENGTH: [illegible]
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  OTHER INFORMATION: Incyte ID No: [illegible]

  Query Match [illegible]
  Best Local Similarity [illegible]
  Matches [illegible]; Conservative 0; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];
```

```
Qy       1179 [illegible] 1238

Qy       1240 [illegible] ----------AGGAAGAC 1287

Db       1169 ACAG[illegible]AAG[illegible]CC 1228

Qy       1288 A[illegible] 1347

Db       1229 [illegible] 1288

Qy       1348 CACAGTCAGGGC 1359

Db       1289 [illegible] 1300


RESULT 11
US-09-620-312D-42
; Sequence 42, Application US/09620312D
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  [illegible], Vinod
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  [illegible]
;  APPLICANT:  Chen, Rui-hong
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Yang, Yonghong
;  APPLICANT:  [illegible]
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  [illegible]
;  APPLICANT:  John Tillinghast
;  APPLICANT:  [illegible]
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 784CIP2B
;  CURRENT APPLICATION NUMBER: US/09/620,312D
;  CURRENT FILING DATE:  2000-07-19
;  PRIOR APPLICATION NUMBER: 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  NUMBER OF SEQ ID NOS: 1105
;  SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 42
;   LENGTH: 1887
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (55)..(156[illegible])
US-09-620-312D-42

  Query Match             17.6%;  Score 243.4;  DB 5;  Length 1887;
  Best Local Similarity   57.9%;  Pred. No. 9.7e-46;
  Matches  452;  Conservative    0;  Mismatches  326;  Indels    [illegible];  Gaps    1;

Qy        5[illegible] [illegible]AAAA[illegible]ACAACACT 559

Db        677 G[illegible]C 736

Qy        560 TGGTGATCGGGGCATTGGAGAGTGCCTTTCAGGAATGTGATGAGGTGATCGGCCGGAGC 619

Db        737 [illegible]TGA[illegible] 796

Qy        620 TGGA[illegible]CCAA 679

Db        797 GGAGTTCATATAATATA[illegible]CCA 856

Qy        680 A[illegible]GATATA[illegible] 739

Db        857 A[illegible] 916

Qy        740 CC[illegible] 799

Db        917 TCCCA[illegible]AGAA[illegible]GAT 976

Qy        800 TT[illegible]A 859

Db        977 TCA[illegible]TATAT 1036

Qy        860 AG[illegible] 919

Db       1037 [illegible]TAT 1096

Qy        920 A[illegible] 979

Db       1097 [illegible] 1156

Qy        980 [illegible] 1039

Db       1157 [illegible] 1216

Qy       1040 [illegible] 1099

Db       1217 [illegible] 1276

Qy       1100 ATGGGA[illegible] 1159

Db       1277 [illegible] 1336

Qy       1160 G[illegible]TTGA 1219

Db       1337 [illegible]TAA[illegible] 1396

Qy       1217 [illegible] 1276

Db       1397 A[illegible] 1456

Qy       1277 G 1277
              |
Db       1457 G 1457


RESULT 12
US-10-349-781-23865
; Sequence 23865, Application US/10349781
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.; Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.; Starr, Laura L.
;  APPLICANT:  Mullahy, Sara J.; Naughton, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIV
;  FILE REFERENCE: P[illegible]N
;  CURRENT APPLICATION NUMBER: US/10/349,781
;  CURRENT FILING DATE:  2[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1997-12-[illegible]
;  PRIOR APPLICATION NUMBER: 60/032,838
;  PRIOR FILING DATE: 1996-12-1[illegible]
;  PRIOR APPLICATION NUMBER: 08/734,[illegible]
;  PRIOR FILING DATE: 1996-10-18
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 199[illegible]-10-2[illegible]
;  PRIOR APPLICATION NUMBER: 08/73[illegible],814
;  PRIOR FILING DATE: 1996-10-18
;  PRIOR APPLICATION NUMBER: [illegible],8[illegible]4
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: 08/7[illegible]
;  PRIOR FILING DATE: 1996-12-[illegible]
;  PRIOR APPLICATION NUMBER: 60/00[illegible],794
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: [illegible]
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: [illegible]
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: [illegible]
;   OTHER INFORMATION: [illegible]
[illegible]

  Query Match          [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative    [illegible];  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]

Db   [illegible]


RESULT [illegible]
[illegible]
; Sequence [illegible], Application [illegible]
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT: KABLE, Amy E.
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: SWARNAKAR, Anita
;  APPLICANT: [illegible]
;  APPLICANT: HAFALIA, April J.A.
;  APPLICANT: EMERLING, Brooke M.
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: GRIFFIN, Jennifer A.
;  APPLICANT: [illegible]
;  APPLICANT: BAUGHN, Mariah R.
;  APPLICANT: CHAWLA, Narinder K.
;  APPLICANT: [illegible]
;  APPLICANT: KHARE, Reena
;  APPLICANT: LEE, Sally
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: KINASES AND PHOSPHATASES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: [illegible]
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: [illegible]
[illegible]

  Query Match          [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative    [illegible];  Mismatches  [illegible];  Indels   [illegible];  Gaps    [illegible];

Qy   [illegible]
Db    577 [illegible]

Qy   [illegible]
Db    637 [illegible]

Qy   [illegible]
Db    697 [illegible]

Qy   [illegible]
Db    757 [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   1117 [illegible]

Qy   [illegible]
Db   1177 [illegible]

Qy   [illegible]
Db   [illegible]
```

```
RESULT 14
PCT-US02-39126-64
; Sequence 64, Application PCT/US0239126
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  KABLE, Amy E.
;  APPLICANT:  CHIEN, David
;  APPLICANT:  WILSON, Amy D.
;  APPLICANT:  SWARNAKAR, Anita
;  APPLICANT:  GORVAD, Ann E.
;  APPLICANT:  HAFALIA, April J.A.
;  APPLICANT:  EMERLING, Brooke M.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  JIN, Pei
;  APPLICANT:  GRIFFIN, Jennifer A.
;  APPLICANT:  MARQUIS, Joseph P.
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  CHAWLA, Narinder K.
;  APPLICANT:  LEHR-MASON, Patricia M.
;  APPLICANT:  KHARE, Reena
;  APPLICANT:  LEE, Sally
;  APPLICANT:  HAWKINS, Phillip P.
;  APPLICANT:  BECHA, Shanya D.
;  APPLICANT:  LEE, Soo Yeun
;  APPLICANT:  SPRAGUE, William W.
;  APPLICANT:  ZEBARJADIAN, Yeganeh
;  TITLE OF INVENTION: KINASES AND PHOSPHATASES
;  FILE REFERENCE: PF-1315 PCT
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE:  2002-12-06
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: 2001-12-07
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: 2002-12-04
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2002-02-15
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PERL Program
; SEQ ID NO 64
;   LENGTH: 1472
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;    OTHER INFORMATION: Incyte ID No: 7507107CB1
PCT-US02-39126-64

  Query Match             12.2%;  Score 168.8;  DB 1;  Length 1472;
  Best Local Similarity   65.3%;  Pred. No. 7.7e-29;
  Matches  248;  Conservative    0;  Mismatches  132;  Indels    0;  Gaps    0;

Qy        536 AAAAGGTCA[illegible] 595
              [illegible]
Db        516 AGAA[illegible] 575

Qy        596 [illegible] 655
              [illegible]
Db        576 [illegible] 635

Qy        656 TGGTGGCTGTGTCCCTGCAGGGAAAGCTGTACATGGCCAATGCTGGGGATAGCAGGGCCA 715
              [illegible]
Db        636 [illegible] 695

Qy        716 [illegible] 775
              [illegible]
Db        696 [illegible] 755

Qy        776 [illegible] 835
              [illegible]
Db        756 [illegible] 815

Qy        836 [illegible] 895
              [illegible]
Db        816 [illegible] 875

Qy        896 [illegible] 915
              [illegible]
Db        876 [illegible] 895


RESULT 15
US-10-349-781-46051/c
; Sequence 46051, Application US/10349781
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.; Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.; Stuve, Laura L.
;  APPLICANT:  Mullahy, Sara J.; Naughton, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIV
;  FILE REFERENCE: PB-1028-2 CON
;  CURRENT APPLICATION NUMBER: US/10/349,781
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1997-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]/006,111
;  PRIOR FILING DATE: 1995-10-24
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1995-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-12-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1995-12-14
;  PRIOR APPLICATION NUMBER: [illegible]/772,[illegible]
;  PRIOR FILING DATE: 1996-12-23
;  Remaining Prior Application data removed - See File Wrapper [illegible]
;  NUMBER OF SEQ ID NOS: 61458
;  SOFTWARE: PERL Program
; SEQ ID NO 46051
;   LENGTH: 183
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. [illegible]
US-10-349-781-46051

  Query Match             4.6%;  Score 62.8;  DB 6;  Length 183;
  Best Local Similarity   74.5%;  Pred. No. 4.7e-05;
  Matches   79;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy        736 ATA[illegible] 795
              [illegible]
Db        183 ATA[illegible] 124

Qy        796 [illegible] 841
              [illegible]
Db        123 GTA[illegible] 78


Search completed: February [illegible], 2003, [illegible]
Job time : [illegible] secs
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                      GenCore version 5.1.3
          Copyright (c) 1993 - 2003 Compugen Ltd.

 Nucleic - nucleic search, using sw model

Run on:          February 24, 2003, 04:51:04 ; Search time 2236 Seconds
                                              (without alignments)
                                              5395.425 Million cell updates/sec

Title:           US-09-866-987-3
Perfect score:   1380
Sequence:        1 atgtcccgccaactgtttcct..........[illegible]aacactga 138[illegible]

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:      32[illegible]

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :        EST:*
                 1:  em_estba:*
                 2:  em_esthum:*
                 3:  em_estin:*
                 4:  em_estmu:*
                 5:  em_estov:*
                 6:  em_estpl:*
                 7:  em_estro:*
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                 16:  em_estom:*
                 17:  gb_gss:*
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                 19:  em_gss_inv:*
                 20:  em_gss_pln:*
                 21:  em_gss_vrt:*
                 22:  em_gss_fun:*
                 23:  em_gss_mam:*
                 24:  em_gss_mus:*
                 25:  em_gss_other:*
                 26:  em_gss_pro:*
                 27:  em_gss_rod:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                               SUMMARIES
                %
Result          Query
  No.   Score   Match Length DB  ID                        Description
  ----- ------- ----- ------ --- ------------------------  ----------------
     1    1027   74.4   1737  11  AK013149                  AK013149 Mus musc
     2  [illegible]   57.5    908  13  BI911260                  BI911260 [illegible]
     3     742   53.8    796  16  AW960759                  AW960759 [illegible]
     4   591.6   42.9   1192  11  AK017245                  AK017245 [illegible]
     5   555.2   40.3    760  13  BI909341                  BI909341 [illegible]
  c  6     547   39.6    547  14  BM719494                  BM719494 [illegible]
     7     536   38.8    547   9  AA292266                  AA292266 [illegible]
     8   520.6   37.7    [illegible]  12  BG[illegible]79142               [illegible]
     9     498   36.1    [illegible]  15  BM[illegible]                    [illegible]
    10     498   36.1   1018  15  BM[illegible]742                 [illegible]
    11   496.6   36.0    639  10  AW742[illegible]                 AW742[illegible]
    12     494   35.7    494  12  BF[illegible]                    [illegible]
    13   488.6   35.4    [illegible]  13  BI544[illegible]                 [illegible] MA
    14   483.4   35.0    556  13  BI847[illegible]                 [illegible] MA
    15   478.2   34.7    580  12  BF41[illegible]112               [illegible]
    16   476.4   34.5    512  10  AW[illegible]481[illegible]              [illegible] MA
    17     473   34.3    473   9  AI924511                  AI924511 [illegible]
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    22   446.2   32.3    [illegible]  1[illegible]  BF[illegible]822                [illegible]
    23     433   31.4    [illegible]  12  BF419191                  [illegible]
    24     431   31.2   1058  12  BE913261                  [illegible]
    25   426.4   30.9    798  12  BG754589                  [illegible]
  c 26   425.2   30.8    472  12  BE[illegible]                    [illegible]
    27   413.4   [illegible]    [illegible]4  1[illegible]  AW434[illegible]                 [illegible]
    28   409.2   29.7    446   9  AA633370                  AA633370 [illegible]
    29   407.2   29.5    [illegible]  1[illegible]  AW434[illegible]                 [illegible]
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    31   397.6   28.8    4[illegible]2   9  AI4[illegible]626                 [illegible]
    32   390.4   28.3    657  12  BF509035                  [illegible]
    33   387.2   28.1    [illegible]   9  AA1[illegible]660                 [illegible]
    34     379   27.5    [illegible]  12  BF75[illegible]                  [illegible]
    35     373   27.0    4[illegible]  10  AW630065                  [illegible]
    36   372.2   27.0    6[illegible]7   9  AI256[illegible]                 [illegible]
    37   365.2   26.5    4[illegible]  12  BF41[illegible]84                [illegible]
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    40   36[illegible].1   2[illegible]    [illegible]  1[illegible]  [illegible]               [illegible]
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    42   356.8   25.9    478   9  AI390672                  AI390672 [illegible]
  c 43     356   25.8    [illegible]   9  AI[illegible]15[illegible]               [illegible]
    44     [illegible]   25.7    51[illegible]  10  AW[illegible]                    [illegible] MA
    45   351.2   25.4    396  10  BE486988                  BE486988 [illegible]

                               ALIGNMENTS

RESULT 1
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LOCUS       AK013149                1737 bp    mRNA    linear   EST 1[illegible]-JAN-2[illegible]
DEFINITION  Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
            enriched library, clone:2810423[illegible] [illegible] phosphatase 2C
            containing protein, full insert sequence.
ACCESSION   AK013149
VERSION     AK013149.1  GI:128[illegible]
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) 10, 11 days embryo cDNA to mRNA,
            clone_lib:RIKEN full-length enriched mouse cDNA library
            clone:2810423[illegible].
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
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REFERENCE   [illegible]
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. [illegible] ([illegible]) [illegible] ([illegible])
  MEDLINE   [illegible]
   PUBMED   [illegible]
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 ([illegible]) [illegible] ([illegible])
  MEDLINE   [illegible]
   PUBMED   11217851
REFERENCE   [illegible] (bases 1 to [illegible])
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., [illegible],
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hirozane,K., Hiraoka,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kondo,M., Koya,S.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
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            [illegible], [illegible], Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,K., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa [illegible], Japan (E-mail:genex@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:[illegible],
            Fax:[illegible])
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [illegible] GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN-3'), cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. cDNA went
            through one round of normalization to Rot=[illegible] and subtraction to
            Rot=[illegible]. Second strand cDNA was prepared with the primer adapter
            of sequence [illegible]
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATC[illegible]). cDNA was cleaved
            with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
            Host: SOLR.
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                     /db_xref="MGD:MGI:[illegible]"
                     /db_xref="taxon:10090"
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                     /dev_stage="10, 11 days embryo"
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                     putative"
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                     CVCPSDPQFVEEKGIQAEDLVIGALENAFQECDDVIGRELEASGQVGGCTALVAVFLQ
                     GKLYVANAGDSRAILVRRHEIRQLSSEFTPETERQRIQQLAFIYPELLAGEFTRLEFP
                     RRLK[illegible]QKVLFRDHHMPGWSYKRVEKSDLKYPLIHG[illegible]GRQARLTLLAVSRGFGD
                     H[illegible]RVLPHHQLKPFLLSTPQVTVLDVHQLAVQ[illegible]EDVVVMATDGLW[illegible]VLSNE[illegible]VALLV
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                     SHR"
BASE COUNT   [illegible] a   [illegible] c   [illegible] g   [illegible] t
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Db        [illegible]

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Qy        [illegible]
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Qy        [illegible]
Db        [illegible]
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Qy        563 [illegible] 622
              [illegible]
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Qy        623 AGGCCTCAGGCCAGATGGGCGGCTGCACAGCCCTGGTGG[illegible]TTGTTCCTGCAGGCAAAGC 682
              [illegible]
Db        602 AGGCCTCAGGACAGGTGGGTGGCTGTACAGCCCTGGTGGCGGTGTTCCTGCAAGGAAGC 661

Qy        683 TGTACAT[illegible] 742
              [illegible]
Db        662 TGTATGTGGTCAATGCTGGGGACAGCAGGGCCATCTTGGTGGGAGACATGAGATACGGC 721

Qy        743 [illegible] 802
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Db        722 [illegible] 781

Qy        803 [illegible] 862
              [illegible]
Db        782 [illegible] 841

Qy        863 [illegible] 922
              [illegible]
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Qy        923 [illegible] 982
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Db        902 [illegible] 961

Qy        983 [illegible] 1042
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Db        962 [illegible] 1021

Qy       1043 [illegible] 1102
              [illegible]
Db       1022 ACACGGACATCCAGCTGAAGGCCTTCCTACTCTCATCCCTCAGGTGACTGTGCTGGATG 1081

Qy       1103 [illegible] 1162
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RESULT 2
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LOCUS       BI911260                 908 bp    mRNA    linear   EST 16-[illegible]-2001
DEFINITION  [illegible] NIH_MGC_118 Homo sapiens cDNA clone IMAGE:[illegible] 5',
            mRNA sequence.
ACCESSION   BI911260
VERSION     BI911260.1  GI:16174900
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  [illegible]
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; [illegible]
REFERENCE   1  (bases 1 to 908)
  AUTHORS   [illegible]
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM[illegible]  row: [illegible]  column: 4
            High quality sequence start: 35
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FEATURES             Location/Qualifiers
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                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from [illegible]
                     non-activated adult donors. Library is oligo-dT primed
                     and directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.[illegible] kb. Insert size range
                     [illegible] kb. Library is normalized and enriched for
                     full length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code [illegible]. Note:
                     this is a NIH_MGC Library."
BASE COUNT      178 a    [illegible] c    [illegible] g    [illegible] t
ORIGIN

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  Best Local Similarity   [illegible];  Pred. No. [illegible];
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Qy        623 [illegible] 682
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Db        [illegible]

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Db        [illegible]


RESULT 3
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DEFINITION  [illegible] MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW[illegible]
VERSION     AW[illegible]  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Hegde,P., Qi,R., Abernathy,K., Gharrap,S., Gaspard,R., [illegible], Hoff
            [illegible], Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
  TITLE     Assessment of gene expression patterns in a model of [illegible]
            metastasis using a 10,000 element cDNA microarray
  JOURNAL   Unpublished (2000)
COMMENT     Contact: [illegible]
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: [illegible]
            Fax: [illegible]
            Email: [illegible]
            [illegible]
            Seq primer: Reverse.
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Qy        [illegible]

Db        [illegible]

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Qy        485 [illegible] 544

Db        241 [illegible]

Qy        545 [illegible]

Db        [illegible]

Qy        605 [illegible] 664

Db        361 [illegible] 420

Qy        665 [illegible] 724

Db        421 [illegible] 480

Qy        725 [illegible] 784

Db        481 [illegible] 540

Qy        785 [illegible] 844

Db        541 [illegible] 600

Qy        845 [illegible]

Db        601 [illegible] 660

Qy        905 [illegible] 964

Db        661 [illegible] 720

Qy        965 [illegible]

Db        721 [illegible]

Qy        [illegible]

Db        781 [illegible]


RESULT 4
AK017245
LOCUS       AK017245                1182 bp    mRNA    linear   HTC 19-JAN-2002
DEFINITION  Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched
            library, clone:[illegible]:protein phosphatase 2C containing
            protein, full insert sequence.
ACCESSION   AK017245
VERSION     AK017245.1  GI:[illegible]
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) 6 days neonate head cDNA to mRNA,
            clone_lib:RIKEN full-length enriched mouse cDNA library,
            clone:5430400123.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   [illegible]
   PUBMED   [illegible]
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
```

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JOURNAL     Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE     20499374
PUBMED      11042159
REFERENCE   3
AUTHORS     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE       RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
JOURNAL     Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE     20530913
PUBMED      11076861
REFERENCE   4
AUTHORS     Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y
TITLE       Functional annotation of a full-length mouse cDNA collection
JOURNAL     Nature 409 (6821), 685-690 (2001)
MEDLINE     21085660
PUBMED      11217851
REFERENCE   5  (bases 1 to 1182)
AUTHORS     Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kondo,S., Kouda,M.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y
TITLE       Direct Submission
JOURNAL     Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5'-GAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTTVN-3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. cDNA went
            through one round of normalization to Rot = 10.0 and subtraction to
            Rot = 100.0. Second strand cDNA was prepared with the primer
            adapter of sequence [5'-
            GAGAGAGAGATCTCGAGCTAACTAAACTAAACTAA[illegible]-3'], cDNA was cleaved
            with BamHI and XhoI. Vector: a modified pBluescript SK(-) after
            bulk excision from lambda FLC1. Cloning sites: 5' end: SalI; 3'
            end: BamHI. Host: DH10B.
FEATURES             Location/Qualifiers
     source          1..1182
                     /organism "Mus musculus"
                     /strain "C57BL/6J"
                     /db_xref "FANTOM DB:[illegible]"
                     /db_xref "MGD:MGI:[illegible]"
                     /db_xref "taxon:10090"
                     /clone "[illegible]"
                     /tissue_type "head"
                     /clone_lib "RIKEN full-length enriched mouse cDNA library"
                     /dev_stage "6 days neonate"
     CDS             <1..766
                     /note "Protein phosphatase 2C containing protein
                     data source:Pfam, source key:PF00481, evidence:ISS
                     putative"
                     /codon_start 2
                     /protein_id "BAB[illegible].1"
                     /db_xref "GI:12856386"
                     /db_xref "MGD:MGI:[illegible]"
                     /translation "[illegible]
                     SEFIPETERQRIQQLAFIYPELLAGELIRLEEPRRLKGLDLGQKVIEKDHHMPWSYK
                     RVEKSDLKYFLIHGQGRQARLLGTLAVSRGIGDHQLRV[illegible]
                     [illegible]SFLAKMIHN
                     [illegible]SKENGAPE[illegible]VSYIDVSVTVIPLHSQAQEGSGH"
     polyA_signal    1161..1166
                     /note "putative"
     polyA_site      1182
                     /note "putative"
BASE COUNT      276 a    294 c    330 g    282 t
ORIGIN

  Query Match             42.9%;  Score 551.6;  DB 11;  Length 1182;
  Best Local Similarity   86.7%;  Pred. No. 3.5e-124;
  Matches  664;  Conservative    0;  Mismatches   99;  Indels    3;  Gaps    1;

Qy        618 [illegible]
Db          1 [illegible]

Qy        678 [illegible]
Db         61 [illegible]

Qy        738 [illegible]
Db        121 [illegible]

Qy        798 [illegible] 857
Db        181 [illegible] 240

Qy        858 [illegible]
Db        241 [illegible]

Qy        918 [illegible]
Db        301 [illegible]

Qy        978 [illegible]
Db        361 [illegible]

Qy       1038 [illegible]
Db        421 [illegible]
```

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Qy       1098 [illegible] 1157
              [illegible]
Db        481 [illegible] 540

Qy       1158 [illegible] 1217
              [illegible]
Db        541 [illegible] 600

Qy       1218 [illegible] 1274
              [illegible]
Db        601 TCAAAAGGATGACCCACACAGGTTTCCAGAGTTGCCAAAATGCTGATACACAACACTTCA 660

Qy       1275 [illegible] 1334
              [illegible]
Db        661 AGGAAAGGACAATGGTGCCACCGGAGAGGGCAGGTATCCTACGACGATGTCTCGTGTT 720

Qy       1335 CGTGATTCCTTTGCACAGTCAGGCCAAGAGAGCAGTGACCACTGA 1380
              [illegible]
Db        721 TGTGATTCCTTTGCACAGTCAGGCCAAGAAGGCAGTGGCCACTGA 766


RESULT 5
BI909841
LOCUS       BI909841                 760 bp    mRNA    linear   EST [illegible]
DEFINITION  603065418F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5214292 5',
            mRNA sequence.
ACCESSION   BI909841
VERSION     BI909841.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 760)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11538  row: d  column: 05
            High quality sequence stop: 751.
FEATURES             Location/Qualifiers
     source          1..760
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5214292"
                     /clone_lib="NIH_MGC_118"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from anonymous pool of
                     non-activated adult donors.  Library is oligo-dT primed
                     and directionally cloned  (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb.  Library is normalized and enriched for
                     full length clones and was constructed by C. Gruber
                     (Invitrogen).  Research Genetics tracking code 027. Note:
                     this is a NIH_MGC Library."
BASE COUNT      170 a     202 c     218 g     161 t
ORIGIN

  Query Match             40.3%;  Score 596.2;  DB 13;  Length 760;
  Best Local Similarity   90.1%;  Pred. No. 3.5e-116;
  Matches  [illegible];  Conservative    0;  Mismatches   [illegible];  Indels    2;  Gaps    2;

Qy        788 AGCAGCTGGCTTTGGTCATCTGGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCC 847
              [illegible]
Db          1 AGCAGCTGGCTTTGGTCATCTGGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTTC 60

Qy        848 [illegible] 907
              [illegible]
Db         61 [illegible] 119

Qy        908 [illegible] 967
              [illegible]
Db        120 GTGGCTGGAGTACAAACTGGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGAC 179

Qy        968 [illegible] 1027
              [illegible]
Db        180 AGGTTAGGCAGGCTCGGTTACTAGGAACACTGGCTGTCTCCCGGGGCTGGGAGACCATC 239

Qy       1028 [illegible] 1087
              [illegible]
Db        240 AGCTCAGAGTCTGGACACAAACATCCAGCTCAAGCCTTCTTGCTCTCTGTGCCACAGG 299

Qy       1088 TGACTGTGCTGGA-TGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCA 1146
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        300 TGACTGTGCTGGACTGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCA 359

Qy       1147 ACTGATGGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTC 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 ACTGATGGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTC 419

Qy       1207 [illegible] 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        420 [illegible] 479

Qy       1267 [illegible]CTACGATGACGTC 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 [illegible]CTACGATGACGTC 539

Qy       1327 [illegible]AAGAGAGCAGT 1371
              [illegible]
Db        540 TCTGTGTACTTGATTCCTTGCACAGTCAGGGCAAGAGAGCAGT 584


RESULT 6
BM719494/c
LOCUS       BM719494                 547 bp    mRNA    linear   EST 01-MAR-2002
DEFINITION  UI-E-EJ1-ajt-m-24-0-UI.r1 UI-E-EJ1 Homo sapiens cDNA clone
            UI-E-EJ1-ajt-m-24-0-UI 5', mRNA sequence.
ACCESSION   BM719494
VERSION     BM719494.1  GI:19038162
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 547)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
```

```
FEATURES             Location/Qualifiers
     source          1..547
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /clone_lib="UI-E-EJ1"
                     /tissue_type="fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     Choroid"
                     /dev_stage="fetal and adult"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EJ1 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tags for this library are: fetal eyes, AGAATCAACA
                     ; lens, CGATTAGCGA; eye anterior segment, AATGCCCCAT;
                     optic nerve, CCATTAACTC; retina, CCCCG; Retina Foveal and
                     Macular, CTCG; RPE and Choroid, ACCTA. This library was
                     created for the program, Gene Discovery in the Visual
                     System, supported by National Eye Institute (NEI)."
BASE COUNT      [illegible] a    179 c    134 g    117 t
ORIGIN

  Query Match             39.6%;  Score 547;  DB 14;  Length 547;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-114;
  Matches  547;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        672 GCAGGGAAAGCTGTACATGGCCAATGCTGGGCATACCACCCCCATCTTGCTGCCCACACA 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GCAGGGAAAGCTGTACATGGCCAATGCTGGGCATACCACCCCCATCTTGCTGCCCACACA 488

Qy        732 [illegible] 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 [illegible] 428

Qy        792 GCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCCCTCG 851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 GCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCCCTCG 368

Qy        852 [illegible] 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GCGGCTGAAC[illegible] 308

Qy        912 CTGGA[illegible] 971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGGA[illegible] 248

Qy        972 [illegible]
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 TA[illegible] 188

Qy       1032 CAGAGTCCTGGACACAAACATCCAGTTCAAGGCC[illegible]CAGGTGAC 1091
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CAGAGTCCTGGACACAAACATCCAGTTCAAGGCC[illegible]CAGGTGAC 128

Qy       1092 TGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGA 1151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGA 68

Qy       1152 TGGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTCCTCCC 1211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TGGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTCCTCCC 8

Qy       1212 TGGGAAC 1218
              |||||||
Db          7 TGGGAAC 1


RESULT 7
AA292266
LOCUS       AA292266                 547 bp    mRNA    linear   EST 08-AUG-1997
DEFINITION  zt50f12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGE:725807 5' similar to SW:P2C2_ARATH P49598 PROTEIN PHOSPHATASE
            2C ;, mRNA sequence.
ACCESSION   AA292266
VERSION     AA292266.1  GI:1940246
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 547)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
            ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
            ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
            Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
            Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1457   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 479.
FEATURES             Location/Qualifiers
     source          1..547
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:725807"
                     /clone_lib="Soares ovary tumor NbHOT"
                     /sex="Female"
                     /tissue_type="ovarian tumor"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     [illegible]TACCAATCTGAAGTGGGAGCGGCCGCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. "
BASE COUNT      [illegible] a    [illegible] c    171 g    [illegible] t
ORIGIN

  Query Match             38.8%;  Score 536;  DB 9;  Length 547;
  Best Local Similarity   99.8%;  Pred. No. 1.1e-111;
  Matches  547;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy        792 GCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCCCTCG 851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCCCTCG 60

Qy        852 [illegible] 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGGCTGA[illegible] 120

Qy        912 CTGGAGC[illegible] 971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGGA[illegible] 180
```

```
Qy       [illegible] [illegible]
Db       [illegible] [illegible]

Qy       [illegible] [illegible]
Db       [illegible] [illegible]

Qy       [illegible] [illegible]
Db       [illegible] [illegible]

Qy       [illegible] [illegible]
Db       [illegible] [illegible] 419

Qy       [illegible] [illegible]
Db       [illegible] [illegible] 479

Qy       [illegible] [illegible]
Db       [illegible] [illegible]

Qy       [illegible] [illegible]
Db       [illegible] [illegible]


RESULT 8
[illegible]
LOCUS       [illegible]                 631 bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible] NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
            [illegible] 5', mRNA sequence.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; [illegible]
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 631)
  AUTHORS   Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka
            ,T.S., Carter,M.G. and Ko,M.S.H.
  TITLE     Verification and initial annotation of NIA mouse 15K cDNA clone set
  JOURNAL   Unpublished (2001)
COMMENT     Other ESTs: [illegible]
            Contact: George J. Kargul
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: [illegible]
            This clone set has been freely distributed to the community. Please
            visit http://lgsun.grc.nia.nih.gov/cDNA/ [illegible]
            Plate: [illegible] row: [illegible] column: [illegible]
            Seq primer: [illegible]
            High quality sequence stop: [illegible]
            PolyA No.
FEATURES             Location/Qualifiers
     source          1..631
                     /organism="Mus musculus"
                     /strain="[illegible]"
                     /db_xref="[illegible]"
                     /db_xref="taxon:10090"
                     /clone="[illegible]"
                     /clone_lib="NIA Mouse 15K cDNA Clone Set"
                     /sex="Clones arrayed from a variety of cDNA libraries"
                     /dev_stage="Clones arrayed from a variety of cDNA
                     libraries"
                     /lab_host="[illegible]"
                     /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
                     clone is among a rearrayed set of 15,247 clones from 11
                     embryo cDNA libraries (including preimplantation stage
                     embryos from unfertilized egg to blastocyst, embryonic
                     part of E7.5 embryos, extraembryonic part of E7.5 embryos
                     , [illegible]
                     ovary cDNA library. Average insert size 1.5 kb. All
                     source libraries are cloned unidirectionally with oligo(dT
                     ) Not primers. References include: (1) Genome-wide
                     expression profiling of mid-gestation placenta and embryo
                     using a 15,000 mouse developmental cDNA microarray, 2000,
                     Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)
                     Large-scale cDNA analysis reveals phased gene expression
                     patterns during preimplantation mouse development, 2000,
                     Development, 127: 1737-1749; (3) Genome-wide mapping of
                     unselected transcripts from extraembryonic tissue of
                     7.5-day mouse embryos reveals enrichment in the t-complex
                     and under-representation on the X chromosome, 1998, Hum
                     Mol Genet 7: 1967-1978."
BASE COUNT      138 a    154 c    214 g    125 t
ORIGIN

  Query Match             [illegible]%;  Score 520.6;  DB 12;  Length 631;
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  562;  Conservative    0;  Mismatches   69;  Indels    0;  Gaps    0;

Qy        436 [illegible] 495
Db          1 [illegible] 60

Qy        496 [illegible] 555
Db         61 [illegible] 120

Qy        556 [illegible] 615
Db        121 [illegible] 180

Qy        616 [illegible] 675
Db        181 [illegible] 240

Qy        676 [illegible] 735
Db        241 GGGAAGCTGTATGTGGCTAATGTGGGGACAGCAGGGCCATCTTGGTGGGGAGACATGAG 300

Qy        736 ATACGGCCACTGAGCTTCGAGTTCACCCAGAGACTGAGGGCAGGGATCCAGCAGCTG 795
              ||||||    ||||| |    ||||||||||||| ||  |||||||||||||||||||||
Db        301 ATACGGCAGCTGAGTTCTGAGTTCACCCAGAAACAGAGGGCAGCGGATCCAGCAGCTG 360

Qy        796 GCCTTTGTCTATCCTGAGTTTCTGGCTGGTGAGTTCACCGACTGGAGTTCC[illegible] 855
Db        361 [illegible] 420

Qy        856 [illegible] 915
Db        421 [illegible] 480

Qy        916 [illegible] 975
Db        481 [illegible] 540

Qy        976 [illegible] 1035
Db        541 [illegible] 600

Qy       1036 GTCCTGGA ATAAACATCCAGCTCAAGCCCT 1066
Db        601 [illegible]GACACCGACATCCAGCTGAAGCCCT 631


RESULT 9
BM563697
LOCUS       BM563697                 997 bp    mRNA    linear   EST [illegible] FEB 2002
DEFINITION  AGENCOURT_6580[illegible] NIH_MGC_[illegible] Homo sapiens cDNA clone IMAGE:[illegible]
```

```
            5', mRNA sequence.
ACCESSION   BM563697
VERSION     BM563697.1  GI:18811842
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 997)
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1916  row: i  column: 12
            High quality sequence stop: 697.
FEATURES             Location/Qualifiers
     source          1..997
                     /organism "Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone "IMAGE:5441819"
                     /clone_lib "NIH_MGC_98"
                     /tissue_type "astrocytoma grade IV, cell line"
                     /lab_host "DH10B (phage-resistant)"
                     /note "Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      245 a    274 c    271 g    207 t
ORIGIN

  Query Match             [illegible]%;  Score 498;  DB [illegible];  Length 997;
  Best Local Similarity   100.0%;  Pred. No. [illegible];
  Matches  498;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        88[illegible] [illegible] 942
              [illegible]
Db          1 [illegible] 60

Qy        943 CTTAAGTACCCACTGATGCATGGACAGGGTAGGCAGGCTCGGTTACTAGGAACACTGGCT 1002
              [illegible]
Db         61 [illegible] 120

Qy       1003 GTCTGCGGGCCTGGGAGACCATCAGCTCAGAGTCCTGGACATAAACATCCAGCTCAAG 1062
              [illegible]
Db        121 [illegible] 180

Qy       106[illegible] [illegible] 1122
              [illegible]
Db        181 [illegible] 240

Qy       1123 [illegible] 1182
              [illegible]
Db        241 [illegible]

Qy       118[illegible] [illegible]
              [illegible]
Db        [illegible] [illegible]

Qy       124[illegible] [illegible]
              [illegible]
Db        [illegible] [illegible]
```

```
Qy       130[illegible] [illegible] 1362
              [illegible]
Db        4[illegible]1 [illegible]

Qy       13[illegible] [illegible] 1380
              [illegible]
Db        461 GAGAGCAGTGACCACTGA 498


RESULT 10
BM563742
LOCUS       BM563742               1018 bp    mRNA    linear   EST [illegible]
DEFINITION  AGENCOURT_6587[illegible] NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5441849
            5', mRNA sequence.
ACCESSION   BM563742
VERSION     BM563742.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1916  row: m  column: 14
            High quality sequence stop: 607.
FEATURES             Location/Qualifiers
     source          1..1018
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "IMAGE:5441849"
                     /clone_lib "NIH_MGC_98"
                     /tissue_type "astrocytoma grade IV, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note "Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      251 a    285 c    268 g    214 t
ORIGIN

  Query Match             [illegible]%;  Score 466;  DB 15;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-103;
  Matches  4[illegible];  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        88[illegible] [illegible] 942
              [illegible]
Db          1 [illegible]

Qy        9[illegible] [illegible] 100[illegible]
              [illegible]
Db         [illegible] [illegible] 12[illegible]

Qy       100[illegible] [illegible] 1062
              [illegible]
Db        [illegible] [illegible]

Qy       106[illegible] [illegible] 1122
```

```
Db        181 [illegible] 240

Qy       [illegible] [illegible]
              [illegible]
Db        241 [illegible] 300

Qy       [illegible] [illegible]
              [illegible]
Db        301 [illegible] 360

Qy       [illegible] [illegible]
              [illegible]
Db        361 [illegible] 420

Qy       [illegible] [illegible] 1362
              [illegible]
Db        421 [illegible] 480

Qy       [illegible] [illegible]
              [illegible]
Db        481 [illegible]


RESULT [illegible]
AW[illegible]
LOCUS       AW[illegible]    [illegible] bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible] NMIE Mus musculus cDNA clone IMAGE:[illegible]
            [illegible] mRNA
            sequence.
ACCESSION   AW[illegible]
VERSION     AW[illegible]  GI:[illegible]
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   NCI-CGAP http://[illegible]
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished ([illegible])
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40RP from Gibco
            High quality sequence stop: [illegible].
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="Mus musculus"
                     /strain="[illegible]"
                     /db_xref="taxon:[illegible]"
                     /clone="IMAGE:[illegible]"
                     /clone_lib="Soares mouse NMIE"
                     /sex="[illegible]"
                     /dev_stage="[illegible]"
                     /lab_host="DH10B"
                     /note="Organ: [illegible] inner ear, [illegible] pooled; Vector: pT7T3D-Pac;
                     Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed
                     with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCACA[illegible]TTTTTTTTTTTTTTTTTTT
                     3'], double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not
                     I and Eco RI sites of the modified pT7T3 vector. Library
                     is normalized and was constructed and donated by Bento
                     Soares and M.Fatima Bonaldo (University of Iowa) and P.
                     Hardisty, A. Varela-Carver, E. Morris and S.D.M. Brown (MRC
                     UK Mouse Genome Centre and Mammalian Genetics Unit,
                     Harwell, UK)."
BASE COUNT      [illegible] a    [illegible] c    [illegible] g    [illegible] t
ORIGIN
```

```
  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   86.1%;  Pred. No. [illegible];
  Matches [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy        562 [illegible] 621
              [illegible]
Db          1 [illegible] 60

Qy        622 [illegible] 681
              [illegible]
Db         61 [illegible] 120

Qy        682 [illegible] 741
              [illegible]
Db        121 [illegible] 180

Qy        742 CCACTGAGCTTCGAGTTCAGCCAGAGACTGAGCGGCAGCGGATCCAGCAGCTGGCCTTT 801
              [illegible]
Db        181 [illegible] 240

Qy        802 [illegible] 861
              [illegible]
Db        241 [illegible] 300

Qy        [illegible] [illegible]
              [illegible]
Db        301 [illegible] 360

Qy        [illegible] [illegible]
              [illegible]
Db        361 [illegible]

Qy        [illegible] [illegible]
              [illegible]
Db        421 [illegible] 480

Qy       1042 [illegible]
              [illegible]
Db        481 [illegible]

Qy       1102 [illegible]
              [illegible]
Db        541 [illegible] 600

Qy       1162 [illegible] 1190
              [illegible]
Db        601 [illegible] 639


RESULT 12
BF059521
LOCUS       BF059521             [illegible] bp    mRNA    linear   EST [illegible]
DEFINITION  7k[illegible] NCI_CGAP_[illegible] Homo sapiens cDNA clone IMAGE:[illegible]
            similar to TR:Q9ULK5 Q9ULK5 KIAA1[illegible] PROTEIN ;, mRNA sequence.
ACCESSION   BF059521
VERSION     BF059521.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   NCI-CGAP http://[illegible]/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., [illegible]
            F. Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 467.
FEATURES             Location/Qualifiers
     source          1..494
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:348[illegible]"
                     /clone_lib="NCI_CGAP_GC6"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                     from the normalized library NCI_CGAP_GC4 was prepared, and
                     ss circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (clonelds
                     1257196 1258631, 1469064 1470983, and 1475562 1476743).
                     Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       91 a    16[illegible] c    153 g     86 t      1 others
ORIGIN

  Query Match             85.7%;  Score 493;  DB 12;  Length 494;
  Best Local Similarity   99.8%;  Pred. No. [illegible];
  Matches  493;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         75 [illegible] 134

Db          1 [illegible] 60

Qy        135 [illegible] 194

Db         61 [illegible]

Qy        195 [illegible] 254

Db        121 [illegible]

Qy        255 [illegible] 314

Db        181 [illegible] 240

Qy        315 [illegible] 374

Db        241 AGAGTGGCTGACCCTGTGCCCAGAGGAGTTCCTGACAGGCCATTACTGGGCACTGTTCGA 300

Qy        375 TGGGCACGGCGGTCCTGCAGCAGCCATCTTGGCTGCCAACACCCTGCACTCCTGCTTGCG 434

Db        301 TGGGCACGGCGGTCCTGCAGCAGCCATCTTGGCTGCCAACACCCTGCACTCCTGCTTGCG 360

Qy        435 [illegible] 494

Db        361 [illegible] 420

Qy        495 [illegible] 554

Db        421 [illegible]

Qy        555 AGACTTGGTGATCG 568

Db        481 AGACTTGGTGATCG 494


RESULT 1[illegible]
BI344088
LOCUS       BI344088                 597 bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible]72433 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BI344088
VERSION     BI344088.1  GI:15[illegible]
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 597)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 13
            and -minmatch 12 options.
            PCR PRIMERS
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGAC
            Plate: 1[illegible]  row: L  column: 22
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1..597
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 2PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from testis, ovary,
                     endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT      114 a    141 c    221 g    121 t
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB 13;  Length 597;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  537;  Conservative    0;  Mismatches   54;  Indels    [illegible];  Gaps    1;

Qy        237 [illegible]

Db          1 [illegible] 60

Qy        297 TGAGTTTGGG[illegible]TGAAG------AAGAGTGG[illegible] 350

Db         61 [illegible]

Qy        351 [illegible] 410

Db        121 [illegible]

Qy        411 [illegible]

Db        181 [illegible]

Qy        471 [illegible]

Db        241 [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible]
```

```
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]


RESULT 14
[illegible]
LOCUS       [illegible]                    bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible] MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.L., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: [illegible]
            Fax: [illegible]
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and QV trimmed with phred
            [illegible]. Vector identified by cross match with the minscore 18
            and minmatch 12 options.
            PCR PRIMERS
            FORWARD: [illegible]
            BACKWARD: [illegible]
            Plate: [illegible] row: A column: [illegible]
            Seq primer: [illegible]
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="Sus scrofa"
                     /db_xref="taxon:[illegible]"
                     /clone_lib="MARC 2PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT 6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from testis, ovary,
                     endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT  [illegible]
ORIGIN

  Query Match             [illegible]
  Best Local Similarity   [illegible]  Pred. No. [illegible]
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
```

```
Db     181 [illegible]

Qy     708 [illegible]
Db     241 [illegible]

Qy     768 [illegible]
Db     [illegible]

Qy     828 [illegible]
Db     [illegible]

Qy     888 [illegible]
Db     421 [illegible]

Qy     948 [illegible]
Db     481 [illegible]

Qy    1008 [illegible]
Db     541 [illegible]


RESULT 15
[illegible]
LOCUS       [illegible]                   bp    mRNA    linear   EST [illegible] NOV [illegible]
DEFINITION  UI-R-BJ2-bcu-h-04-0-UI.s1 UI-R-BJ2 Rattus norvegicus cDNA clone
            UI-R-BJ2-bcu-h-04-0-UI 3', mRNA sequence.
ACCESSION   [illegible]
VERSION     [illegible]  GI:[illegible]
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   [illegible]
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242 USA
            Tel: 319 335 8250
            Fax: 319 335 [illegible]
            Email: msoares@blue.weeg.uiowa.edu
            Polyd(T) track not found. Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab. Clone Distribution: Clones will be available through
            Research Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA No.
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="Rattus norvegicus"
                     /strain="Sprague Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-BJ2-bcu-h-04-0-UI"
                     /clone_lib="UI-R-BJ2"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; UI-R-BJ2
                     library is a subtracted library derived from [illegible]
                     tissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc,
                     atrium at 16.5 dpc, ventricle at 18 dpc, ventricle at [illegible]
```

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                    dpc, AV canal at 15 dpc.  For a detailed description of
                    the library from which this clone was derived, please
                    visit our web site at [illegible]. The
                    subtraction has been previously described in (Bonaldo,
                    Lennon and Soares, Genome Research 6:791-806, 1996)
                    TAG_SEQ None found"
BASE COUNT     [illegible] a     140 c     156 g     [illegible] t
ORIGIN

  Query Match             34.7%;  Score 478.2;  DB 12;  Length 589;
  Best Local Similarity   88.4%;  Pred. No. 1.7e-98;
  Matches  519;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy        496 [illegible] 555

Db          3 GGCGGCTGTGTCTGCTCCAGTGACCCACAGTTCGTGGAAGAAAAGGGCAT[illegible]AGAA 62

Qy        556 [illegible] 615

Db         63 [illegible] 122

Qy        616 [illegible] 675

Db        123 [illegible] 182

Qy        676 [illegible] 735

Db        183 [illegible]GAGAGATGAG 242

Qy        736 [illegible] 795

Db        243 [illegible] 302

Qy        796 [illegible] 855

Db        303 GCCTTTACCTACCCCGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTTCCACGGCGG 362

Qy        856 [illegible]GACTGGCTGG 915

Db        363 CTGAAGGGGATGACTTGGGGCAGAAGGTTCTGTTCAGGGATCATCACATGAGAGGCTGG 422

Qy        916 [illegible] 975

Db        423 [illegible] 482

Qy        976 [illegible] 1035

Db        483 [illegible] 542

Qy       1036 [illegible] 1082

Db        543 [illegible] 589


Search completed: February 23, 2003, 09:12:27
Job time : 2254 secs
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                    GenCore version 5.1.5
         Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         February 23, 2003, 03:42:41 ; Search time 3765 Seconds
                                              (without alignments)
                                              10667.364 Million cell updates/sec

Title:          US-09-866-987-3
Perfect score:  1388
Sequence:       1 atgtccgccgagtaattccg..........aaattacaatgccactgtga 1388

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters:      4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        GenEmbl:*
                1:  gb_ba:*
                2:  gb_htg:*
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                32:  em_htg_other:*
                33:  em_htg_mus:*
                34:  em_htg_pln:*
                35:  em_htg_rod:*
                36:  em_htg_mam:*
                37:  em_htg_vrt:*
                38:  em_sy:*
                39:  em_htgo_hum:*
                40:  em_htgo_mus:*
                41:  em_htgo_other:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES

Result          Query
   No.   Score  Match Length DB  ID                    Description
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     1    1388  100.0   1388  6  AX352514              AX352514 Sequence
     2    1377   99.2   1867  6  AX202274              AX202274 Sequence
     3  1076.4   77.6   2121  9  AK096681              AK096681 Homo sapi
     4    1049   75.6   2154  9  HSM803792             AL832294 Homo sapi
     5  1014.4   73.1   2423  9  AK056894              AK056894 Homo sapi
     6     787   56.7    182  9  BC033644              BC033644 Homo sapi
     7   283.8   20.4   1687  9  AK093270              AK093270 Homo sapi
     8   283.8   20.4   1695  9  BC011833              BC011833 Homo sapi
     9   264.8   19.2   2518  6  AX411118              AX411118 Sequence
    10   264.8   19.2   2518  9  HSM801407             AL133644 Homo sapi
    11   264.4   19.2    900  6  AX419116              AX419116 Sequence
    12   262.6   19.0   1198  6  AX400071              AX400071 Sequence
c   13   260.2   18.9  82590  9  AC006252              AC006252 Homo sapi
c   14   260.2   18.9 171848  9  AC112045              AC112045 Homo sapi
    15   260.2   18.9  21410  9  AC[illegible]21       AC[illegible]21 Homo sapi
c   16   260.2   18.9 240204  2  AC044892              AC044892 Homo sapi
    17   243.4   17.6   5791  6  AX397499              AX397499 Sequence
    18   243.4   17.6   5791  9  AK032983              AK032983 Homo sapi
    19   242.4   17.6   1993  9  AK023315              AK023315 Homo sapi
    20   167.4   12.1    657  9  HSA336006             AJ336006 Homo sapi
    21   162.6   11.8    688  9  HSA332762             AJ332762 Homo sapi
    22   159.4   11.6    852  9  HSA336051             AJ336051 Homo sapi
    23     157   11.4    472  9  HSNL30048             X[illegible] H.sapiens
    24   154.4   11.2 24[illegible]  2  AC044892       AC044892 Homo sapi
    25   129.2    9.4    744  9  HSA330026             AJ330026 Homo sapi
    26   101.2    7.3   2651  3  AY070581              AY070581 Drosophil
    27   101.2    7.3  18791  2  AC017940              AC017940 Drosophil
c   28   101.2    7.3 144746  3  AC130649              AC130649 Drosophil
    29   101.2    7.3 179886  3  AC104515              AC104515 Drosophil
c   30   101.2    7.3 206643  2  AC011760              AC011760 Drosophil
c   31   101.2    7.3 274888  3  AE003574              AE003574 Drosophil
c   32    68.6    5.0 125932  9  AL129315              AL129315 Homo sapi
    33    66.2    4.8 125932  9  AL129315              AL129315 Homo sapi
c   34    64.8    4.7 157343  2  AC115413              AC115413 Rattus n
c   35    62.6    4.5  44686  3  AF014695              AF014695 Caenorhab
c   36    61.2    4.4 135733  2  AC128114              AC128114 Rattus n
    37    58.6    4.2 111747  2  AC129004              AC129004 Rattus n
c   38    58.2    4.2 129000  2  AC127988              AC127988 Rattus no
    39    58.2    4.2 178857  2  AC121435              AC121435 Rattus no
c   40    58.2    4.2  20842  2  AC094216              AC094216 Rattus n
    41    58.2    4.2 277389  2  AC099419              AC099419 Rattus n
c   42      58    4.2 161237  2  AC106114              AC106114 Rattus n
c   43      58    4.2  16282  2  AC117388              AC117388 Rattus n
c   44    57.8    4.2  56[illegible]  2  AC[illegible]414  AC[illegible]414 Rattus n
    45    57.8    4.2 214287  2  AC105656              AC105656 Rattus n

                              ALIGNMENTS

RESULT 1
AX352514
LOCUS       AX352514                1388 bp    DNA     linear   PAT 07-FEB-2002
DEFINITION  Sequence 3 from Patent WO0192491.
ACCESSION   AX352514
VERSION     AX352514.1  GI:18617749
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Plowman,G.D., Whyte,D., Sudarsanam,S., Manning,G., Caenepeel,S.,
            Martinez,R., Hunter,T. and Flanagan,P.
  TITLE     Mammalian protein phosphatases
  JOURNAL   Patent: WO 0192491-A 3 06-DEC-2001;
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            [illegible], Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1380
                     /organism "synthetic construct"
                     /db_xref "[illegible]"
                     /note "Synthetic phosphatase nucleotide"
BASE COUNT      274 a    395 c    449 g    262 t
ORIGIN

  Query Match             100.0%;  Score 1380;  DB 1;  Length 1380;
  Best Local Similarity   100.0%;  Pred. No. [illegible];
  Matches 1380;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 [illegible] 60
Db          1 [illegible] 60

Qy         61 [illegible] 120
Db         61 [illegible] 120

Qy        121 [illegible] 180
Db        121 [illegible] 180

Qy        181 [illegible] 240
Db        181 [illegible] 240

Qy        241 [illegible] 300
Db        241 [illegible] 300

Qy        301 [illegible] 360
Db        301 [illegible] 360

Qy        361 [illegible] 420
Db        361 [illegible] 420

Qy        421 [illegible] 480
Db        421 [illegible] 480

Qy        481 [illegible] 540
Db        481 [illegible] 540

Qy        541 [illegible] 600
Db        541 [illegible] 600

Qy        601 [illegible] 660
Db        601 [illegible] 660

Qy        661 [illegible] 720
Db        661 [illegible] 720

Qy        721 [illegible] 780
Db        721 [illegible] 780

Qy        781 [illegible] 840
Db        781 [illegible] 840

Qy        841 [illegible] 900
Db        841 [illegible] 900

Qy        901 [illegible] 960
Db        901 CACATGAGTGGCTGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATC 960

Qy        961 [illegible] 1020
Db        961 [illegible] 1020

Qy       1021 [illegible] 1080
Db       1021 [illegible] 1080

Qy       1081 [illegible] 1140
Db       1081 [illegible] 1140

Qy       1141 [illegible] 1200
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Qy       1201 [illegible] 1260
Db       1201 AGCTTCCTCCCTGGGAACCAAGAGGACCCACACAGGTTCTCAAAGCTGGCCCAGATGCTG 1260

Qy       1261 [illegible] 1320
Db       1261 [illegible] 1320

Qy       1321 [illegible] 1380
Db       1321 [illegible] 1380


RESULT 2
AX202234
LOCUS       AX202234                1837 bp    DNA     linear   PAT [illegible]-AUG-2001
DEFINITION  Sequence 19 from Patent WO0153469.
ACCESSION   AX202234
VERSION     AX202234.1  GI:15392009
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1837)
  AUTHORS   Bandman,O., Tang,Y.T., Azimzai,Y., Yue,H., Baughn,M.R.,
            Hillman,J.L., Lal,P., Wang,E., Gandhi,A.R., Policky,J.L. and
            Mathur,P.
  TITLE     Phosphatases
  JOURNAL   Patent: WO [illegible]-A [illegible] 26-JUL-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1837
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /note "Incyte ID No: 1723447CB1"
BASE COUNT      392 a    527 c    555 g    363 t
ORIGIN

  Query Match             99.2%;  Score 1369;  DB 6;  Length 1837;
  Best Local Similarity   99.9%;  Pred. No. 2.6e-260;
  Matches [illegible];  Conservative    [illegible];  Mismatches    [illegible];  Indels    1;  Gaps    1;

Qy          1 [illegible] 60
Db          1 [illegible] 60

Qy         61 [illegible] 120
Db         61 [illegible] 120

Qy        121 [illegible] 180
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Db        121 [illegible] 180

Qy        181 [illegible] 240

Db        181 [illegible] 240

Qy        241 [illegible] 300

Db        241 [illegible] 300

Qy        301 [illegible] 360

Db        301 [illegible] 360

Qy        361 [illegible] 420

Db        361 [illegible] 420

Qy        421 [illegible] 480

Db        421 [illegible] 480

Qy        481 [illegible] 540

Db        481 [illegible] 540

Qy        541 [illegible] 600

Db        541 [illegible] 600

Qy        601 [illegible] 660

Db        601 [illegible] 660

Qy        661 [illegible] 720

Db        661 [illegible] 720

Qy        721 [illegible] 780

Db        721 [illegible] 780

Qy        781 [illegible] 840

Db        781 [illegible] 840

Qy        841 [illegible] 900

Db        841 [illegible] 900

Qy        901 [illegible] 960

Db        901 [illegible] 960

Qy        961 [illegible] 1020

Db        961 [illegible] 1020

Qy       1021 [illegible] 1080

Db       1021 [illegible] 1080

Qy       1081 [illegible] 1140

Db       1081 [illegible] 1140

Qy       1141 [illegible] 1200

Db       1141 [illegible] 1200

Qy       1201 [illegible] 1260

Db       1201 [illegible] 1260

Qy       1261 [illegible]

Db       1261 [illegible]

Qy       1321 [illegible]

Db       1321 [illegible]

Qy       1380 A 1380
              |
Db       1381 A 1381


RESULT 3
AK096681
[illegible]     AK096681                2121 bp    mRNA    linear   [illegible]
DEFINITION  Homo sapiens cDNA FLJ[illegible] fis, clone FEBLM[illegible], weakly similar
            to PROTEIN PHOSPHATASE 2C HOMOLOG [illegible] (EC 3.1.3.16).
ACCESSION   AK096681
VERSION     AK096681.1  GI:[illegible]
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens peripheral blood mononuclear cells (HBPMC[illegible]) cDNA to
            mRNA, clone lib:FEBLM, clone:FEBLM2005282.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K.,
            Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
            Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
            Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
            Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
            Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B.,
            Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and
            Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2121)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI team); [illegible]
            Kazusa Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-[illegible])
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
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                     /cell_type="peripheral blood mononuclear cells
                     (HBPMC[illegible])"
                     /clone_lib="FEBLM"
                     /note="cloning vector: pME18SFL3; primary culture
                     peripheral blood mononuclear cells"
     CDS             411..1782
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="BAC[illegible].1"
                     /db_xref="GI:[illegible]"
                     /translation="MEEN[illegible]ESDPQEVPEEK[illegible]
                     [illegible]AGDSRAILVRRGE[illegible]
                     QLVGALSMLAVK[illegible]GP"
BASE COUNT      [illegible] a    [illegible] c    [illegible] g    [illegible] t
ORIGIN
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Qy        194 [illegible] 253
Db            [illegible]

Qy        254 [illegible] 313
Db            [illegible]

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Qy       1239 [illegible]
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Qy       1299 [illegible] 1358
Db       1259 [illegible]

Qy       1359 [illegible] 1380
Db       [illegible]


RESULT 4
HSM803792
LOCUS       HSM803792              2184 bp    mRNA    linear   [illegible]
DEFINITION  Homo sapiens mRNA; cDNA DKFZp[illegible] (from clone DKFZp[illegible])
ACCESSION   AL[illegible]
VERSION     AL[illegible]  GI:21[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2184)
  AUTHORS   [illegible]
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) [illegible] Heidelberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de
            sequenced by DKFZ (German Cancer Research Center,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp[illegible]) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://[illegible]/cDNA/.
FEATURES             Location/Qualifiers
     source          1..2184
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp[illegible]"
                     /tissue_type="[illegible]"
                     /clone_lib="[illegible] (synonym: [illegible]). Vector pSport1; Site1 [illegible]
                     [illegible] sites [illegible]"
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     polyA_signal    [illegible]
     polyA_site      [illegible]
BASE COUNT   [illegible]
ORIGIN

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  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches 1156; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
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Db        128 CATCGGAGATG[illegible]AAGAAGAG[illegible]AGGAGTT 187

Qy        345 [illegible]GACA[illegible]CATTACT[illegible]GGAT[illegible]CAGCA[illegible]CATCTT 404

Db        188 [illegible]GACA[illegible]CATTACT[illegible]GGATGGCA[illegible]CATCTT 247

Qy        405 GGCTGCCAA[illegible]GCAC[illegible]TGG[illegible]GGCAG[illegible]GGAAGGCTT 464

Db        248 [illegible]AACAC[illegible]GGAAGG[illegible] 307

Qy        465 [illegible] 524

Db        308 [illegible] 367

Qy        525 GTTGTGGA[illegible]GAAAAGG[illegible]CAGAAGACT[illegible] 584

Db        368 GT[illegible]GAAAAGGCATCA[illegible]CAGAAGACT[illegible] 427

Qy        585 [illegible] 644

Db        428 [illegible] 487

Qy        645 [illegible]GCAGGGAAAG[illegible] 704

Db        488 [illegible]GCAGGGAAAG[illegible] 547

Qy        705 [illegible] 764

Db        548 [illegible] 607

Qy        765 AGAGACTGAGGGCAGGGATCCAGCAGCT ----------  ----------- ---  - 794

Db        608 [illegible] 667

Qy        795 - ------------------------------------------  ------ ------    794

Db        668 GAAGCTCAACTCCTGGGTCCAGGGCCATAAGAAGGAGTTA[illegible] 727

Qy        795 -------GGGCTTGTCTATCCTGAGCTTCTGGCTGGTGA[illegible]GACTGGAGTTCC 847

Db        728 CACCCAGGGCTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCAG[illegible]GACTGGAGTTCC 787

Qy        848 CTGGGCGGCTGAAGGGGGATGACTTGGGACAGAAGGTTTTG[illegible]CAGGGATCA[illegible]CACATGA 907

Db        788 [illegible]GAAGGGGGATGACTTGGGACAGAAGGTTTT[illegible]CAGGGATCA[illegible]CACATGA 847

Qy        908 CTGGCTG[illegible]AAA[illegible]GGAGAAATGGGAT[illegible] 967

Db        848 [illegible] 907

Qy        968 [illegible] 1027

Db        908 [illegible] 967

Qy       1028 [illegible] 1087

Db        968 AGCTCAGA[illegible]GGACACAAAGAT[illegible]AAG[illegible] 1027

Qy       1088 [illegible] 1147

Db       1028 [illegible] 1087

Qy       1148 [illegible] 1207

Db       1088 [illegible] 1147

Qy       1208 [illegible] 1267

Db       1148 [illegible]GGAAGCAAGAGGA[illegible]CAGAGG[illegible]CAAA[illegible] 1207

Qy       1268 [illegible] 1327

Db       1208 [illegible] 1267

Qy       1328 [illegible] 1387

Db       1268 [illegible] 1327


RESULT 5
AK056894
LOCUS       AK056894                2429 bp    mRNA    linear   [illegible]
DEFINITION  Homo sapiens cDNA FLJ32332 fis, clone PROST2005121, weakly similar
            to PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16).
ACCESSION   AK056894
VERSION     AK056894.1  GI:16552415
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens prostate cDNA to mRNA, clone_lib:PROST2
            clone:PROST2005121.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishii,S.,
            [illegible],Y., Hotuta,T., Hirakawa,S., Murakawa,K., Takiguchi,S.,
            Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishii,M.,
            Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
            Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
            Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y.,
            Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A.,
            Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2429)
  AUTHORS   Isogai,T., Otsuki,T. and Sugiyama,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-[illegible]) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: RAB and
            HRI.
FEATURES             Location/Qualifiers
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                     /clone="PROST2005121"
                     /tissue_type="prostate"
                     /clone_lib="PROST2"
                     /note="cloning vector: pME18SFL3"
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                     /codon_start=1
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                     /db_xref="GI:16552416"
                     /translation="MHLNGF[illegible]FVLEKG[illegible]
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                     [illegible]LARKL[illegible]LAVSE[illegible]LPVLL[illegible]SVP[illegible]VV
                     [illegible]AWAWVGASSKEK"
BASE COUNT      527 a    [illegible] c    [illegible] g    [illegible] t
ORIGIN

  Query Match             73.[illegible]%;  Score 1614.4;  DB 9;  Length 2429;
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Qy        [illegible] GA[illegible]AA[illegible]GAA[illegible]AA[illegible] 24[illegible]

Db        [illegible]AAG[illegible] 24[illegible]
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[illegible]

RESULT [illegible]
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LOCUS       [illegible]    [illegible] bp    mRNA    linear   [illegible]
DEFINITION  [illegible] sapiens, [illegible] MGC:[illegible] IMAGE:[illegible], mRNA, complete cds.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD [illegible]
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA [illegible]
            Web site: http://www-shgc.stanford.edu
            Contact: (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: [illegible]
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="MGC:[illegible] IMAGE:[illegible]"
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                     /clone_lib="NIH_MGC_[illegible]"
                     /lab_host="[illegible]"
                     /note="Vector: pCMV-SPORT6"
     CDS             [illegible]..[illegible]
                     /codon_start=1
                     /product="Unknown (protein for MGC:[illegible])"
                     /protein_id="AAH[illegible].1"
                     /db_xref="GI:[illegible]"
                     /translation="[illegible]
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                     [illegible]
                     [illegible]
                     [illegible]VSY[illegible]VSVFVIP[illegible]HS[illegible]SSDH"
BASE COUNT      [illegible] a    [illegible] c    [illegible] g    [illegible] t
ORIGIN

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length [illegible];
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[illegible]
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Qy  [illegible] [illegible] 957
Db  525 [illegible] 584

Qy  958 [illegible] 1017
Db  585 [illegible] 644

Qy  1018 [illegible] 1077
Db  645 [illegible] 704

Qy  1078 [illegible] 1137
Db  705 [illegible] 764

Qy  1138 [illegible] 1197
Db  765 [illegible] 824

Qy  1198 [illegible] 1257
Db  825 [illegible] 884

Qy  1258 [illegible] 1317
Db  885 [illegible]

Qy  1318 [illegible] 1377
Db  945 [illegible]

Qy  1378 TGA 1380
         ||
Db  1005 TGA 1007


RESULT 7
AK093270
LOCUS       AK093270               1687 bp    mRNA    linear   PRI 15-JUL-2002
DEFINITION  Homo sapiens cDNA [illegible], [illegible]
            to PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16).
ACCESSION   AK093270
VERSION     AK093270.1  GI:21752092
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens testis cDNA to mRNA, clone_lib:TEST12
            clone:TEST12012104.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishidao,S.,
            Ono,Y., Hotuta,T., Hiraoka,S., [illegible]
            Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
            Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., [illegible]
            Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
            Saito,K., Nishikawa,T., Kimura,K., [illegible], Nakamura,Y.,
            Sekine,M., Kikuchi,H., Kanda,K., [illegible], Takahashi-Fujii,A.,
            Oshima,A., Sugiyama,A., [illegible]
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1687)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            [illegible]
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     [illegible]
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center [illegible]
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="TEST12012104"
                     /tissue_type="testis"
                     /clone_lib="TEST12"
                     /note="cloning vector: pME18SFL3"
BASE COUNT      336 a    [illegible] c    [illegible] g    326 t
ORIGIN

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  Best Local Similarity   54.6%;  Pred. No. 1.3e-45;
  Matches  [illegible];  Conservative    [illegible];  Mismatches  547;  Indels  [illegible];  Gaps  [illegible];

Qy   67 [illegible] 126
Db  194 [illegible]

Qy  127 [illegible]
Db  254 [illegible]

Qy  [illegible] [illegible]
Db  [illegible] [illegible]

Qy  [illegible] [illegible] 324
Db  374 [illegible]

Qy  325 [illegible] 384
Db  434 CGTA---[illegible] [illegible]

Qy  385 [illegible] 444
Db  [illegible] [illegible] 550

Qy  445 [illegible]
Db  551 [illegible]

Qy  [illegible] [illegible]
Db  611 [illegible]

Qy  [illegible] [illegible]
Db  671 [illegible]

Qy  [illegible] [illegible]
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Qy  [illegible] [illegible]
Db  [illegible] [illegible]

Qy  [illegible] [illegible]
Db  [illegible] [illegible]

Qy  [illegible] [illegible]
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Qy  [illegible] [illegible]
Db  [illegible] [illegible]
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Qy      [illegible]
Db      [illegible]

Qy      [illegible]
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Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]

Db      [illegible]

RESULT [illegible]
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LOCUS       [illegible]                    [illegible] bp    mRNA    linear   [illegible] 2001
DEFINITION  Homo sapiens, Similar to RIKEN cDNA [illegible] gene, clone
            MGC:[illegible] IMAGE:[illegible], mRNA, complete cds.
ACCESSION   [illegible]
VERSION     [illegible]  GI:[illegible]
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            [illegible]
            Tissue Procurement: [illegible]
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: [illegible]
            Shevchenko,Y., [illegible], [illegible], Bouffard,G.G.,
            [illegible], Blakesley,R.W., [illegible], [illegible],
            [illegible], [illegible], Gupta,J., [illegible], [illegible],
            Lim,M., Maduro,Q., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J.,
            [illegible], [illegible], [illegible], Wetherby,K.,
            [illegible],B. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAT Plate: 27 Row: p Column: 10
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: [illegible].
FEATURES             Location/Qualifiers
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                     [illegible]SYS"
BASE COUNT     [illegible] a   [illegible] c   [illegible] g   [illegible] t
ORIGIN

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Db        [illegible]

Qy        147 [illegible]
Db        [illegible]

Qy        [illegible]
Db        267 [illegible]

Qy        [illegible]
Db        327 [illegible]

Qy        327 [illegible]
Db        387 [illegible]

Qy        [illegible] 444
Db        444 [illegible]

Qy        445 [illegible]
Db        504 [illegible]

Qy        494 [illegible] 554
Db        [illegible]

Qy        [illegible]
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Qy        [illegible]
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Db        684 [illegible] 743

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Db        744 [illegible]

Qy        712 [illegible] 771

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Qy        772 [illegible]

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Qy        832 [illegible]

Db        924 [illegible]

Qy        892 [illegible]

Db        984 [illegible]

Qy        952 [illegible]

Db       1044 [illegible]

Qy       1012 GGCTGGGA[illegible]

Db       1104 [illegible]

Qy       1072 [illegible]

Db       1164 [illegible]

Qy       1132 [illegible]

Db       1224 [illegible]

Qy       1192 [illegible]

Db       1284 [illegible]

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Db       1344 [illegible]

Qy       1297 [illegible]

Db       1404 [illegible]

Qy       1357 [illegible] 1359

Db       1464 [illegible] 1466


RESULT 4
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LOCUS       AX419118                2518 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 3 from Patent WO0218565.
ACCESSION   AX419118
VERSION     AX419118.1  GI:[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            [illegible]
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human protein phosphatase [illegible]-like enzyme
  JOURNAL   Patent: WO 0218565-A [illegible] 07-MAR-2002;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
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                     /translation="MA[illegible]
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                     [illegible]GSYS"
BASE COUNT      507 a    768 c    759 g    484 t
ORIGIN

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  Best Local Similarity   [illegible];  Pred. No. 2.7e-42;
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Db       [illegible]

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Db       1548 [illegible]

Qy        685 [illegible] 744

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Qy        745 [illegible] 804

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Db       [illegible]

Qy        [illegible]

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Qy        925 [illegible]

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Qy       [illegible] 1164

Db       2028 [illegible] 2087

Qy       1165 [illegible]

Db       2088 [illegible] 2147
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Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]


[illegible]
[illegible]
LOCUS       [illegible]                2518 bp    mRNA    linear   PRI 18-FEB-2000
DEFINITION  Homo sapiens mRNA; cDNA DKFZp434[illegible] (from clone DKFZp434[illegible]);
            partial cds.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    [illegible]
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2518)
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., [illegible] and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) MIPS, Am Klopferspitz [illegible]
            Martinsried, GERMANY
COMMENT     [illegible] S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
            sequenced by [illegible] within the cDNA Sequencing Consortium of the German
            Genome Project.
            This clone (DKFZp434[illegible]) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, [illegible]
            Berlin-Charlottenburg, GERMANY; Email: [illegible] Further
            information about the clone and the sequencing project is available
            at http://www.mips.biochem.mpg.de/proj/cDNA/.
FEATURES             Location/Qualifiers
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                     [illegible] sites NotI + SalI"
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                     [illegible]
                     [illegible]KKA[illegible]VMA[illegible]VIP[illegible]KV[illegible]EIVEVVY[illegible]
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[illegible]
[illegible]
[illegible]
ORIGIN

  [illegible] Match [illegible]
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Qy     [illegible]
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Qy     [illegible]
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Qy     [illegible]
Db     1548 [illegible]

Qy     [illegible]
Db     1608 [illegible]

Qy     [illegible]
Db     [illegible]

Qy     805 [illegible]
Db     [illegible]

Qy     865 [illegible]
Db     [illegible]

Qy     925 [illegible]
Db     1848 [illegible]

Qy     985 [illegible]GGGGCTGGGAGACCATCAGCTCAGAG[illegible] 1044
Db     1908 [illegible]GAGGCTGGGAGACCACAGCCTAAGG[illegible] 1967

Qy     1045 [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     2148 [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]


RESULT 11
AX4[illegible]
LOCUS       AX4[illegible]             [illegible] bp    DNA     linear   PAT [illegible]
DEFINITION  Sequence [illegible] from Patent WO[illegible].
ACCESSION   AX4[illegible]
VERSION     AX4[illegible]  GI:[illegible]
KEYWORDS    .
SOURCE      human.
```

```
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human protein phosphatase [illegible] like enzyme
  JOURNAL   Patent: WO 0218565 A 1 07 MAR 2002;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1..900
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      [illegible] a    247 c    292 g    [illegible] t
ORIGIN

  Query Match             1[illegible].2%;  Score 264.4;  DB [illegible];  Length 900;
  Best Local Similarity   58.8%;  Pred. No. 3.8e-12;
  Matches  [illegible];  Conservative    0;  Mismatches  [illegible];  Indels   17;  Gaps    2;

Qy        523 [illegible] 582
Db         37 [illegible] 96

Qy        583 [illegible] 642
Db         97 [illegible] 156

Qy        643 [illegible] 702
Db        157 GGCTGCTGTGACTGGTTGTGATGTACCTGTTAGGTAAGGTGTATGGGCAATGCAGGC 216

Qy        703 [illegible] 762
Db        217 [illegible] 276

Qy        763 [illegible] 822
Db        277 [illegible] 336

Qy        823 [illegible] 882
Db        337 [illegible] 396

Qy        883 [illegible] 942
Db        397 [illegible] 456

Qy        943 [illegible] 1002
Db        457 [illegible] 516

Qy       1003 [illegible] 1062
Db        517 [illegible] 576

Qy       1063 [illegible] 1122
Db        577 [illegible] 636

Qy       1123 [illegible] 1182
Db        637 [illegible] 696

Qy       118[illegible] [illegible] 12[illegible]
Db        697 [illegible] 75[illegible]

Qy       1240 [illegible] 1287
Db        7[illegible]7 [illegible]

Qy       1288 [illegible] 1347
```

```
Db        817 [illegible] 876

Qy       1348 [illegible] 1359
Db        877 [illegible] 888


RESULT 12
AX400071
LOCUS       AX400071                1198 bp    DNA     linear   PAT 1[illegible]-JUN-2002
DEFINITION  Sequence 242 from Patent WO0218424.
ACCESSION   AX400071
VERSION     AX400071.1  GI:21[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tang,[illegible], [illegible],V., Zhou,[illegible], Xue,A.J., Ren,F., Zhao,[illegible],
            Wang,J.R., Zhou,[illegible].A., Wang,[illegible], [illegible], [illegible] and [illegible]
  TITLE     Nucleic acids and polypeptides
  JOURNAL   Patent: WO 0218424 A 242 07 MAR 2002;
            HYSEQ, INC. (US)
FEATURES             Location/Qualifiers
     source          1..1198
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             182..1198
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAD3351[illegible].1"
                     /db_xref="GI:21336494"
                     /translation="[illegible]
                     HILGPQSCWSSQKEV[illegible]HESLVV[illegible]AIENAP[illegible]LM[illegible]MARERRGH[illegible]V[illegible]ALVVIYLL
                     [illegible]
                     [illegible]
                     [illegible]
                     [illegible]VLSAYEPNE[illegible]RYIALAQALVLGARGTPRDR[illegible]WRLPNNKL[illegible]
                     [illegible]SYS"
BASE COUNT      [illegible] a    [illegible] c    [illegible] g    2[illegible] t
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB 6;  Length 1198;
  Best Local Similarity   [illegible];  Pred. No. [illegible]e-42;
  Matches  495;  Conservative    0;  Mismatches  329;  Indels   1[illegible];  Gaps    2;

Qy        [illegible] [illegible]
Db        [illegible] [illegible]

Qy        [illegible] [illegible]
Db        [illegible] [illegible]

Qy        [illegible] [illegible]
Db        [illegible] [illegible]

Qy        71[illegible] [illegible]
Db        [illegible] [illegible]

Qy        77[illegible] [illegible]
Db        [illegible] [illegible]

Qy        [illegible] [illegible]
Db        [illegible] [illegible]

Qy        [illegible] [illegible]
```

[illegible]

```
[illegible]
AC[illegible]
LOCUS       AC[illegible]          [illegible] bp    DNA     linear   [illegible] FEB [illegible]
DEFINITION  Homo sapiens [illegible] clone [illegible] (Roswell Park Cancer
            Institute Human BAC Library) complete sequence.
ACCESSION   AC[illegible]
VERSION     AC[illegible]  GI:[illegible]
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Muzny,D., Abramson,A.D., Bouck,J., [illegible], Chen,[illegible], Chen,Z.,
            [illegible], Ding,Y., Dugan,S.P., Durbin,K.J., [illegible],
            [illegible],
            He,X., Hernandez,[illegible], Jackson,L.R., Kondejewski,N., [illegible],
            [illegible], Liu,W., [illegible], Lu,J., Martinez,[illegible], Moore,S.,
            [illegible], Nguyen,N., [illegible],
            [illegible],
            [illegible], Wei,Y., Williamson,A.L., Worley,K., [illegible],X.,
            Naylor,[illegible] and Gibbs,R.A.
  TITLE     [illegible]
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to [illegible])
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible] FEB [illegible]) Molecular and Human Genetics, Baylor
            College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to [illegible])
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (27 FEB [illegible]) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Mar 1, [illegible] this sequence version replaced gi:[illegible].
            INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
            [illegible]

            [illegible]: this sequence does not necessarily represent the
            entire insert of this clone. Overlapping regions of clones are only
            sequenced and submitted once, so the sequence for the remainder of
            the insert may be found in the record for the adjacent clone(s).
            Overlapping clones are noted at the beginning and end of the
            features listing.

            ANNOTATION OF FEATURES:
               STSs are identified using ePCR (Genome Res. 7:541-550) searches
            of a local database that includes entries from dbSTS, GDB, and
            local mapping efforts.
               Repeats are identified using RepeatMasker (A. Smit and P. Green,
            unpublished.) for Human and Mouse sequences.
               Genes and Region of sequence similarity are identified by BLAST
            (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
            EST and cDNA sequences. Genes demonstrate at least two exons
            flanked by consensus splice sites that maintained sequence
            continuity across the splice junctions. Sequences that are not
            identical matches are annotated as similar.

            SEQUENCING READ COVERAGE:Sequencing is completed to a minimum
            standard of double strand coverage with a minimum of [illegible]
            reads with no ambiguities or 2 chemistries with a minimum of [illegible]
            [illegible] and [illegible] reads with no ambiguities. If the sequence quality for
            a region does not meet this standard, it will be indicated in the
            annotation as [illegible].

            QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality
            standards (estimated error rate less than 1 per [illegible] bases).
            Reports of lowest quality individual bases and measures of base
            quality are listed below. Description of the metrics can be found
            at URL: http://[illegible]/quality_info/genbank_annotation.
            html.

            QUALSTAT REPORT [illegible]

                               Summary Statistics
            Contig length:                                       [illegible]
            Phrap values in estimate:                            [illegible]
            Average error rate (RMS Phrap estimate):             [illegible]
            Fraction of Phrap values less than 40 :              [illegible]
            Number of consensus changing edits:                  [illegible]
            Number of N's in consensus :                         [illegible]

                               Consensus changing edits
            Position         Original-Context                 Edited-Context
            [illegible]      [illegible](n)[illegible]        [illegible](a)[illegible]
            [illegible]      [illegible](n)[illegible]        [illegible](a)[illegible]
            [illegible]148   attaaaaaga(n)atacatttt           attaaaaaga(a)atacatttt
            [illegible]      [illegible](n)[illegible]        [illegible](a)[illegible]
            [illegible]      [illegible](n)[illegible]        [illegible](a)[illegible]
            [illegible]      [illegible](n)[illegible]        [illegible](t)[illegible]

                       Distribution of Quality [illegible] Bases

                       [illegible]|                                 *
                       [illegible]|                                 *
                       [illegible]|                                 *
            #          [illegible]|                                 *
            bases      [illegible]|                           *     *
                       [illegible]|                           *     *
                       [illegible]|                           *     *
                       [illegible]|                           *     *
                       2000|                     *     *     *
                       [illegible]|         *     *     *     *     *
                       [illegible]|  *     *     *     *     *     *     *     *
                          ----------------------------------------------
                              5    10    15    20    25    30    35    40
                                       Phrap Value Range

            Version: [illegible]
```

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FEATURES             Location/Qualifiers
     source          1..182098
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="RP[illegible]-1157M2[illegible]"
                     /note="Eukaryota; Metazoa; Chordata, Vertebrata, Mammalia,
                     Eutheria; Primates; Catarrhini; Hominidae; Homo."
     repeat_region   1..169
                     /rpt_family="Alu"
     repeat_region   78..[illegible]
                     /rpt_family="AluSx"
     gene            complement(join(588..1542,1865..2013,2124..22[illegible],
                     2487..255[illegible],2734..285[illegible]))
                     /gene="Unigene cluster containing AI[illegible]78477, [illegible]80596,
                     AA2275[illegible], [illegible], AA728[illegible], [illegible], and AA2[illegible]2266."
     STS             [illegible]47..783
                     /standard_name="stSG[illegible]882"
                     /db_xref="GDB:456[illegible]425"
     STS             695..860
                     /standard_name="G[illegible]"
                     /db_xref="dbSTS:32797"
     misc_feature    5[illegible]21..526[illegible]
                     /note="Region: Similar to H.sapiens genomic DNA, X87[illegible]."
     repeat_region   5178..52[illegible]
                     /rpt_family="GC_rich"
     repeat_region   5290..5[illegible]
                     /rpt_family="GC_rich"
     misc_feature    55[illegible]..5[illegible]
                     /note="Region: Similar to H.sapiens genomic DNA, X87[illegible]."
     repeat_region   6[illegible]..[illegible]2
                     /rpt_family="AluSx"
     repeat_region   complement(7672..7745)
                     /rpt_family="L1M4"
     repeat_region   complement(7747..7[illegible])
                     /rpt_family="AluSp"
     repeat_region   8106..8173
                     /rpt_family="MER4A1"
     repeat_region   complement(8[illegible]7..8[illegible]1)
                     /rpt_family="AluSx"
     repeat_region   complement(8542..8591)
                     /rpt_family="AluSp"
     repeat_region   9144..9289
                     /rpt_family="MER4[illegible]"
     repeat_region   complement(9421..9582)
                     /rpt_family="FRAM"
     repeat_region   complement(9586..9631)
                     /rpt_family="(TAGA)n"
     repeat_region   complement(9663..9894)
                     /rpt_family="AluJo"
     repeat_region   9935..10052
                     /rpt_family="MIR"
     repeat_region   complement(10124..10260)
                     /rpt_family="L2"
     repeat_region   11050..11126
                     /rpt_family="L2"
     repeat_region   11143..11426
                     /rpt_family="AluSp"
     repeat_region   11960..12050
                     /rpt_family="GC_rich"
     gene            join(12104..1219[illegible],16081..1[illegible]158,1[illegible]..1[illegible],1[illegible]..2[illegible],
                     20[illegible]2..2[illegible]317,21117..21267,214[illegible]..21[illegible],21[illegible]..22[illegible])
                     /gene="Unigene cluster containing AI[illegible], AA[illegible],
                     W9[illegible]722, [illegible]451, AA[illegible], [illegible], and AA2[illegible]."
     repeat_region   complement(14187..1429[illegible])
                     /rpt_family="MIR"
     repeat_region   complement(148[illegible]6..151[illegible])
                     /rpt_family="AluSq"
     repeat_region   complement(15623..1572[illegible])
                     /rpt_family="(CA)n"
     repeat_region   complement(17254..1754[illegible])
                     /rpt_family="AluY"
     repeat_region   complement(18166..1845[illegible])
                     /rpt_family="AluSp"
     STS             18[illegible]52..1[illegible]
                     /standard_name="[illegible]"
                     /db_xref="dbSTS:7[illegible]"
     STS             223[illegible]..22[illegible]
                     /standard_name="stSG[illegible]"
                     /db_xref="GDB:4564423"
     repeat_region   complement(22[illegible]..2[illegible]2[illegible])
                     /rpt_family="MLT1[illegible]"
     repeat_region   complement(24[illegible]..24822)
                     /rpt_family="L2"
     repeat_region   complement(2[illegible]..2[illegible]124)
                     /rpt_family="AluSp"
     repeat_region   complement([illegible]..[illegible]874)
                     /rpt_family="(GGGA)n"

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible]e-41;
  Matches  262;  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy        [illegible]4 [illegible]
              [illegible]
Db       4222 [illegible]

Qy        [illegible]94 [illegible]
              [illegible]
Db       4162 [illegible]

Qy        454 [illegible]
              [illegible]
Db       4102 [illegible]

Qy        [illegible]14 [illegible]
              [illegible]
Db       4042 [illegible]

Qy        [illegible]74 TTGGAGAGT[illegible]TT[illegible]AGGAATGTG [illegible]98
              [illegible]
Db       [illegible]82 TTGGAGAG[illegible] [illegible]

RESULT 14
AC092045/c
LOCUS       AC092045               [illegible] bp    DNA     linear   [illegible]
DEFINITION  Homo sapiens chromosome [illegible] clone RP11-[illegible], complete sequence.
ACCESSION   AC092045 AC024148
VERSION     AC092045.2  GI:[illegible]
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 17[illegible])
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,[illegible] and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 17[illegible])
  AUTHORS   Kaul,R.K., [illegible],M.V., Raymond,[illegible], [illegible], [illegible] and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]-JUN-[illegible]) Genome Center, University of Washington,
            Box [illegible], Seattle, WA [illegible], USA
REFERENCE   3  (bases 1 to 17[illegible])
  AUTHORS   Kaul,R.K., [illegible],M.V., Zhou,Y., James,R.A., Raymond,[illegible] and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
COMMENT     On Aug 23, 2001 this sequence version replaced gi:[illegible].
                 [illegible] Genome Center
                 Center: University of Washington Genome Center
                 Center code: UWGC
                 Web site: http://www.genome.washington.edu
```

[illegible] with no [illegible]
Finishing Center: BCM
Project Information
Center project name: chr [illegible]
Center clone name: RP11-[illegible] ([illegible])
Summary Statistics
Sequencing vector: M13; [illegible]% of reads
Sequencing vector: plasmid; [illegible]% of reads
Chemistry: Dye-terminator [illegible]; [illegible]% of reads
Chemistry: Dye-primer Bodipy; [illegible]% of reads
Chemistry: Dye-terminator Big Dye; [illegible]% of reads
Assembly program: Phrap; version [illegible]
Consensus quality: 171265 bases at least Q40
Consensus quality: [illegible] bases at least Q30
Consensus quality: [illegible] bases at least Q20
Insert size: [illegible]; [illegible]% error; agarose-fp
Insert size: [illegible]; sum-of-contigs
Quality coverage: [illegible]x in Q20 bases; agarose-fp
Quality coverage: 8.8x in Q20 bases; sum-of-contigs

Overlapping Sequences:
5': RP11-[illegible] (GWGC:[illegible]) AC[illegible]
3': RP11-[illegible] (GWGC:[illegible]) AC[illegible]

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero; quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally available from the Genbank flat file format but are available as part of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted: all regions were either double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The experimentally digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a size of [illegible] (approximately [illegible] bp) are not resolved in the fingerprint and hence don't appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines.

BamHI		EcoRI		HindIII	
SequenceMap	Fingerprint	SequenceMap	Fingerprint	SequenceMap	Fingerprint
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	3511
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	6014	6008	2098	[illegible]
[illegible]	[illegible]	2571	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	4002	1016	[illegible]
[illegible]	2914	1146	1134	[illegible]	[illegible]
[illegible]	[illegible]	25656	[illegible]	[illegible]	[illegible]
9003	9073	1677	1655	92	800
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
2941	[illegible]	[illegible]	6341	4990	[illegible]
3542	3563	1927	1952	716	800
[illegible]	[illegible]	[illegible]	8714	[illegible]	[illegible]
[illegible]	[illegible]	1190	1130	[illegible]	[illegible]
1561	1603	3490	3407	6471	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
1061	1062	227	800	[illegible]	[illegible]
[illegible]	[illegible]	3880	3954	127	[illegible]
113	[illegible]	25557	26655	8945	[illegible]
66	800	3966	3954	255	800
7458	7445	8435	8744	4368	4251
6637	6697	18224	18042	5477	5454
[illegible]	[illegible]	7	800	14272	[illegible]
1044	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
2008	[illegible]			1858	[illegible]
[illegible]	1478			6412	[illegible]
3867	3920			6309	6187
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
259	800			3408	3511
[illegible]	[illegible]				
[illegible]	[illegible]				
[illegible]	5208				
[illegible]	[illegible]				
[illegible]	8404				
[illegible]	[illegible]				
[illegible]	[illegible]				

FEATURES Location/Qualifiers

```
     source          1..171343
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /chromosome "3"
                     /clone "RP11 168J18"
                     /clone_lib "RPCI human BAC library 11"
BASE COUNT    [illegible] a  40163 c  45178 g  [illegible] t
ORIGIN

  Query Match             18.9%;  Score 260.2;  DB 9;  Length 171343;
  Best Local Similarity   98.9%;  Pred. No. 1.2e-41;
  Matches  262;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        334 [illegible] 393
              || | | ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     165894 CCTGTGCAGTTCCTGACAGGCCATTACTGGGCACTGTTCGATGGGCACGGCGGTCCTGCA 165835

Qy        394 [illegible] 453
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Db     165834 [illegible] 165775

Qy        454 [illegible] 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     165774 GTGGAAGGCTGGTGGCCACTCAGCCCCCCATGCACTTCAATGGCGGTGCATCTGCCCC 165715

Qy        514 AGTGACCCTCAGTTTGTGGAGGAAAAGGGTATCAGGGGAGAAGACTGGGTGATCGGGGCA 573
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db     165714 [illegible] 165655

Qy        574 TTGGAGATTGCCTTTTCAGGAATGTG 598
              ||||||||||||||||||||||||||
Db     165654 TTGGAGATTGCCTTTTCAGGAATGTG 165630


RESULT 15
AC094021
LOCUS       AC094021               214160 bp    DNA     linear   PRI 27-MAR-2002
DEFINITION  Homo sapiens chromosome 3 clone RP11 801L18, complete sequence.
ACCESSION   AC094021 AC069253
VERSION     AC094021.2  GI:19745061
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-2002) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
COMMENT     On Mar 27, 2002 this sequence version replaced gi:15584339.
            ------------ Genome Center
                Center: University of Washington Genome Center
                Center code: UWGC
                Web site: http://www.genome.washington.edu
                Contact: uwgcht@u.washington.edu
                Draft Center: BCM
            ------------ Project Information
                Center project name: chr-3
                Center clone name: RP11 801L18 (bcm565)
            ------------      Summary Statistics
                Sequencing vector: M13; L08821; 19% of reads
                Sequencing vector: plasmid; 81% of reads
                Chemistry: Dye-terminator ET; 86% of reads
                Chemistry: Dye-primer Bodipy; 11% of reads
                Chemistry: Dye terminator big dye; [illegible]% of reads
                Assembly program: Phrap; version [illegible]
                Consensus quality: [illegible] bases at least Q40
                Consensus quality: 211[illegible] bases at least Q30
                Consensus quality: 211[illegible] bases at least Q20
                Insert size: 2116[illegible]; sum of contigs
                Quality coverage: [illegible]x in Q20 bases; sum of contigs
            ------------
            Overlapping Sequences:
                5': Mapping in progress
                3': [illegible] (UWGC:[illegible]) AC006208
            ------------
            Sequence Quality Assessment:
             This entry has been annotated with sequence quality
             estimates computed by the Phrap assembly program.
             All manually edited bases have been reduced to quality zero.
             Quality levels above 40 are expected to have less than
             1 error in 10,000 bp.
             Base by base quality values are not generally available in the
             GenBank flat file format but are available as part
             of this entry's ASN.1 file.

            This sequence was finished as follows unless otherwise noted:
            all regions were either double-stranded or sequenced with an
            alternate chemistry or covered by high quality data (i.e., Phred
            quality >= 30); an attempt was made to resolve all sequencing
            problems, such as compressions and repeats; all regions were
            covered by at least one plasmid subclone or more than one M13
            subclone; and the assembly was confirmed by restriction digest.
            ------------
            Sequence Validation:
             This sequence has been validated by Multiple Complete Digest
             fingerprinting. Comparison of the experimentally derived digest
             fragments with sequence-predicted fragments is given below.
             The electronically digested sequence consists of both insert and
             vector, in order to accurately represent the entire circular BAC.
             Small fragments below a variable cutoff (approximately 4 - 800 bp)
             are not resolved in the fingerprint and hence do not appear
             in the table. There are no significant remaining discrepancies
             between the experimental and predicted values. Unique clones
             fragments are separated by dashed lines.
                     BglII                      EcoRI                      HindIII
            -------                    ------                                     --
            SeqDerMap    FngrPrnt      SeqDerMap   FngrPrnt       SeqDerMap   FngrPrnt
            ---------    --------      ---------   --------       ---------   --------
            ----                       -                          ---
                 3254         [illegible]       86[illegible]        8704       [illegible]      [illegible]
            ------                     ------
                 2067         [illegible]       [illegible]        [illegible]       [illegible]      [illegible]
            --------                   -----
                 1[illegible]         [illegible]       4872        4941       [illegible]      [illegible]
              -------                  --------                   ----
                 14477        14184      7[illegible]        7549       44[illegible]      [illegible]
              --------                 ------
                 6169         6264       1627        1647       [illegible]      [illegible]
            ----------                 --------
                 11235        10936      1465        1443       1481      [illegible]
            ------                     ----                       -------
                 1606         [illegible]       4[illegible]        4941       [illegible]      [illegible]
             -----                     --                         --
                 [illegible]         [illegible]       [illegible]        5277       4[illegible]      [illegible]
            -----
                 42[illegible]         [illegible]       [illegible]        6041       [illegible]      [illegible]
                                        ----
                 1426         [illegible]       80[illegible]        8002       [illegible]      [illegible]
               ---                     --------
                 15           [illegible]       753         [illegible]       72[illegible]      72[illegible]
            ------                     ---
                 5962         [illegible]       8244        8387       [illegible]      [illegible]
     3530     3570        2219     2147         628    [illegible]
     2713     2758        3014     3012        1117      595
     9212     9087        2374     2384         305    [illegible]
     8003     9087        4571     4633       13279    10159
      336  [illegible]    1146     1130          92    [illegible]
     2644     2738       25960    26349        2927     2934
     3512     3570        1677     1642        4995     5017
     1408     1579       14734    11140         715    [illegible]
    10087    19976        1490     1443        3758     3771
     6637     6645        3499     3525       11877    11690
     9657     9657        5208     5277        6471     6448
     1041     1570         227  [illegible]   17175    12857
       33  [illegible]    3889     3971        5598     5511
     2998     2968       27037  [illegible]    5475     5511
     5002     4075        3966     3971       11272    13913
     3967     3923        8405     8397        7112     7204
     1250     1244       18224    17531        9299     9276
    19019    19976        8662     8754        1878     1877
      259  [illegible]     284  [illegible]    6112     6448
     6540     6645         241  [illegible]    6399     6448
     2293     2230       25108    26349       13796    13913
     5173     5211         449  [illegible]    3293     3316
     1022     1531        2174     2502        3498     3529
     8390     8419                             5150     5517
     1267     1266                             1165     1154
     2000     1575                             8966     8642
     1505     1503                             5120     5017
     5655     5626                            14017    13913
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     2518     2519
    16009    15788
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FEATURES             Location/Qualifiers
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BASE COUNT    47581 a  57396 c  57428 g  48755 t
ORIGIN

  Query Match             18.9%;  Score 260.2;  DB 9;  Length 211160;
  Best Local Similarity   98.9%;  Pred. No. 1.1e-41;
  Matches  262;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        334 GCAGAGGAGTTCCTGACAGGCATTACTGGGCACTGTTCGATGGGCACGGCGGTCCTGCA 393
              || | | | ||||||||||||||||||||||||||||||||||||||||||||||||||
Db      25941 GCTGTGCAGTTCCTGACAGGCATTACTGGGCACTGTTCGATGGGCACGGCGGTCCTGCA 26000

Qy        394 GCAGCCATCTTGGCTGCCAACACCCTGCACTCCTGCTTGCGCCGGCAGCTGGAGGCCGTG 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26001 GCAGCCATCTTGGCTGCCAACACCCTGCACTCCTGCTTGCGCCGGCAGCTGGAGGCCGTG 26060

Qy        454 GTGGAAGGCTGGTGGGCACTCAGCTCCCATGCACCTCAATGGCCGCTGCATCTGCCCC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26061 GTGGAAGGCTGGTGGGCACTCAGCTCCCATGCACCTCAATGGCCGCTGCATCTGCCCC 26120

Qy        514 AGTGACTCCAGCCCCTGCAGGAAAGCCCACCAGGGAGAAGACTTGGTGATCCGGGCA 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      26121 AGTGACTCCAGCCCCTGCAGGAAAGCCCACCAGGGAGAAGACTTGGTGATCCGGGCA 26180

Qy        574 TTGGAGAGTGCCTTTCAGGAATGTG 598
              |||||||||||||||||||||||||
Db      26181 TTGGAGAGTGCCTTTCAGGAATGTG 26205


Search completed: February 23, 2003, 08:59:56
Job time : 4684 secs
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                    GenCore version 5.1.3
         Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 23, 2003, 00:38:49 ; Search time 319 Seconds
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                                              9742.187 Million cell updates/sec

Title:           US-09-866-987-3
Perfect score:   1380
Sequence:        1 atgtcccccagctggttccg..........aagaagcaatgaccactga 1380

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters:      4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 24: [illegible]

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result             Query
  No.    Score   Match Length  DB  ID                               Description
-------------------------------------------------------------------------------
   1      1369    99.2   1837  22  AAH22961                         Human phosphatase
   2       917    66.4    917  24  ABA94426                         Human protein phos
   3       536    38.8    547  24  ABL79[illegible]                 Human ovarian canc
   4     264.8    19.2   2518  24  ABK47452                         DNA encoding human
   5     262.4    19.0   4262  17  AAT38484                         Rat petrin cDNA el
   6     262.4    19.0   4515  17  AAT38486                         Rat petrin cDNA.
   7     243.4    17.6   1917  23  AAS93640                         DNA encoding novel
   8     243.4    17.6   1887  22  AAI58166                         Human polynucleoti
   9     243.4    17.6   [illegible]  24  ABK46163                  cDNA encoding [illegible]
  10     242.4    17.6   1993  22  AAH17958                         Human cDNA sequence
  11       178    12.9    479  17  AAT38482                         Rat petrin cDNA el
  12     109.2     7.9    759  21  AAA62311                         Human [illegible] cancer
  13       103     7.5    566  2[illegible]  AAL12841               Human [illegible] express
  14     102.8     7.4   [illegible]  2[illegible]  AAX88954        Human validated [illegible]
  15     101.2     7.3   2087  23  ABL25549                         Drosophila melanog
  16     101.2     7.3   5107  23  ABL25548                         Drosophila melanog
  17        98     7.1    55[illegible]  24  ABL82482               Human ovarian canc
  18        95     6.9   [illegible]  20  AAX88437                  Human cancer [illegible]
  19      87.6     6.3   [illegible]  21  AAA[illegible]            Human [illegible]
  20      83.6     6.1    244  21  AAA[illegible]                   Human [illegible]
  21      81.2     5.9   2258  23  ABV22179                         Human prostate exp
  22      81.2     5.9   2258  23  ABV23186                         Human prostate exp
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  25      81.2     5.9   2258  23  ABV28[illegible]                 Human prostate exp
c 26      76.8     5.6    582  22  AAH16[illegible]                 Human cDNA clone (
  27        68     4.9    434  17  AAT38480                         Rat petrin cDNA el
  28      50.4     3.7   1643  22  AAS06065                         [illegible]
c 29      49.8     3.6   [illegible]  21  AAZ459[illegible]         Nucleotide sequenc
c 30      49.8     3.6   [illegible]  21  AAZ15[illegible]          Nucleotide sequenc
c 31      49.8     3.6   [illegible]  21  AAZ159[illegible]         Nucleotide sequenc
c 32      49.4     3.6   [illegible]  22  AAK754[illegible]         Human immune/haema
  33      49.2     3.6    750  22  AAI59952                         Human polynucleoti
c 34        49     3.6   [illegible]  24  ABK47453                  Protein phosphatas
c 35      48.8     3.5   [illegible]  24  AB[illegible]8452         Listeria monocytog
c 36      48.2     3.5   [illegible]  2[illegible]  AAX15147        Nucleotide sequenc
c 37      48.2     3.5   [illegible]  24  AA[illegible]6162         Human Smad[illegible] DNA.
c 38        48     3.5   [illegible]  24  ABQ37014                  Oligonucleotide fo
  39        48     3.5   [illegible]  24  ABQ37015                  Oligonucleotide fo
  40      47.6     3.4   [illegible]  12  AAL1124[illegible]        HSV [illegible]K [illegible]
c 41      47.4     3.4   [illegible]  22  AAK75[illegible]          Human immune/haema
  42        47     3.4   [illegible]  2[illegible]  AAZ2[illegible] Zea mays [illegible]
c 43      46.8     3.4   [illegible]  21  ABN0[illegible]           Gene [illegible] used t
c 44      46.8     3.4   [illegible]  21  AB[illegible]             Lung cancer relate
c 45      46.8     3.4   [illegible]  24  ABL65219                  Lung cancer relate

                              ALIGNMENTS

RESULT 1
AAH22961
ID   AAH22961 standard; DNA; 1837 BP.
XX
AC   AAH22961;
XX
DT   17-SEP-2001  (first entry)
XX
DE   Human phosphatase (HI) encoding cDNA (Clone ID [illegible]).
XX
KW   phosphatase; [illegible]; alzheimer's disease; Huntington's disease; human;
KW   immune disorder; cancer; nootropic; immunomodulatory; cytostatic;
KW   neuroprotective; anticonvulsant; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             [illegible]
FT                   /*tag= a
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XX
PN   WO200153469-A2.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US-0[illegible].
XX
PR   21-JAN-2000; 2000US-0177[illegible].
PR   28-JAN-2000; 2000US-0178[illegible].
PR   25-FEB-2000; 2000US-0185[illegible].
PR   17-MAR-2000; 2000US-0190[illegible].
XX
```

```
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   [illegible]
PI   [illegible]
XX
DR   [illegible]
DR   [illegible]
XX
PT   Novel phosphatases useful for treating diseases associated with
PT   decreased expression of functional phosphatases, e.g., Alzheimer's
PT   diseases, Huntington's diseases, immune disorders, and cancers
XX
PS   Claim [illegible]; Page [illegible]; [illegible] English.
XX
CC   The invention provides human phosphatases (PP) and polynucleotides
CC   that encode the phosphatases. The polypeptides can be expressed by standard
CC   recombinant methodology. The PP are useful for treating a disease or
CC   condition associated with decreased expression of functional
CC   phosphatases. Compositions containing agonists or antagonists of PP may
CC   be used to treat a disease associated with decreased expression or
CC   [illegible] of PP, respectively. Such diseases may include
CC   Alzheimer's disease, Huntington's disease, immune disorders, and
CC   cancers. The present sequence represents a human phosphatase encoding
CC   cDNA.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches [illegible];  Conservative    [illegible];  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

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Db        61 [illegible] 120

Qy       121 [illegible]
Db       121 [illegible]

Qy       181 [illegible] 240
Db       181 [illegible] 240

Qy       241 [illegible]
Db       241 [illegible]

Qy       301 [illegible] 360
Db       301 [illegible] 360

Qy       361 [illegible]
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Qy       481 [illegible]
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Qy       541 [illegible]
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Qy       721 [illegible]
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Qy       781 [illegible]
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Qy       901 [illegible]
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Qy       961 [illegible]
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Qy      1021 [illegible] 1080
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Qy      1081 [illegible] 1140
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Qy      1201 [illegible]
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Qy      1261 [illegible]
Db      1261 [illegible] 1320

Qy      1321 [illegible]
Db      1321 [illegible]

Qy      1380 A 1380
             |
Db      1381 A 1381


RESULT 2
ABA64129
ID   ABA64129 standard; cDNA; [illegible] BP.
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AC   ABA64129;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human protein phosphatase SHP[illegible] encoding cDNA.
XX
KW   Protein phosphatase; serine threonine phosphatase; [illegible]; SH[illegible]; [illegible]
KW   cytostatic; immunosuppressive; gastrointestinal; analgesic; hypertensive;
KW   hypotensive; [illegible]; neuroprotective; virucide; antibacterial; human;
KW   fungicide; ophthalmological; antiinflammatory; cardiant; antimigraine;
KW   antiarthritic; vasculotropic; antiasthmatic; osteopathic; antipsoriatic;
KW   antiarteriosclerotic; antiallergic; antidiabetic; tranquilliser; cancer;
KW   neuroleptic; antiparkinsonian; anorectic; gene therapy; ss.
XX
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```
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FT                   /note= "sequence coding for approximately another 154
FT                          amino acid residues in the corresponding protein
FT                          is not printed in the specification."
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PN   WO200[illegible]2491-A2.
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PD   [illegible]-2001.
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PF   [illegible]-MAY-2001; 2001WO-US17[illegible].
XX
PR   30-MAY-2000; 2000US-208291P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   [illegible] CD,  Whyte D,  Sudarsanam S,  Manning G,  Caenepeel S;
PI   Martinez R,  Hill RJ,  Flanagan P;
XX
DR   WPI; 2002-114346/15.
DR   P-PSDB; ABB67364.
XX
PT   New phosphatase polypeptides for treating e.g., cancers, immune-related
PT   diseases and disorders, cardiovascular diseases, or brain or
PT   neuronal-associated diseases -
XX
PS   Claim 28; Fig 1A; 161pp; English.
XX
CC   The invention relates to human protein phosphatase polypeptides and
CC   polynucleotides. The phosphatase polypeptides are useful for diagnosing
CC   and treating various phosphatase-related diseases and conditions, such as
CC   cancers, immune-related diseases and disorders, cardiovascular diseases
CC   (e.g., reperfusion restenosis), brain or neuronal-associated diseases,
CC   metabolic disorders (e.g., diabetes or obesity), central or peripheral
CC   nervous system diseases and conditions (e.g., pain, migraine, mood
CC   disorders, hypotension, or hypertension), psychotic and neurological
CC   disorders (e.g., anxiety, schizophrenia), neurodegenerative diseases
CC   (e.g., Alzheimer's or Parkinson's disease), infections caused by virus
CC   (e.g., human immunodeficiency virus (HIV)), bacterial, fungal or prion-
CC   agents, ocular diseases (macular degeneration), and inflammatory disorders
CC   (e.g., rheumatoid arthritis, multiple sclerosis, osteoarthritis). The
CC   polypeptides may also be used for screening for small molecule compounds
CC   that inhibit the catalytic activity of the encoded protein phosphatase
CC   with potential use for treating the above mentioned diseases, for
CC   generating antibodies or hybridomas, and as a diagnostic tool for
CC   detecting a disease or disorder. Genetic sequences of phosphatases are
CC   useful in gene therapy. The present sequence represents a cDNA encoding
CC   a novel human serine threonine phosphatase (STP)-like phosphatase
CC   polypeptide SGP[illegible].
XX
SQ   Sequence 917 BP; 161 A; 27[illegible] C; 31[illegible] G; 17[illegible] T;   other;

  Query Match             6[illegible].4%;  Score 917;  DB 24;  Length 917;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-[illegible];
  Matches  917;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 [illegible] 60

Qy         61 [illegible] 120
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Db         61 [illegible] 120

Qy        121 [illegible] 180
              [illegible]
Db        121 [illegible] 180

Qy        181 [illegible] 240
              [illegible]
Db        181 [illegible] 240

Qy        241 [illegible] 300
              [illegible]
Db        241 [illegible] 300

Qy        301 [illegible]
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Qy        541 [illegible]
              [illegible]
Db        541 [illegible]

Qy        601 [illegible]
              [illegible]
Db        601 [illegible]

Qy        661 GCTGTGTCCCTGCAGGAAAGCTGTACATGGCCAATGCTGGGATAGCAGGCCATCTTG 720
              [illegible]
Db        661 GCTGTGTCCCTGCAGGAAAGCTGTACATGGCCAATGCTGGGATAGCAGGCCATCTTG 720

Qy        721 [illegible] 780
              [illegible]
Db        721 [illegible] 780

Qy        781 [illegible] 840
              [illegible]
Db        781 [illegible] 840

Qy        841 [illegible]
              [illegible]
Db        841 [illegible]

Qy        901 CACATGAGTGGCTGGAG 917
              [illegible]
Db        901 [illegible] 917


RESULT
ABL7[illegible]
ID   ABL7[illegible] standard; cDNA; [illegible] BP.
XX
AC   ABL7[illegible];
XX
DT   17-MAY-2002  (first entry)
XX
DE   Human ovarian cancer related cDNA clone SEQ ID NO:2968.
XX
KW   Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO[illegible] A2.
XX
PD   06-DEC-2001.
XX
PF   25-MAY-2001; 2001WO-US1[illegible].
XX
PR   26-MAY-2000; 2000US-20[illegible]484P.
```

```
XX
PA   [illegible]
XX
PI   A[illegible] PA, Harlocker [illegible]
XX
DR   WPI; 2002-[illegible].
XX
PT   Composition for therapy and diagnosis of ovarian cancer comprising
PT   polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT   polypeptide, antibody specific to polypeptide or T cell expressing
PT   polypeptide
XX
PS   Claim [illegible]; SEQ ID 2068; [illegible]pp; English.
XX
CC   The present invention describes a composition (I) comprising: carriers
CC   and immunostimulants; and a polypeptide (II) of a ovarian tumour
CC   polypeptide encoded by a polynucleotide (III) having a cDNA sequence
CC   (S1) from the 1042 nucleotide sequences as given in ABL77023 to
CC   AB[illegible]4, (III) encoding (II) having a sequence (S2), a T cell
CC   population of (II), or antigen presenting cells that express (II).
CC   (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC   (S1) can be used for detecting ovarian cancer in a patient's biological
CC   sample preferably serum or ovarian tissue. The method comprises
CC   contacting a biological sample from a patient with (IV), detecting the
CC   amount of polynucleotide hybridising to (IV) and comparing the amount to
CC   a predetermined cutoff value and thereby detecting ovarian cancer in the
CC   patient, where the amount of polynucleotide hybridising to (IV) is
CC   detected preferably by polymerase chain reaction (PCR). (I) comprising
CC   (III) and/or (II) is useful for stimulating and/or expanding T cells
CC   specific for an ovarian tumour protein comprising contacting T cells
CC   with (II) or (III). (III) is useful in design and preparation of
CC   ribozyme molecules for inhibiting expression of the tumour polypeptides
CC   and proteins in tumour cells; and to isolate a full length gene from a
CC   suitable library, e.g., a tumour cDNA library, using well known
CC   techniques.
XX
SQ   Sequence 547 BP; 123 A; 135 C; 171 G; 118 T; 0 other;

  Query Match             98.8%;  Score [illegible];  DB 21;  Length 547;
  Best Local Similarity   [illegible]%;  Pred. No. 1.9e-11[illegible];
  Matches  54[illegible];  Conservative    0;  Mismatches    [illegible];  Indels    1;  Gaps    1;

Qy        [illegible]
Db          1 [illegible]

Qy        [illegible]
Db         61 [illegible] 120

Qy        [illegible]
Db        [illegible]

Qy        [illegible] 1031
Db        [illegible] 240

Qy        [illegible]
Db        [illegible]

Qy        [illegible] 1151
Db        [illegible]

Qy        [illegible]
Db        [illegible] 419

Qy        [illegible] 1271
Db        [illegible]

Qy       1272 [illegible]
Db        [illegible]

Qy       1332 [illegible]
Db        540 [illegible] 547


RESULT 4
ABK47452
ID   ABK47452 standard; DNA; 2518 BP.
XX
AC   ABK47452;
XX
DT   18-JUN-2002  (first entry)
XX
DE   DNA encoding human protein phosphatase II C-like (PPIIC) enzyme.
XX
KW   Protein phosphatase II C like; agonist; antagonist; apoptosis; AIDS;
KW   Acquired immunodeficiency virus; genetic immunodeficiency; PPIIC;
KW   neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW   retinitis pigmentosa; amyotropic lateral sclerosis; myelodysplasia;
KW   aplastic anaemia; ischaemic injury; myocardial infarction; stroke;
KW   reperfusion injury; toxin induced disease; cirrhosis; wasting disease;
KW   cachexia; viral infection; hepatitis; osteoporosis; cancer; diabetes;
KW   central nervous system disorder; CNS disorder; cardiovascular disorder;
KW   inflammatory disorder; chronic obstructive pulmonary disease; COPD;
KW   gene; ds; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1410..2309
FT                   /*tag=  a
FT                   /product= "PPIIC"
FT                   /note= "Protein phosphatase IIC like enzyme,
FT                          Specifically claimed in claim 1"
FT   misc_binding    1410..1434
FT                   /*tag=  b
FT                   /note= "Bound by the antisense oligonucleotide shown
FT                          in ABK47461"
XX
PN   WO200218[illegible]-A2.
XX
PD   07-MAR-2002.
XX
PF   20-AUG-2001; 2001WO-EP09558.
XX
PR   30-AUG-2000; 2000US-228[illegible]P.
PR   02-APR-2001; 2001US-280115P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Xiao Y;
XX
DR   WPI; 2002-292261/33.
DR   P-PSDB; AA[illegible]8802.
XX
PT   New protein phosphatase IIC like enzyme and polynucleotide, useful for
PT   treating a disease associated with an increase or decrease in
PT   apoptosis, e.g. neurodegenerative diseases, viral infections,
PT   myelodysplasia, cancer, diabetes
XX
PS   Disclosure; Fig 3; 125pp; English.
XX
CC   The invention describes an isolated polynucleotide (I) which encodes a
CC   protein phosphatase IIC (PPIIC)-like enzyme (II). (I) and (II) can be
CC   used in diagnostic assays for detecting diseases and abnormalities or
CC   susceptibility to diseases and abnormalities related to the presence of
CC   mutations in the nucleic acid sequences encoding the enzyme. (I) and (II)
CC   or its antagonists, agonists, or modulators are useful for treating a
CC   disease or disorder associated with an increase in apoptosis such as AIDS
CC   or other infectious or genetic immunodeficiencies, neurodegenerative
CC   diseases (e.g. Alzheimer's disease or Parkinson's disease, retinitis
CC   pigmentosa, or amyotropic lateral sclerosis), myelodysplasia (e.g.
CC   aplastic anaemia), ischaemic injuries (e.g. myocardial infarction, stroke
CC   or reperfusion injury), toxin induced diseases (e.g. alcohol induced
CC   liver damage or cirrhosis), wasting diseases (e.g. cachexia), viral
CC   infections (e.g. hepatitis B or C), and osteoporosis, or a decrease in
CC   apoptosis such as cancer, diabetes, CNS disorders, cardiovascular
CC   disorders, chronic obstructive pulmonary disease (COPD), and inflammatory
CC   disorders. Regulation of human PPIIC-like enzyme can be used to treat
CC   disorders such as diabetes, CNS disorders, cardiovascular disorders,
CC   COPD, and cancers (e.g. leukaemia, lymphoma, or cancers of the organs).
CC   This sequence encodes the novel human protein phosphatase IIC-like enzyme
CC   described in the invention.
XX
SQ   Sequence 2518 BP; 607 A; 762 C; 752 G; 484 T;   other;

  Query Match             19.2%;  Score 264.8;  DB 24;  Length 2518;
  Best Local Similarity   57.7%;  Pred. No. 7.8e-52;
  Matches  587;  Conservative    0;  Mismatches  377;  Indels   16;  Gaps    4;

Qy        445 [illegible] 504
Db       1369 [illegible] 1428

Qy        505 [illegible] 564
Db       1429 [illegible] 1487

Qy        565 ATGGGGCATTGGAGAGTGCCTTTCAGGAATGTGATGAGGTGATGGGGGGAGCTGGAG 624
Db       1488 [illegible] 1547

Qy        625 [illegible] 684
Db       1548 [illegible] 1607

Qy        685 [illegible] 744
Db       1608 [illegible] 1667

Qy        745 [illegible] 804
Db       1668 [illegible] 1727

Qy        805 [illegible] 864
Db       1728 [illegible] 1787

Qy        865 [illegible] 924
Db       1788 [illegible] 1847

Qy        925 [illegible] 984
Db       1848 [illegible] 1907

Qy        985 [illegible] 1044
Db       1908 [illegible] 1967

Qy       1045 [illegible] 1104
Db       1968 [illegible] 2027

Qy       1105 [illegible] 1164
Db       2028 [illegible] 2087

Qy       1165 [illegible] 1221
Db       2088 [illegible] 2147

Qy       1222 [illegible]
Db       2148 [illegible]

Qy       1280 [illegible]
Db       2208 [illegible]

Qy       1340 [illegible] 1369
Db       2268 [illegible] 2297


RESULT 5
AAT38484
ID   AAT38484 standard; cDNA; 4262 BP.
XX
AC   AAT38484;
XX
DT   16-JAN-1997  (first entry)
XX
DE   Rat petrin cDNA clone [illegible].
XX
KW   Petrin; neurite outgrowth associated protein; CNS;
KW   central nervous system; myelin; protein phosphatase [illegible]; stroke;
KW   neurodegeneration; gene therapy; ss.
XX
OS   Rattus sp.
XX
FH   Key                 Location/Qualifiers
FT   misc_difference     3825
FT                       /*tag=  a
FT                       /note= "Base 3825 is given as b in the
FT                              specification."
XX
PN   WO9632476-A1.
XX
PD   17-OCT-1996.
XX
PF   12-APR-1996;   96WO-CA00214.
XX
PR   13-APR-1995;   95US-0421701.
XX
PA   (MOUN-) MOUNT SINAI HOSPITAL CORP.
XX
PI   Labes M,  Lozano A,  Roach A,  Roder J;
XX
DR   WPI; 1996-477127/47.
DR   P-PSDB; AAW04327.
XX
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, Petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 2; Page [illegible]; [illegible]pp; English.
XX
CC   A cDNA sequence (AAT38484) encodes rat petrin (AAW04327), a protein
CC   involved in modulating neurite growth inhibition. It was derived
CC   from Trapasso's [illegible] clone [illegible] (see also AAT38485) isolated from an
CC   adult rat brain cDNA library in lambda gt11 by screening with
CC   a monoclonal antibody that blocks the effect on neurites in cultures
CC   of CNS myelin inhibitors. The petrin gene is expressed in neurons
CC   in brain tissue, partic. in cerebellum Purkinje cells. It can be
CC   used to produce petrin protein and to prepare probes. Antisense
CC   sequences (see also AAT38485) can be used in gene therapy to enhance
CC   axonal regeneration.
XX
SQ   Sequence 4262 BP; 921 A; 1164 C; 1156 G; 1002 T; 19 other;

  Query Match             [illegible];  Score 257.4;  DB 17;  Length 4262;
  Best Local Similarity   [illegible];  Pred. No. [illegible]e-51;
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible] 1137

Qy   [illegible]
Db   [illegible] 1257

Qy   [illegible]
Db   [illegible] 1317

Qy   [illegible]
Db   [illegible] 1377

Qy   [illegible]
Db   [illegible] 1437

Qy   [illegible]
Db   [illegible] 1497

Qy   [illegible]
Db   [illegible] 1557

Qy   [illegible]
Db   [illegible]

RESULT [illegible]
AAT[illegible]
ID   AA[illegible] standard; cDNA; [illegible] BP.
XX
AC   AAT[illegible];
XX
DT   [illegible]-JAN-[illegible] (first entry)
XX
DE   Rat petrin cDNA.
XX
KW   [illegible] with [illegible] protein; CNS;
KW   [illegible] nervous system; [illegible] protein phosphatase [illegible] stroke;
KW   [illegible] degeneration; gene therapy; ss.
XX
OS   [illegible]
XX
FH   Key             Location/Qualifiers
FT   [illegible]
FT                   /*tag= a
FT                   /product= petrin
FT   misc_difference 962
FT                   /*tag= b
FT                   /note= "base 962 is given as N in the
FT                          specification"
XX
PN   WO9[illegible]-A1.
XX
PD   17-OCT-1996.
XX
PF   12-APR-1996;    96WO-CA[illegible].
XX
PR   1[illegible]-APR-1995;   95US-0[illegible].
XX
PA   (MOUN-) MOUNT SINAI HOSPITAL CORP.
XX
PI   Labes M,  [illegible] A,  Roach A,  Roder J;
XX
DR   WPI; 1996-[illegible].
DR   P-PSDB; AAW[illegible].
XX
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, Petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 4; Fig 2; [illegible]pp; English.
XX
CC   A nucleotide sequence (AAT[illegible]) codes for petrin (AAW[illegible]), a protein
CC   involved in mediating neurite growth inhibition.  It was isolated
CC   from an adult rat brain cDNA library in lambda gt11 by screening
CC   with probes based on partial petrin clones (see also AAT38479-81).
CC   The human petrin locus was localised to chromosome 12.  The gene
CC   is expressed in neurons in brain tissue, partic. in cerebellum
CC   Purkinje cells.  It can be used to produce petrin protein and to
CC   prepare probes.  Antisense sequences (see also AAT38485) can be used
CC   in gene therapy to enhance axonal regeneration.
XX
SQ   Sequence 4[illegible] BP; 986 A; 1240 C; 1236 G; 1052 T; 1 other;

  Query Match             [illegible]%;  Score 262.4;  DB 17;  Length 4515;
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  459;  Conservative    0;  Mismatches  306;  Indels    0;  Gaps    1;

Qy        498 [illegible]
Db       1091 [illegible]

Qy        [illegible]
Db       1151 [illegible]

Qy        [illegible]
Db       1211 [illegible]

Qy        [illegible]
Db       1271 [illegible]

Qy        [illegible]
Db       1331 [illegible]

Qy        [illegible]
Db       1391 [illegible]

Qy        [illegible]
Db       1451 [illegible]
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Qy        918 [illegible] 977
Db       1511 [illegible] 1570

Qy        978 GGCTCGGTTACTAGGAACACTGGCTGTCTCCGGGGCTGGGAGACCATCAGCTCAGAGT 1037
Db       1571 [illegible]

Qy       1038 [illegible]
Db       1631 [illegible]

Qy       1098 [illegible] 1157
Db       1691 [illegible]

Qy       1158 [illegible]
Db       1751 [illegible]

Qy       1218 [illegible]
Db       1811 [illegible]


RESULT 7
AAS[illegible]
ID   AAS[illegible] standard; cDNA; 1617 BP.
XX
AC   AAS[illegible];
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #29444.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   [illegible]
XX
PD   11-OCT-2001.
XX
PF   [illegible]
XX
PR   [illegible]
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-6[illegible]62/73.
DR   [illegible]
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 1; SEQ ID No 29444; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS94197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at [illegible]/published pct sequences.
XX
SQ   Sequence 1617 BP; [illegible] A; 442 C; 467 G; 325 T; 0 other;

  Query Match             [illegible];  Score 24[illegible];  DB 2[illegible];  Length 1617;
  Best Local Similarity   57.9%;  Pred. No. 6.5e-47;
  Matches  452;  Conservative    [illegible];  Mismatches  326;  Indels    [illegible];  Gaps    [illegible];

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        791 [illegible]

Qy        620 [illegible]
Db        871 [illegible]

Qy        680 [illegible]
Db        911 [illegible]

Qy        740 [illegible]
Db        971 [illegible]

Qy        800 [illegible]
Db       [illegible]

Qy        860 [illegible]
Db       [illegible]

Qy        920 [illegible]
Db       1151 [illegible]

Qy        980 [illegible]
Db       1211 [illegible]

Qy       1040 [illegible]
Db       1271 [illegible]

Qy       1100 [illegible]
Db       [illegible]

Qy       1160 [illegible]
Db       1391 [illegible]

Qy       1217 [illegible]
Db       1451 [illegible]

Qy       1277 G 1277
              |
Db       1511 G 1511
```

```
RESULT 8
AAL[illegible]
ID   AAL[illegible] standard; cDNA; 1467 BP.
XX
AC   AAL[illegible];
XX
DT   [illegible] (first entry)
XX
DE   Human polynucleotide SEQ ID NO 369.
XX
KW   Human; [illegible]; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO[illegible]-A2.
XX
PD   [illegible]
XX
PF   [illegible] 2000WO-US[illegible].
XX
PR   [illegible]
PR   [illegible] 2000US-[illegible].
PR   [illegible]
PR   [illegible]
PR   [illegible] 2000US-[illegible].
PR   [illegible]
PR   [illegible]
PR   29-NOV-2000; 2000US-[illegible].
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI   Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI   Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
DR   WPI; 2001-[illegible]/47.
DR   P-PSDB; AAM[illegible].
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries
XX
PS   Claim [illegible]; SEQ ID NO [illegible]; [illegible]pp; English.
XX
CC   The invention relates to human nucleic acids (AAL[illegible]-AAL[illegible]) and
CC   the encoded polypeptides (AAM[illegible]-AAM[illegible]) with neutrophic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: immune system suppression,
CC   [illegible] activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   CNS disorders.
CC   Note: the sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence 1467 BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible]  Score [illegible]  DB [illegible]  Length 1467;
  Best Local Similarity   [illegible]  Pred. No. [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

Qy        500 [illegible] 559
              [illegible]
Db        677 [illegible] 736

Qy        560 [illegible] 619
              [illegible]
Db        737 [illegible] 796

Qy        620 [illegible] 679
              [illegible]
Db        797 [illegible] 856

Qy        680 [illegible] 739
              [illegible]
Db        857 [illegible] 916

Qy        740 [illegible] 799
              [illegible]
Db        917 [illegible] 976

Qy        800 [illegible] 859
              [illegible]
Db        977 [illegible] 1036

Qy        860 [illegible] 919
              [illegible]
Db       1037 [illegible] 1096

Qy        920 [illegible] 979
              [illegible]
Db       1097 [illegible] 1156

Qy        980 [illegible] 1039
              [illegible]
Db       1157 [illegible] 1216

Qy       1040 [illegible] 1099
              [illegible]
Db       1217 [illegible] 1276

Qy       1100 [illegible] 1159
              [illegible]
Db       1277 [illegible] 1336

Qy       1160 [illegible] 1216
              [illegible]
Db       1337 [illegible] 1396

Qy       1217 [illegible] 1276
              [illegible]
Db       1397 [illegible] 1456

Qy       1277 G 1277
              
Db       1457 G 1457


RESULT 9
ABK46163
ID   ABK46163 standard; cDNA; [illegible] BP.
XX
AC   ABK46163;
XX
DT   05-JUN-2002  (first entry)
XX
DE   cDNA encoding colon tumour antigen protein, SEQ ID NO 1714.
XX
KW   Human; colon tumour; vaccine; colon cancer; immunoagent[illegible];
KW   gene therapy; [illegible]; ss.
XX
OS   Homo sapiens.
XX
PN   WO[illegible]-A2.
```

```
XX
PD   14-FEB-2002.
XX
PF   [illegible]
XX
PR   [illegible] 2000; [illegible] US-226284P.
PR   28-MAR-2001; 2001US-279763P.
PR   29-JUN-2001; [illegible]
XX
PA   (CORI-) CORIXA CORP.
XX
PI   King GE,  Meagher MJ,  Xu J,  Secrist H;
XX
DR   WPI; 2002-241[illegible]/29.
XX
PT   New colon cancer polypeptides and polynucleotides, useful as vaccines,
PT   for diagnosing, preventing, and treating colon cancer, and as markers
PT   for the progression of cancer -
XX
PS   Claim 1; SEQ ID No 1714; 147pp; English.
XX
CC   The invention relates to polynucleotides encoding colon tumour proteins.
CC   The polynucleotides and encoded polypeptides are useful in pharmaceutical
CC   compositions, such as vaccines, for the diagnosis, prevention, and
CC   treatment of colon cancer. Polynucleotide sequences may be used as
CC   hybridisation probes or primers, and in the design and preparation of
CC   ribozyme molecules for inhibiting expression of tumour polypeptides and
CC   proteins in tumour cells. The compositions are useful for stimulating an
CC   immune response against cancer, particularly for the immunotherapy of
CC   colon cancer, and as markers for the progression of cancer.
CC   ABK41159-ABK46247 represent coding sequences of human colon tumour
CC   proteins of the invention.
CC   Note: With the exception of SEQ ID No 1 and 2, the sequence data
CC   for this patent did not form part of the printed specification but was
CC   supplied by the European Patent Office.
XX
SQ   Sequence 5791 BP; 1436 A; 1312 C; 1395 G; 1648 T; 0 other;

  Query Match             17.6%;  Score 243.4;  DB 24;  Length 5791;
  Best Local Similarity   57.9%;  Pred. No. [illegible]e-47;
  Matches  452;  Conservative    0;  Mismatches  [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy        500 [illegible] 559
Db        [illegible]
Qy        560 [illegible] 619
Db        [illegible]
Qy        620 [illegible] 679
Db        521 [illegible]
Qy        [illegible]
Db        581 [illegible] 64[illegible]
Qy        740 [illegible] 799
Db        641 [illegible] 70[illegible]
Qy        800 [illegible] 859
Db        701 [illegible]
Qy        860 [illegible] 919
Db        761 [illegible] 820
Qy        920 [illegible] 979
Db        [illegible]
Qy        980 [illegible]
Db        881 [illegible]
Qy        1040 [illegible]
Db        941 [illegible]
Qy        [illegible]
Db        1001 [illegible]
Qy        1160 [illegible]
Db        1061 [illegible]
Qy       1217 [illegible] 1276
Db       1121 [illegible]
Qy       1277 G 1277
              |
Db       1181 G 1181


RESULT 11
AAH17958
ID   AAH17958 standard; cDNA; [illegible] BP.
XX
AC   AAH17958;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:[illegible].
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs
XX
PS   Claim 8; SEQ ID NO [illegible]; [illegible]pp; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5' end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3' end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the 5' end and/or
CC   the 3' end sequence/5' end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the protein encoded by
CC   the full length cDNA. The primers allow obtaining of the full length
CC   cDNA easily without any specialised methods. AAH[illegible] to AAH[illegible] and
CC   AAH[illegible] to AAH[illegible] represent human cDNA sequences; AAB[illegible] to
CC   AAB[illegible] represent human amino acid sequences; and AAH[illegible] to AAH[illegible]
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence [illegible] BP; 111 A; [illegible] other;

  Query Match             [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity   [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]
```

```
RESULT 11
AAI[illegible]
ID   AAI[illegible] standard; cDNA; 4[illegible] BP.
XX
AC   AAI[illegible];
XX
DT   16-JAN-[illegible]  (first entry)
XX
DE   Rat petrin cDNA clone DI 413.
XX
KW   Petrin; neurite outgrowth associated protein; CNS;
KW   central nervous system; myelin; protein phosphatase 2C; stroke;
KW   neurodegeneration; gene therapy; ss.
XX
OS   Rattus sp.
XX
PN   WO9[illegible] A1.
XX
PD   [illegible]
XX
PF   12-APR-1996;   96WO-US[illegible].
XX
PR   13-APR-1995;   95US-042[illegible].
XX
PA   (MOUN-) MOUNT SINAI HOSPITAL CORP.
XX
PI   Haber M,  Lozano A,  Roach A,  Roder J;
XX
DR   WPI; 1996-4[illegible].
XX
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, Petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 2; Page 4[illegible]; [illegible]pp; English.
XX
CC   A cDNA clone (AAI[illegible]), designated DI 413, is a fragment of clone
CC   DI (see also AAI[illegible] and AAI[illegible]) that codes for petrin (AAW[illegible]),
CC   a protein involved in mediating neurite growth inhibition. It
CC   was isolated from an adult rat brain cDNA library by screening with
CC   a monoclonal antibody capable of neutralising the inhibition of
CC   neurite growth by several neuronal types on CNS myelin substrates.
CC   The gene is expressed in neurons in brain tissue, partic. in
CC   cerebellum Purkinje cells. It can be used to produce petrin
CC   protein and to prepare probes. Antisense sequences (see also
CC   AAI[illegible]) can be used in gene therapy to enhance axonal regeneration.
XX
SQ   Sequence 47[illegible] BP; 14[illegible] A; 10[illegible] C; 127 G; 107 T; 0 other;

  Query Match             [illegible]; Score [illegible]; DB [illegible]; Length 4[illegible];
  Best Local Similarity   [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
```

```
Db        267 [illegible]

Qy       1054 [illegible] 1113

Db        327 [illegible]

Qy       1114 [illegible]

Db        387 [illegible]

Qy       1174 AA[illegible] 1187

Db        447 AA[illegible]


RESULT 12
AAA[illegible]
ID   AAA[illegible] standard; cDNA; 729 BP.
XX
AC   AAA[illegible];
XX
DT   19-MAY-2000  (first entry)
XX
DE   Human colon cancer cell line polynucleotide sequence SEQ ID NO:[illegible].
XX
KW   Human; colon cancer; tumour; diagnosis; gene expression product;
KW   probe; detection; cancerous state; metastasis; identification;
KW   breast cancer; oestrogen receptor-positive breast cancer; therapy;
KW   oestrogen receptor negative breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   W[illegible]75-A2.
XX
PD   18-NOV-1999.
XX
PF   14-MAY-1999;    99WO-US[illegible].
XX
PR   14-MAY-1998;    98US-[illegible].
PR   15-MAY-1998;    98US-[illegible].
PR   15-MAY-1998;    98US-[illegible].
PR   21-OCT-1998;    98US-0105234.
PR   27-OCT-1998;    98US-0105877.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Williams LT,  Escobedo J,  Innis MA,  Garcia PD,  Sudduth-Klinger J;
PI   Reinhard C,  Giese K,  Randazzo F,  Kennedy GC,  Pot D,  Kassam A;
PI   Lamson G,  Drmanac R,  Crkvenjakov R,  Dickson M,  Drmanac S,  Labat I;
PI   Leshkowitz D,  Kita D,  Garcia V,  Jones LW,  Stache-Crain B;
XX
DR   WPI; 2000-12[illegible]/11.
XX
PT   Polynucleotide library used to determine cancerous states of mammalian
PT   cells -
XX
PS   Claim 1; Page [illegible]; 1097pp; English.
XX
CC   AAA[illegible] to AAA42716 represent polynucleotides isolated from cDNA
CC   libraries constructed from human colon cancer cell lines. The present
CC   invention also describes a method of detecting differentially expressed
CC   genes correlated with a cancerous state of a mammalian cell, comprising
CC   detecting at least one differentially expressed gene product in a test
CC   sample derived from a cell suspected of being cancerous, where detection
CC   of the differentially expressed gene product is correlated with a
CC   cancerous state of the cell from which the test sample was derived.
CC   The polynucleotides sequences can be used in a method for detecting
CC   differentially expressed genes correlated with a cancerous state of a
CC   mammalian cell. The polynucleotides can also be used as probes for
CC   detecting and mapping related genes. They can be used in diagnosis and
CC   prognosis of diseases and disorders (e.g. identification of
CC   pre-metastatic or metastatic cancerous states, stages of cancer, or
CC   responsiveness of cancer to therapy). This is particularly for breast
CC   cancer, oestrogen receptor positive breast cancer, oestrogen receptor
CC   negative breast cancer, lung cancer, and colon cancer.
XX
SQ   Sequence 729 BP; [illegible] A; [illegible] C; [illegible] G; 161 T; 5 other;

  Query Match             [illegible]%;  Score [illegible];  DB 21;  Length 729;
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches [illegible];  Conservative    [illegible];  Mismatches  [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy        891 [illegible]

Db         24 [illegible]

Qy        951 [illegible]

Db         84 [illegible]

Qy       1011 [illegible]

Db        144 [illegible]

Qy       1071 [illegible]

Db        205 [illegible]

Qy       1131 [illegible]

Db        265 [illegible] 324

Qy       1191 [illegible]

Db        325 [illegible]

Qy       1248 [illegible]

Db        385 [illegible] 444

Qy       [illegible]

Db        444 [illegible]

Qy       [illegible]

Db       [illegible]


RESULT 13
AAZ12841
ID   AAZ12841 standard; cDNA; [illegible] BP.
XX
AC   AAZ12841;
XX
DT   [illegible]  (first entry)
XX
DE   Human gene expression product cDNA sequence SEQ ID NO:[illegible].
XX
KW   Human; gene; gene expression product; diagnosis; therapy; probe;
KW   detection; [illegible]; tissue typing; profiling; forensic; cancer;
KW   genetic analysis; [illegible] cancer; breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   W[illegible]-A2.
XX
PD   [illegible] AUG 1999.
XX
PF   28-JAN-1999;    99WO-US[illegible].
XX
PR   06-APR-1998;    98US-[illegible].
PR   28-JAN-1998;    98US-[illegible].
PR   24-FEB-1998;    98US-[illegible].
PR   31-MAR-1998;   98US-0080111.
PR   03-APR-1998;   98US-0080611.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Crkvenjakov R,  Dickson M,  Drmanac R,  Drmanac S;
PI   Escobedo J,  Garcia PD,  Garcia V,  Giese K,  Innis MA;
PI   Jones LW,  Kassam A,  Kennedy GC,  Kita D,  Labat I;
PI   Lamson G,  Leshkowitz D,  Pot D,  Randazzo F,  Reinhard C;
PI   Stache-Crain B,  Sudduth-Klinger J,  Williams LT;
XX
DR   WPI; 1999-404092/41.
XX
PT   Novel human genes and their expression products which are
PT   differentially expressed in different cell types
XX
PS   Claim 1; Page 732-733; 2179pp; English.
XX
CC   The present invention describes a library of human polynucleotides
CC   comprising the sequences given in AAZ12532 to AAZ17779. Also described is
CC   a method of detecting differentially expressed genes correlated with the
CC   cancerous state of a mammalian cell, comprising detecting at least one
CC   differentially expressed gene product in a test sample from a cell
CC   suspected of being cancerous, where the gene product is encoded by one
CC   of the 5218 polynucleotide sequences given in AAZ12532 to AAZ17779. The
CC   polynucleotides can be used as a source of primers and probes, which can
CC   be used for a variety of purposes, e.g. detection of expression levels,
CC   mapping, tissue typing or profiling, forensics, genetic analysis and
CC   detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC   can be used for raising antibodies for experimental, diagnostic and
CC   therapeutic purposes. The polynucleotides may also be used to construct
CC   arrays for diagnostics (which may be used to determine function of an
CC   encoded protein); and to detect differences in expression levels between
CC   two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC   identify a genetic predisposition or susceptibility to a disease such as
CC   cancer). The polynucleotides of the invention are especially used in the
CC   diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC   and lung cancer. The polynucleotides can also be used to screen for
CC   peptide analogues and antagonists.
XX
SQ   Sequence 300 BP; 66 A; 78 C; 91 G; 65 T; 0 other;

  Query Match             7.5%;  Score 103;  DB 26;  Length 300;
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  [illegible];  Conservative    0;  Mismatches  [illegible];  Indels    [illegible];  Gaps    0;

Qy       [illegible]
Db         1 [illegible] 60

Qy       [illegible]
Db        61 [illegible] 120

Qy      1013 [illegible] 1072
Db       121 [illegible] 180

Qy      1073 [illegible] 1132
Db       181 [illegible] 240

Qy      1133 [illegible] 1187
Db       241 [illegible] 295


RESULT 14
AAX[illegible]
ID   AAX[illegible] standard; cDNA; [illegible] BP.
XX
AC   AAX[illegible];
```

```
XX
DT   24-SEP-1999  (first entry)
XX
DE   Human validated cancer cell derived cDNA #276.
XX
KW   Cancer; human; colon; breast; lung; transmembrane receptor; ATPase;
KW   integral membrane protein; aspartyl protease; GATA family; wnt family;
KW   transcription factor; G-protein alpha subunit; protein phosphatase;
KW   phorbolester binding protein; diacylglycerol binding protein; trypsin;
KW   protein kinase; tyrosine phosphatase; developmental signalling protein;
KW   ww/rsp5/WWP domain; therapy; forensic; genetic mapping; diagnostic;
KW   detection; treatment; cervical; melanoma; colorectal adenocarcinoma;
KW   Wilm's tumour; retinoblastoma; sarcoma; myosarcoma; lung carcinoma;
KW   leukemia; lymphoma; dysplasia; hyperplasia; endometrium; adrenal;
KW   prostate; ss.
XX
OS   Homo sapiens.
XX
PN   WO9933982-A2.
XX
PD   08-JUL-1999.
XX
PF   22-DEC-1998;   98WO-US27610.
XX
PR   21-DEC-1998;   98US-0217471.
PR   23-DEC-1997;   97US-0068755.
PR   03-APR-1998;   98US-0080664.
PR   21-OCT-1998;   98US-0105234.
PR   27-OCT-1998;   98US-0105877.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Crkvenjakov R,  Dickson M,  Drmanac R,  Drmanac S;
PI   Escobedo J,  Garcia PD,  Garcia V,  Giese K,  Innis MA;
PI   Jones LW,  Kassam A,  Kennedy GC,  Kita D,  Labat I;
PI   Lamson G,  Leshkowitz D,  Pot D,  Randazzo F,  Reinhard C;
PI   Stache-Crain B,  Sudduth-Klinger J,  Williams LT;
XX
DR   WPI; 1999-433243/36.
XX
PT   New isolated human polynucleotides
XX
PS   Claim 1; Page 524; 561pp; English.
XX
CC   This invention describes novel isolated human polynucleotides obtained
CC   by screening for differential expression in colon cancer, breast cancer
CC   and lung cancer cell lines. The polynucleotides of the invention are
CC   represented in AAX06277-X06318 and encode polypeptides of protein
CC   families selected from 4 transmembrane segments integral membrane
CC   proteins, 7 transmembrane receptors, ATPases associated with various
CC   cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of
CC   transcription factors, G-protein alpha subunit, phorbolesters or
CC   diacylglycerol binding proteins, protein kinase, protein phosphatase 2C,
CC   protein tyrosine phosphatase, trypsin, wnt family of developmental
CC   signalling proteins and ww/rsp5/WWP domain containing proteins. The
CC   encoded polypeptides also have a functional domain selected from Ank
CC   repeat, basic region plus leucine zipper transcription factors,
CC   bromodomain, EF-hand, SH3 domain, WD domain/G-beta repeats, zinc finger
CC   (C2H2 type), zinc finger (CCHC class), and zinc-binding metalloprotease
CC   domain. The polynucleotides encode polypeptides with similarity to known
CC   protein families and are predicted to have similar properties. The novel
CC   polynucleotides can be used to develop products for use as therapeutic
CC   agents and in forensics, genetic analysis, mapping and diagnostic
CC   applications. In particular, the product can be used for the detection
CC   and management of cancers. They can be used for treating e.g. cervical
CC   cancers, melanomas, colorectal adenocarcinomas, Wilm's tumour, sarcomas,
CC   retinoblastoma, myosarcomas, lung carcinomas, leukemias, such as chronic
CC   myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and
CC   myeloid leukemia, and lymphomas such as histiocytic lymphoma, anhydrotic
CC   hereditary ectodermal dysplasia, congenital alveolar dysplasia,
CC   epithelial dysplasia of the cervix, fibrous dysplasia of bone, and
CC   mammary dysplasia, hyperplasias, e.g. endometrial, adrenal, breast,
CC   prostate or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of
CC   the skin.
XX
SQ   Sequence 75[illegible] BP; 179 A; 20[illegible] C; 182 G; 180 T; 1[illegible] other;

  Query Match             [illegible]%;  Score 102.8;  DB 2[illegible];  Length 7[illegible];
  Best Local Similarity   54.1%;  Pred. No. 2.[illegible]e-11;
  Matches  257;  Conservative    0;  Mismatches  19[illegible];  Indels   1[illegible];  Gaps   [illegible];

Qy        904 [illegible] 96[illegible]
Db         58 [illegible] 1[illegible]7

Qy        [illegible]64 [illegible] 1[illegible]
Db        118 [illegible] 177

Qy       1024 [illegible] 108[illegible]
Db        178 [illegible] 2[illegible]7

Qy       1084 [illegible] 11[illegible]
Db        2[illegible] [illegible] 2[illegible]

Qy       1144 [illegible] 1[illegible]
Db        29[illegible] [illegible] [illegible]

Qy       120[illegible] [illegible] 12[illegible]
Db        [illegible]58 [illegible] [illegible]17

Qy       12[illegible] [illegible] 1[illegible]
Db        418 [illegible] 47[illegible]

Qy       1308 [illegible] 1[illegible]
Db        478 [illegible] 5[illegible]


RESULT 15
ABL25549
ID   ABL25549 standard; DNA; 2087 BP.
XX
AC   ABL25549;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 2[illegible].
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   W[illegible]171042-A[illegible].
XX
PD   27-SEP-2[illegible]1.
XX
PF   2[illegible]-MAR-2[illegible]; 2[illegible]WO-US0923[illegible]1.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE-) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PW,  Myers EW;
XX
DR   WPI; 2001-[illegible]/75.
XX
PT   New isolated nucleic acid detection reagent for detecting [illegible] or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions
XX
PS   Claim 1; SEQ ID NO 2812; [illegible]pp; Sequence listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 10 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL[illegible]1840-ABL[illegible]) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2087 BP; 51[illegible] A; [illegible]82 C; 594 G; 401 T; 0 other;

  Query Match             [illegible]%;  Score [illegible];  DB 2[illegible];  Length 2[illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  287;  Conservative    [illegible];  Mismatches  25[illegible];  Indels   [illegible];  Gaps   [illegible];

Qy        [illegible]41 [illegible]
Db       1112 [illegible] 11[illegible]

Qy        [illegible]01 [illegible] [illegible]
Db       1172 [illegible] 12[illegible]

Qy        [illegible]61 [illegible] [illegible]
Db       1232 [illegible] 12[illegible]

Qy        921 [illegible] 980
Db       1292 [illegible] 1[illegible]

Qy        [illegible]81 [illegible] 1[illegible]
Db       1352 [illegible] 14[illegible]

Qy       1041 [illegible] 1[illegible]
Db       1412 [illegible] 1471

Qy       1101 [illegible]---         -------------- ----    [illegible] 11[illegible]
Db       1472 [illegible] 15[illegible]

Qy       11[illegible]7 [illegible] 1[illegible]
Db       15[illegible]2 [illegible] 1[illegible]

Qy       1197 [illegible] 12[illegible]
Db       1592 [illegible] 1[illegible]

Qy       [illegible]257 [illegible] [illegible]
Db       1652 [illegible] 1[illegible]75


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          Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                3: [illegible]:*
                4: [illegible]:*
                5: [illegible]:*
                6: [illegible]:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
               %
Result         Query
   No.   Score Match Length DB  ID                          Description
  ----   ----- ----- ------ --  ----------------            --------------
c    1    49.8   3.6   6714  4  US-09-299-141-6             Sequence 6, Appli
c    2    49.8   3.6   6924  4  US-09-299-141-9             Sequence 9, Appli
c    3    49.8   3.6   6924  4  US-09-299-141-10            Sequence 10, Appl
c    4    49.8   3.6   6924  4  US-09-299-141-11            Sequence 11, Appl
c    5    48.2   3.5   1491  4  US-09-082-092-9             Sequence 9, Appli
c    6    48.2   3.5   1817  4  US-09-288-292A-45           Sequence 45, Appl
     7      47   3.4    349  4  US-09-198-1197-94           Sequence 94, Appl
c    8    45.4   3.3    774  3  US-08-415-655-11            Sequence 11, Appl
c    9    45.2   3.3    645  4  US-09-535-008-30            Sequence 30, Appl
    10    44.6   3.2 152431  3  US-09-128-155-16            Sequence 16, Appl
c   11    43.4   3.1   1488  4  US-09-096-776B-3            Sequence 3, Appli
c   12    43.4   3.1   2534  4  US-09-096-776B-1            Sequence 1, Appli
c   13    43.2   3.1   5946  3  US-09-083-351-1             Sequence 1, Appli
c   14    43.2   3.1   [illegible]  1  [illegible]          Sequence 1, Appli
c   15      43   3.1   1028  4  US-08-118-200-1             Sequence 1, Appli
c   16      43   3.1   1028  4  US-08-455-715-1             Sequence 1, Appli
    17    42.8   3.1   8460  1  US-08-469-005A-9            Sequence 9, Appli
    18    42.8   3.1   8519  4  US-09-261-007-1             Sequence 1, Appli
c   19    42.4   3.1    326  4  US-09-165-264-7             Sequence 7, Appli
c   20    42.4   3.1    329  4  US-09-165-264-13            Sequence 13, Appl
c   21    41.4   3.0    319  4  US-09-165-264-8             Sequence 8, Appli
    22    41.4   3.0   4252  2  US-08-475-844-4             Sequence 4, Appli
    23    41.4   3.0   4252  5  PCT-US95-08423-4            Sequence 4, Appli
    24    41.2   3.0   1413  4  US-08-984-709A-52           Sequence 52, Appl
    25    41.2   3.0   6453  1  US-08-306-691B-14           Sequence 14, Appl
    26    41.2   3.0   6453  3  US-09-299-866-10            Sequence 10, Appl
    27    41.2   3.0   6453  3  US-09-356-952-8             Sequence 8, Appli
    28    41.2   3.0  12[illegible]  1  US-08-458-568A-11   Sequence 11, Appl
c   29    40.8   3.0   [illegible]  3  US-08-726-214-1      Sequence 1, Appli
c   30    40.8   3.0   4523  1  US-09-473-716-1             Sequence 1, Appli
c   31    40.4   2.9   3332  4  US-09-423-890-11            Sequence 11, Appl
c   32    40.2   2.9   8438  1  US-07-545-283-1             Sequence 1, Appli
c   33      40   2.9   1413  4  US-08-984-709A-52           Sequence 52, Appl
c   34    39.8   2.9   [illegible]  4  US-09-165-264-11     Sequence 11, Appl
c   35    39.6   2.9   7218  1  US-08-232-463-14            Sequence 14, Appl
c   36    39.4   2.9    700  4  US-09-236-097-7             Sequence 7, Appli
c   37    39.4   2.9   2502  1  US-08-073-384-7             Sequence 7, Appli
c   38    39.4   2.9   2502  1  US-08-254-359A-7            Sequence 7, Appli
c   39    39.4   2.9   2502  1  US-08-483-043-7             Sequence 7, Appli
c   40    39.4   2.9   2502  1  US-08-181-258-7             Sequence 7, Appli
c   41    39.4   2.9   2502  2  US-08-471-968-7             Sequence 7, Appli
c   42    39.4   2.9   2502  2  US-08-184-956-7             Sequence 7, Appli
c   43    39.4   2.9   2502  2  US-08-757-653-7             Sequence 7, Appli
c   44    39.4   2.9   2502  2  US-08-599-491-7             Sequence 7, Appli
c   45    39.4   2.9   2502  2  US-08-756-386-7             Sequence 7, Appli

                              ALIGNMENTS

RESULT 1
US-09-299-141-6/c
; Sequence 6, Application US/09299141
; Patent No. 64[illegible]
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: [illegible]
;  APPLICANT: [illegible], MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: 1999-04-23
;  EARLIER APPLICATION NUMBER: 60/083,025
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.
; SEQ ID NO 6
;   LENGTH: 6714
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p43[illegible]
US-09-299-141-6

  Query Match             3.6%;  Score 49.8;  DB 4;  Length 6714;
  Best Local Similarity   54.7%;  Pred. No. 0.0093;
  Matches   99;  Conservative    0;  Mismatches   82;  Indels    [illegible];  Gaps    [illegible];

Qy         19 [illegible]
              [illegible]
Db       1652 [illegible]

Qy         79 [illegible]
              [illegible]
Db       1[illegible] [illegible]

Qy        139 [illegible]
              [illegible]
Db       15[illegible] [illegible]

Qy        199 [illegible]

Db       1472 [illegible]


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US-09-299-141-9/c
; Sequence 9, Application US/09299141
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: 60/08[illegible],025
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.[illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p43[illegible]GENT AT
US-09-299-141-[illegible]

  Query Match             [illegible];  Score [illegible];  DB 4;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy      [illegible]
Db   1[illegible]2 [illegible]

Qy      [illegible]
Db   1[illegible]2 [illegible]

Qy      [illegible]
Db   1[illegible] [illegible]

Qy      [illegible]

Db   1[illegible]


RESULT [illegible]
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; Sequence [illegible], Application US/[illegible]141
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]/299,141
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: 60/08[illegible],025
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.[illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p43[illegible]GENT[illegible] AT
US-[illegible]-141-10

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  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy      [illegible]
Db   1[illegible]2 [illegible]

Qy      7[illegible] [illegible]
Db   1[illegible]2 [illegible]

Qy      1[illegible] [illegible] 198
Db   1742 [illegible]

Qy      [illegible]

Db   1[illegible]2 [illegible]


RESULT 4
US-09-299-141-11/c
; Sequence 11, Application US/09299141
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: 4[illegible]00.011800
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: 1999-04-23
;  EARLIER APPLICATION NUMBER: 60/08[illegible],025
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 1[illegible]
;  SOFTWARE: PatentIn Ver. 2.[illegible]
; SEQ ID NO 11
;   LENGTH: [illegible]24
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p43[illegible]GENT[illegible] AT
US-09-299-141-11

  Query Match             [illegible];  Score [illegible];  DB 4;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches  8[illegible];  Indels  [illegible];  Gaps  [illegible];

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Db   1[illegible]2 [illegible]

Qy      7[illegible] [illegible]
Db   1[illegible]2 [illegible]

Qy      1[illegible] [illegible]
Db   1742 [illegible]

Qy      [illegible]

Db   1[illegible]2 [illegible]


RESULT 5
US-[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;     APPLICANT:  Nakai, Atsuhito
;     APPLICANT:  [illegible], Anita
;     APPLICANT:  [illegible], Rainer
;    APPLICANT:  Itoh, Susumu
;    APPLICANT:  Afrakhte, Mozhgan
;    APPLICANT:  Souchelnytskyi, Serhiy
;    APPLICANT:  Brodin, Greger
;    APPLICANT:  Landstrom, Marene
;    APPLICANT:  Heldin, Nils-Erik
;    APPLICANT:  Heldin, Carl Henrik
;    APPLICANT:  ten Dijke, Peter
;    TITLE OF INVENTION:  SMAD7 AND USES THEREOF
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  [illegible]
;      FILING DATE:  20-MAY-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/047,221
;      FILING DATE:  20-MAY-1997
;      APPLICATION NUMBER:  60/060,465
;      FILING DATE:  30-SEP-1997
;      APPLICATION NUMBER:  60/075,940
;      FILING DATE:  25-FEB-1998
;      APPLICATION NUMBER:  60/077,[illegible]
;      FILING DATE:  06-MAR-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  [illegible]461/70[illegible]2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO: [illegible]:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-[illegible]

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  Best Local Similarity   54.1%;  Pred. No. 0.015;
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Db        302 [illegible] 243

Qy         65 [illegible] 124

Db        242 [illegible] 183

Qy        125 [illegible] 184

Db        182 [illegible] 123

Qy        185 [illegible] 185

Db        122 [illegible] 122
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RESULT 6
US-09-288-292A-45/c
; Sequence 45, Application US/09288292A
; Patent No. 6359194
; GENERAL INFORMATION:
;  APPLICANT: Dean A. Falb
;  APPLICANT:  Katherine Galvin
;  APPLICANT:  Michael Donovan
;  APPLICANT:  Dennis Huszar
;  APPLICANT:  Michael A. Gimbrone, Jr.
;  TITLE OF INVENTION: Compositions and Methods for the Treatment and Diagnosis of
;  TITLE OF INVENTION:  Cardiovascular Disease
;  FILE REFERENCE: 7853-146-999
;  CURRENT APPLICATION NUMBER: US/09/288,292A
;  CURRENT FILING DATE:  1999-04-08
;  PRIOR APPLICATION NUMBER: 08/870,4[illegible]4
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: 08/799,[illegible]
;  PRIOR FILING DATE: 1997-02-13
;  PRIOR APPLICATION NUMBER: [illegible]/011,787
;  PRIOR FILING DATE: 1996-02-16
;  PRIOR APPLICATION NUMBER: 08/487,[illegible]
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/386,844
;  PRIOR FILING DATE: 1995-02-10
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
;   LENGTH: 1817
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-288-292A-45

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Db        476 [illegible]

Qy         65 [illegible] 124

Db        [illegible]

Qy        125 [illegible] 184

Db        [illegible]

Qy        185 [illegible] 185
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Db        [illegible] 276


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US-09-198-[illegible]-94
; Sequence 94, Application US/[illegible]
; Patent No. 6417428
; GENERAL INFORMATION:
;  APPLICANT:  Thomashow, Michael
;  APPLICANT:  Stockinger, Eric
;  APPLICANT:  Jaglo-Ottosen, Kirsten
;  APPLICANT:  Gilmour, Sarah
;  APPLICANT:  Zarka, Daniel
;  APPLICANT:  Jiang, Cai Zhong
;  TITLE OF INVENTION:  Plant Having Altered Environmental Stress Tolerance
;  FILE REFERENCE:  [illegible] Seq List
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE:  1998-11-2[illegible]
;  PRIOR APPLICATION NUMBER:  US 08/706,270
;  PRIOR FILING DATE:  1998-09-04
;  PRIOR APPLICATION NUMBER:  US [illegible]
;  PRIOR FILING DATE:  [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1998 [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: [illegible]
;   FEATURE:
;   OTHER INFORMATION: [illegible]
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  Best Local Similarity   [illegible];  Pred. No. [illegible];
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Db   [illegible]

Qy   [illegible]
Db   [illegible]

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Db   [illegible]


RESULT [illegible]
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; Patent No. [illegible]
; GENERAL INFORMATION:
;    APPLICANT: [illegible]
;    APPLICANT: [illegible]
;    TITLE OF INVENTION: [illegible]
;    TITLE OF INVENTION: p[illegible]KIP[illegible], A CYCLIN DEPENDENT KINASE INHIBITOR AND USES [illegible]
;    TITLE OF INVENTION: SAME
;    NUMBER OF SEQUENCES: [illegible]
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE: [illegible]
;      STREET: [illegible] Avenue of the Americas
;      CITY: New York
;      STATE: New York
;      COUNTRY: United States of America
;      ZIP: [illegible]
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.[illegible]
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: [illegible]
;      FILING DATE:
;      CLASSIFICATION: [illegible]
;    ATTORNEY/AGENT INFORMATION:
;      NAME: [illegible]
;      REGISTRATION NUMBER: [illegible]
;      REFERENCE/DOCKET NUMBER: [illegible]
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (212) [illegible]
;      TELEFAX: (212) [illegible]
;  INFORMATION FOR SEQ ID NO: [illegible]
;    SEQUENCE CHARACTERISTICS:
;      LENGTH: 774 base pairs
;      TYPE: nucleic acid
;      STRANDEDNESS: single
;      TOPOLOGY: linear
;    MOLECULE TYPE: cDNA
;    HYPOTHETICAL: NO
;    ANTI-SENSE: NO
US-08-[illegible]

  Query Match             [illegible];  Score 46.4;  DB [illegible];  Length 774;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

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Db   [illegible]

Qy   [illegible]
Db   712 [illegible]

Qy   15[illegible]
Db   652 CCCCGGCCCCGG[illegible]CCGGACGCGGCGCCTCAAGAGAGCGC 61[illegible]


RESULT [illegible]
US-09-535-008-30/c
; Sequence 30, Application US/09535008
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible], Alexander K.[illegible]
;  APPLICANT: Tavtigian, Sean V.
;  APPLICANT: [illegible], David H. F.
;  TITLE OF INVENTION: [illegible] IS A TUMOR SUPPRESSOR THAT IS MUTATED IN [illegible] STATE
;  TITLE OF INVENTION: AND OTHER CANCER TYPES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/535,008
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: U.S. 60/12[illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-535-008-[illegible]

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  Matches [illegible];  Conservative    0;  Mismatches   8[illegible];  Indels [illegible];  Gaps [illegible];

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Db   4[illegible]

Qy   [illegible]
Db   4[illegible]

Qy   [illegible]
Db   [illegible]

Qy   186 A[illegible] 191

Db   [illegible]


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; Sequence [illegible], Application US/[illegible]
; Patent No. 6117654
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;  TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 09491/252001
;  CURRENT APPLICATION NUMBER: US/09/128,155
;  CURRENT FILING DATE: 1998-08-03
;  EARLIER APPLICATION NUMBER: US 60/091,650
;  EARLIER FILING DATE: 1998-07-02
;  EARLIER APPLICATION NUMBER: US 60/054,646
;  EARLIER FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 152331
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(152331)
;   OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

  Query Match             3.1%;  Score 43.6;  DB 9;  Length 152331;
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Db    21997 GCCCCCCCCCCGCGCCCCCACCCCCCCGCCCCCCCGCCCCCCCCCCCCCCCCCCACCC 22056

Qy       63 GCCTGGGCCGCATGCCAGCCCCGTGCCCTACCGACGGCCCCCCTTCCTTCCCGCCTCCAG 122
                ||      |||        ||   |  |     ||     ||||| |||||     ||    | |    |  |
Db    22057 CCCACACCCGGCCCACACGCACCCCCCACCCCGACGCCCCCGCCCCCCCCCCCCCCCCAGC 22116

Qy      123 CTCCAGCCCCGGGCCGGCCGACCCCTCCCCCCCCCACACTCCCGGCCCCTCCCCAGCCC 182
              |    |   ||||       || |||  |  |    |  |||    |||  ||| |||    |   |       |   |    |||
Db    22117 CGACGCCCCCCCCCCCGCCCGCCCCGCCCCGCACCCCCGACCCCCCCCGCCGCCCCCCCC 22176

Qy      183 CGCACGAGGACGCACGCTACCC 204
              ||| |      |  |   ||   |||
Db    22177 CCCCCCCCCCCCCCCCCCCCCC 22198


RESULT 11
US-09-096-776B-3/c
; Sequence 3, Application US/09096776B
; Patent No. 6270994
; GENERAL INFORMATION:
;  APPLICANT:  Miyazono, Kohei
;  APPLICANT:  Kawabata, Masahiro
;  TITLE OF INVENTION:   SMAD6 AND USES THEREOF
;  FILE REFERENCE:   L0461/7038
;  CURRENT APPLICATION NUMBER:  US/09/096,776B
;  CURRENT FILING DATE:  1998-06-12
;  PRIOR APPLICATION NUMBER:   US 60/049,990
;  PRIOR FILING DATE:   1997-06-13
;  PRIOR APPLICATION NUMBER:   US 60/053,040
;  PRIOR FILING DATE:   1997-07-18
;  PRIOR APPLICATION NUMBER:   US 60/066,173
;  PRIOR FILING DATE:   1997-11-18
;  NUMBER OF SEQ ID NOS:   10
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1488
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-096-776B-3

  Query Match             3.1%;  Score 43.4;  DB 4;  Length 1488;
  Best Local Similarity   52.5%;  Pred. No. 0.2;
  Matches   95;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy        5 CCGCCGGCTGGTTCCGGCGCCGCTTCCTGCCTGGGGAGCCGCTCCCCGCGCCGCGGCCGC 64
              ||   |    |  |     ||| |  |||      |    |||| ||||| |     |      ||| ||    ||
Db      299 CCAGCCCGGCCTCCGACTCCGACACGGGCCTCGGGAGGCGCCCTGTGGCCGGCGCCTG 240

Qy       65 CTGGGCCGCATGCCAGCCCCGTGCCCTACCGACGGCCCCCCTTCCTTCCCGCCTCCAGCT 124
              |   |      |   |  |   | |     |  || ||||      ||    |       |    |  |||  |
Db      239 CCCGCGATCGCGGCGCCTCGCGGTCCGACGGAGTCCCGGGGCCGCCGGGGGCTACCGAG 180

Qy      125 CCAGCCCCGGGCCGGCCGACCCCTCCCCCCCCCACACTCCCGGCCCCTCCCCAGCCCCG 184
              |    |   ||| ||||| |   |||||     || |  |    |  |    ||       |  |  ||  |  |
Db      179 CGGACTTCGGAGGGGCTGCAGCCTCGGCCCTCTCGTGCCCGCGGGGCAGCTCACCTCGG 120

Qy      185 C 185
              |
Db      119 C 119


RESULT 12
US-09-096-776B-1/c
; Sequence 1, Application US/09096776B
; Patent No. 6270994
; GENERAL INFORMATION:
;  APPLICANT:  Miyazono, Kohei
,  APPLICANT:  Kawabata, Masahiro
,  TITLE OF INVENTION:   SMAD6 AND USES THEREOF
,  FILE REFERENCE:   L0461/7038
;  CURRENT APPLICATION NUMBER: US/09/096,776B
;  CURRENT FILING DATE:  1998-06-12
;  PRIOR APPLICATION NUMBER:   US 60/049,990
;  PRIOR FILING DATE:   1997-06-13
;  PRIOR APPLICATION NUMBER:   US 60/053,040
;  PRIOR FILING DATE:   1997-07-18
;  PRIOR APPLICATION NUMBER:   US 60/066,173
;  PRIOR FILING DATE:   1997-11-18
;  NUMBER OF SEQ ID NOS:   10
,  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 2534
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
,   NAME/KEY: CDS
;   LOCATION: (751)..(2235)
US-09-096-776B-1

  Query Match             3.1%;  Score 43.4;  DB 4;  Length 2534;
  Best Local Similarity   52.5%;  Pred. No. 0.24;
  Matches   95;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy        5 CCGCCGGCTGGTTCCGGCGCCGCTTCCTGCCTGGGGAGCCGCTCCCCGCGCCGCGGCCGC 64
              ||   |    |  |     ||| |  |||      |    |||| ||||| |  |  |      | | ||    ||
Db     1049 CCAGCCCGGCCTCCGACTCCGACACGGGCCTCGGGAGGCGCCCTGTGGCCGGCGCCTG 990

Qy       65 CTGGGCCGCATGCCAGCCCCGTGCCCTACCGACGGCCCCCGGCTTCCTTCCCGCCTCCAGCT 124
              |   |      |   |  |   | |     |  || ||||      ||    |       |    ||  |||  |
Db      989 CCCGCGATCGCGGCGCCTCGCGGTCCGACGGAGTCCCGGGGCCGCCGGGGGCTACCGAG 930

Qy      125 CCAGCCCCGGGCCGGCCGACCCCTCCCCCCCCCACACTCCCGGCCCCTCCCCAGCCCCG 184
              |    |   ||| ||||| |   |||||     || |  |    |  |  |||   |       |  |||| |  |
Db      929 CGGACTTCGGAGGGGCTGCAGCCTCGGCCCTCTCGTGCCCGCGGGGCAGCTCACCTCGG 870

Qy      185 C 185
              |
Db      869 C 869


RESULT 13
US-09-083-351-1/c
; Sequence 1, Application US/09083351
; Patent No. 6087107
;  GENERAL INFORMATION:
,    APPLICANT:  Sheffield, Val C.
```

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;     APPLICANT:  Alward, Wallace L.M.
;     APPLICANT:  Stone, Edwin M.
;     APPLICANT:  Nishimura, Darryl
;     APPLICANT:  Patil, Shiva
;     TITLE OF INVENTION:  THERAPEUTICS AND DIAGNOSTICS FOR
;     TITLE OF INVENTION:  CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
;     TITLE OF INVENTION:  TRANSCRIPTION FACTOR
;     NUMBER OF SEQUENCES:  22
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;       STREET:  One Post Office Square
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02109-2170
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/083,[illegible]
;       FILING DATE:  22 MAY 1998
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Arnold, Beth E.
;       REGISTRATION NUMBER:  35,430
;       REFERENCE/DOCKET NUMBER:  CIA-029.02
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-832-1000
;       TELEFAX:  617-832-7000
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3946 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  475..2133
US-09-083-[illegible]-1

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length 3946;
  Best Local Similarity   57.4%;  Pred. No. 0.3;
  Matches   78;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy         88 [illegible] 147
Db        468 [illegible] 409

Qy        148 [illegible] 207
Db        408 [illegible] 349

Qy        208 AA[illegible] 223
Db        348 [illegible] 333


RESULT 14
US-09-083-[illegible]-1/c
; Sequence 1, Application US/09083[illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;     APPLICANT:  Sheffield, Val C.
;     APPLICANT:  Alward, Wallace L.M.
;     APPLICANT:  Stone, Edwin M.
;     APPLICANT:  Nishimura, Darryl
;     APPLICANT:  Patil, Shiva
;     TITLE OF INVENTION:  GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
;     TITLE OF INVENTION:  BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
;     NUMBER OF SEQUENCES:  22
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;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;       STREET:  One Post Office Square
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02109-2170
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/083,352
;       FILING DATE:  22 MAY 1998
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Arnold, Beth E.
;       REGISTRATION NUMBER:  35,430
;       REFERENCE/DOCKET NUMBER:  UIA-029.01
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-832-1000
;       TELEFAX:  617-832-7000
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  3946 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  475..2133
US-09-083-352-1

  Query Match             [illegible];  Score 43.2;  DB 4;  Length 3946;
  Best Local Similarity   57.4%;  Pred. No. 0.3;
  Matches   78;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy         88 [illegible] 147
Db        468 [illegible] 409

Qy        148 [illegible] 207
Db        408 [illegible] 349

Qy        208 AATGCAGGCTACGCCG 223
Db        348 [illegible] 333


RESULT 15
US-08-118-200-1/c
; Sequence 1, Application US/08118200
; Patent No. 6197500
;  GENERAL INFORMATION:
;     APPLICANT:  SUTHERLAND, Grant R
;     APPLICANT:  RICHARDS, Robert I
;     APPLICANT:  SCHLESSINGER, David
;     APPLICANT:  NAGARAJA, Ramaiah
;     APPLICANT:  KREMER, Eric J
;     APPLICANT:  YU, Sui
;     APPLICANT:  BAKER, Elizabeth
;     APPLICANT:  MULLEY, John C
;     APPLICANT:  MANDEL, Jean-Louis
;     APPLICANT:  PRITCHARD, Melanie April
;     APPLICANT:  LYNCH, Michael
;     TITLE OF INVENTION:  DNA SEQUENCES RELATED TO ISOLATED
;     TITLE OF INVENTION:  FRAGILE X SYNDROME
;     NUMBER OF SEQUENCES:  13
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  [illegible]
;        STREET:  P.O. Box 1404
;        CITY:  Alexandria
;        STATE:  Virginia
;        COUNTRY:  United States
;        ZIP:  22313-1404
;      COMPUTER READABLE FORM:
;        MEDIUM TYPE:  Floppy disk
;        COMPUTER:  IBM PC compatible
;        OPERATING SYSTEM:  PC-DOS/MS-DOS
;        SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;        APPLICATION NUMBER:  US/08/118,200
;        FILING DATE:  09-SEP-1993
;        CLASSIFICATION:  435
;      PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  US 07/802,650
;        FILING DATE:  05 DEC 1991
;      PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  US 07/672,232
;        FILING DATE:  20 MAR 1991
;      PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  US [illegible]
;        FILING DATE:  [illegible] JAN 199[illegible]
;      PRIOR APPLICATION DATA:
;        APPLICATION NUMBER:  US 07/966,517
;        FILING DATE:  23 DEC 1992
;      ATTORNEY/AGENT INFORMATION:
;        NAME:  Crane-Foury, Sharon E
;        REGISTRATION NUMBER:  36,113
;        REFERENCE/DOCKET NUMBER:  020160 164
;      TELECOMMUNICATION INFORMATION:
;        TELEPHONE:  (703) 836-6620
;        TELEFAX:  (703) 836-2021
;    INFORMATION FOR SEQ ID NO:  1:
;      SEQUENCE CHARACTERISTICS:
;        LENGTH:  1028 base pairs
;        TYPE:  nucleic acid
;        STRANDEDNESS:  single
;        TOPOLOGY:  linear
;      MOLECULE TYPE:  DNA (genomic)
US-08-118-200-1

  Query Match              3.1%;  Score 43;  DB 4;  Length 1028;
  Best Local Similarity    57.1%;  Pred. No. [illegible];
  Matches   97;  Conservative    0;  Mismatches   7[illegible];  Indels   [illegible];  Gaps   [illegible];

Qy         45 [illegible] 94

Db        471 [illegible] 422

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Db        421 [illegible] 362

Qy        155 [illegible] 203

Db        361 [illegible] 313


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Job time : 266 secs
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                    GenCore version 5.1.[illegible]
              Copyright (c) 1993 - 2003 Compugen Ltd.

 OM nucleic - nucleic search, using sw model

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Title:          US-09-866-987-3
Perfect score:  1380
Sequence:       1 [illegible]..........[illegible] 1380

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       442118 seqs, 280819700 residues

Total number of hits satisfying chosen parameters:     884236

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Published_Applications_NA:*
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                 2:  [illegible]:*
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                 13: [illegible]:*
                 14: [illegible]:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                               SUMMARIES
                    %
Result            Query
  No.    Score    Match Length DB  ID                          Description
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    1     1380    100.0   1380 10  US-09-866-987-3             Sequence 3, Appl
    2      536     38.8    547 10  US-09-867-701-2068          Sequence 2068, Ap
    3    243.4     17.6   5791 10  US-09-920-366A-1714         Sequence 1714, Ap
    4    243.4     17.6   5791 12  US-10-033-528-1714          Sequence 1714, Ap
    5       98      7.1    551 10  US-09-867-701-5460          Sequence 5460, Ap
c   6     48.2      3.5   1817 10  US-09-924-117-61            Sequence 61, Appl
    7       47      3.4    349  9  US-09-996-141-94            Sequence 94, Appl
c   8     46.8      3.4  43058 10  US-09-954-456-242           Sequence 242, App
c   9     46.8      3.4  43058 10  US-09-954-456-523           Sequence 523, App
c  10     46.8      3.4  43058 10  US-09-880-107-3950          Sequence 3950, Ap
   11     46.4      3.4   3200 10  US-09-925-301-474           Sequence 474, App
   12     44.4      3.2   2561  9  US-09-976-740-48            Sequence 48, Appl
   13     44.4      3.2   2561 12  US-10-023-529-48            Sequence 48, Appl
   14     44.4      3.2   2561 12  US-10-023-523-48            Sequence 48, Appl
c  15     44.2      3.2   4286 10  US-09-899-634A-1            Sequence 1, Appl
c  16     44.2      3.2   5183  9  US-09-954-483A-14           Sequence 14, Appl
c  17     44.2      3.2   6148  9  US-09-954-483A-13           Sequence 13, Appl
   18     43.6      3.2 152301  9  US-10-055-457-18            Sequence 18, Appl
c  19     43.4      3.1   1488 10  US-09-923-922-3             Sequence 3, Appl
c  20     43.4      3.1   2534 10  US-09-923-922-1             Sequence 1, Appl
   21     43.2      3.1   2307  9  US-09-843-519A-87           Sequence 87, Appl
   22       43      3.1   1614  9  US-09-976-740-45            Sequence 45, Appl
   23       43      3.1   1614 12  US-10-023-529-45            Sequence 45, Appl
   24       43      3.1   1614 12  US-10-023-523-45            Sequence 45, Appl
   25       43      3.1  12425  9  US-09-976-740-50            Sequence 50, Appl
   26       43      3.1  12425 12  US-10-023-529-50            Sequence 50, Appl
   27       43      3.1  12425 12  US-10-023-523-50            Sequence 50, Appl
   28     42.2      3.1  42999  9  US-09-799-462A-17           Sequence 17, Appl
   29     42.2      3.1  42999  9  US-10-125-767-17            Sequence 17, Appl
   30     42.2      3.1  42999  9  US-09-855-911A-17           Sequence 17, Appl
c  31     41.4      3.0  12739  9  US-10-032-393-47            Sequence 47, Appl
c  32     41.4      3.0  12739  9  US-10-032-393-8             Sequence 8, Appl
c  33     41.2      3.0    485  9  US-10-034-717-59            Sequence 59, Appl
c  34       41      3.0 155374  9  US-10-026-188-6             Sequence 6, Appl
c  35     40.8      3.0   4523  9  US-10-175-158-1             Sequence 1, Appl
c  36     40.4      2.9    477 10  US-09-864-761-14062         Sequence 14062, A
   37     40.4      2.9   1088 10  US-09-917-800A-1479         Sequence 1479, Ap
   38     40.4      2.9   1155 10  US-09-814-777A-21           Sequence 21, Appl
   39     40.4      2.9   1730 10  US-09-814-777A-19           Sequence 19, Appl
   40     40.4      2.9   1919 10  US-09-814-777A-17           Sequence 17, Appl
c  41     40.4      2.9   3332 12  US-10-000-864-11            Sequence 11, Appl
c  42     40.2      2.9   1157 10  US-09-778-844-166           Sequence 166, App
c  43     40.2      2.9   1183 10  US-09-778-844-167           Sequence 167, App
   44       40      2.9   1496 10  US-09-969-708-132           Sequence 132, App
   45     39.8      2.9   8299  1  US-09-764-879-384           Sequence 384, App

                               ALIGNMENTS

RESULT 1
US-09-866-987-3
; Sequence 3, Application US/09866987
; Patent No. [illegible] A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: MARTINEZ, RICARDO
;  APPLICANT: [illegible], DAVID
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible], JUAN
;  APPLICANT: BELL, RON
;  APPLICANT: [illegible], PETER
;  TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
;  FILE REFERENCE: [illegible]/114
;  CURRENT APPLICATION NUMBER: US/09/866,987
;  CURRENT FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: 60/208,291
;  PRIOR FILING DATE: 2000-05-30
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1380
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: phosphatase nucleotide
US-09-866-987-3

  Query Match             100.0%;  Score 1380;  DB 10;  Length 1380;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1380;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 [illegible]
              [illegible]
Db          1 [illegible]

Qy         [illegible]
              [illegible]
Db         [illegible]
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[illegible]

RESULT 2
US-09-867-[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Algate, Paul A.
;  APPLICANT: Jones, Robert
;  APPLICANT: Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/867,[illegible]
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-867-[illegible]

  Query Match             38.8%;  Score 536;  DB 10;  Length 54[illegible];
  Best Local Similarity   [illegible];  Pred. No. 4.[illegible]e-124;
  Matches [illegible]47;  Conservative    ;  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy        792 [illegible] 8[illegible]
Db          1 [illegible]

[illegible]
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Qy       1332 [illegible] 1339
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Db        540 [illegible] 547


RESULT 3
US-[illegible]-1714
; Sequence 1714, Application US/[illegible]
; Patent No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE:  2001-07-31
;  NUMBER OF SEQ ID NOS: 178[illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1714
;   LENGTH: 5791
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-[illegible]-1714

  Query Match             17.6%;  Score 247.4;  DB [illegible];  Length 5791;
  Best Local Similarity   5[illegible]%;  Pred. No. [illegible];
  Matches  452;  Conservative    [illegible];  Mismatches  [illegible];  Indels    [illegible];  Gaps    [illegible];

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Db        401 [illegible]

Qy        560 [illegible]
Db        461 [illegible]

Qy        620 [illegible]
Db        521 [illegible]

Qy        680 [illegible]
Db        581 [illegible]

Qy        740 [illegible]
Db        641 [illegible]

Qy        800 [illegible]
Db        701 [illegible]

Qy        860 [illegible]
Db        761 [illegible]

Qy        920 [illegible]
Db        821 [illegible]

Qy        980 [illegible]
Db        881 [illegible]

Qy       1040 [illegible]
Db        941 [illegible]

Qy       1100 [illegible]
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Db       [illegible]

Qy       1161 [illegible]
Db       1061 [illegible]

Qy       1217 [illegible]
Db       1121 [illegible]

Qy       1277 G 1277
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Db       1181 G 1181


RESULT 4
US-10-033-528-1714
; Sequence 1714, Application US/[illegible]
; Patent No. US2002[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547C1
;  CURRENT APPLICATION NUMBER: US/10/033,528
;  CURRENT FILING DATE:  [illegible]-12-2[illegible]
;  NUMBER OF SEQ ID NOS: 18[illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1714
;   LENGTH: 579[illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-528-1714

  Query Match             [illegible];  Score 247.4;  DB 12;  Length [illegible];
  Best Local Similarity   57.[illegible]%;  Pred. No. [illegible];
  Matches  452;  Conservative    [illegible];  Mismatches  326;  Indels    [illegible];  Gaps    [illegible];

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       821 [illegible]
```

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[illegible]

RESULT 5
[illegible]
; Sequence [illegible], Application [illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible] A.
;  APPLICANT: [illegible], Robert
;  APPLICANT: [illegible], Susan [illegible]
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: [illegible]
;   OTHER INFORMATION: [illegible]
[illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible]

RESULT 6
US-09-924-417-64/c
; Sequence 64, Application US/09924417
; Patent No. [illegible]
; GENERAL INFORMATION:
;       APPLICANT: [illegible]
;       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;                           THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR
;                           DISEASE
;       NUMBER OF SEQUENCES: [illegible]
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: PENNIE & EDMONDS LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: [illegible]
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: DOS
;             SOFTWARE: FastSEQ Version [illegible]
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/924,417
;             FILING DATE: [illegible]
;             CLASSIFICATION: Unknown
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/[illegible]
;             FILING DATE: [illegible] MAR 1998
;             APPLICATION NUMBER: 08/870,434
;             FILING DATE: [illegible] JUN 1997
;             APPLICATION NUMBER: 08/[illegible]
;             FILING DATE: 13 FEB 1997
;             APPLICATION NUMBER: 60/011,787
;             FILING DATE: [illegible] FEB 1996
;             APPLICATION NUMBER: 08/599,654
;             FILING DATE: 09-FEB-1996
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: 07 JUN 1995
;             APPLICATION NUMBER: 08/[illegible],844
;             FILING DATE: [illegible] FEB [illegible]
;       ATTORNEY/AGENT INFORMATION:
;             NAME: [illegible], Laura A
;             REGISTRATION NUMBER: [illegible]
;             REFERENCE/DOCKET NUMBER: [illegible]
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212)[illegible]
;             TELEFAX: (212)[illegible]
;             TELEX: [illegible] PENNIE
;   INFORMATION FOR SEQ ID NO: 64:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: [illegible] base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: [illegible]
;             TOPOLOGY: unknown
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-09-924-417-64

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]
Db [illegible]

Qy [illegible]
Db [illegible]
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Qy     125 [illegible] 184
           [illegible]
Db     336 [illegible]CAGCTCCG 277

Qy     185 [illegible] 186

Db     276 [illegible] 276


RESULT 7
US-09-996-140-94
; Sequence 94, Application US/09996140
; Patent No. US20020157136A1
; GENERAL INFORMATION:
;  APPLICANT: Thomashow, Michael
;  APPLICANT:  Stockinger, Eric
;  APPLICANT:  Jaglo-Ottosen, Kirsten
;  APPLICANT:  Gilmour, Sarah
;  APPLICANT:  Zarka, Daniel
;  APPLICANT:  Jiang, Cai-Zhong
;  TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL
;  TITLE OF INVENTION:  STRESS TOLERANCE
;  FILE REFERENCE: MRI004US
;  CURRENT APPLICATION NUMBER: US/09/996,140
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: 08/706,270
;  PRIOR FILING DATE: 1996-09-04
;  PRIOR APPLICATION NUMBER: 09/018,233
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/017,816
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,235
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/017,575
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,227
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,234
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/198,119
;  PRIOR FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: PCT/US99/01895
;  PRIOR FILING DATE: 1999-01-28
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94
;    LENGTH: 349
;    TYPE: DNA
;    ORGANISM: Zea maize
US-09-996-140-94

  Query Match             5.4%;  Score 47;  DB 4;  Length 349;
  Best Local Similarity   55.1%;  Pred. No. 0.014;
  Matches   92;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy      19 [illegible] 78
           [illegible]
Db     102 [illegible] 161

Qy      79 [illegible] 138
           [illegible]
Db     162 [illegible] 221

Qy     139 [illegible] 185
           [illegible]
Db     222 [illegible] 268


RESULT 8
US-09-954-456-292/c
; Sequence 292, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using [illegible]
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 68929-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,[illegible]
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,834
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,86[illegible]
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 292
;    LENGTH: 43058
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-954-456-292

  Query Match             5.4%;  Score 46.8;  DB 10;  Length 43058;
  Best Local Similarity   54.7%;  Pred. No. 0.091;
  Matches   93;  Conservative    0;  Mismatches   77;  Indels    0;  Gaps    0;

Qy      18 CCGGCGCCGCTTCCTGCCTGGGCAGCCGCTCCCCGCGCCGCGGCCGCTGGGCCGCATGC 77
           [illegible]
Db   25721 [illegible] 25662

Qy      78 [illegible] 137
           [illegible]
Db   25661 [illegible] 25602

Qy     138 [illegible] 187
           [illegible]
Db   25601 [illegible] 255[illegible]


RESULT 9
US-09-954-456-529/c
; Sequence 529, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using [illegible]
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 68929-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,[illegible]
;   PRIOR FILING DATE: [illegible]
;   PRIOR APPLICATION NUMBER: [illegible]
;   PRIOR FILING DATE: 2000-[illegible]
;   PRIOR APPLICATION NUMBER: [illegible]
;   PRIOR FILING DATE: [illegible]
;   PRIOR APPLICATION NUMBER: US/60/[illegible]
;   PRIOR FILING DATE: 2000-[illegible]
;   PRIOR APPLICATION NUMBER: [illegible]
;   PRIOR FILING DATE: 2000-[illegible]
;   NUMBER OF SEQ ID NOS: [illegible]
;   SOFTWARE: [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-[illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]


RESULT [illegible]
US-[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible], Joseph [illegible]
;  APPLICANT: [illegible], Uwe
;  APPLICANT: Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression in [illegible]
;  FILE REFERENCE: 44[illegible]W
;  CURRENT APPLICATION NUMBER: US/09/[illegible]
;  CURRENT FILING DATE: 2001-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-[illegible]
;  PRIOR APPLICATION NUMBER: US/60/[illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: GenBank Accession No. [illegible]
US-[illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]
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Qy [illegible]

Db 2566[illegible]


RESULT 11
US-09-925-301-474
; Sequence 474, Application US/09925301
; Patent No. US2002[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA[illegible]
;  CURRENT APPLICATION NUMBER: US/09/925,301
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US00/[illegible]
;  PRIOR FILING DATE: 2000-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]/124,[illegible]
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1694
;  SOFTWARE: PatentIn Ver. 2.[illegible]
; SEQ ID NO 474
;   LENGTH: 3209
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (427)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-301-474

  Query Match [illegible].4%; Score 46.4; DB 10; Length 3209;
  Best Local Similarity 48.5%; Pred. No. 0.044;
  Matches 128; Conservative 0; Mismatches 136; Indels [illegible]; Gaps [illegible];

Qy 976 [illegible]

Db 1268 [illegible]

Qy 1036 [illegible]

Db 1328 [illegible]

Qy [illegible]

Db 1388 [illegible]

Qy 1156 [illegible]

Db 1448 [illegible]

Qy 1216 [illegible]

Db 1508 [illegible]


RESULT 12
US-09-976-740-48
; Sequence 48, Application US/09976740
; Publication No. US2002[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Loos, Ann M.
;  APPLICANT: Loos, Robert S.
;  APPLICANT: Law, Simon W.
;  APPLICANT: [illegible], [illegible] A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/09/976,740
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: 09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-09-976-744-48

  Query Match             8.2%;  Score 44.4;  DB 9;  Length 2561;
  Best Local Similarity   55.9%;  Pred. No. 0.13;
  Matches  104;  Conservative    0;  Mismatches   81;  Indels    1;  Gaps    1;

Qy         11 [illegible] 70
Db        620 [illegible] 679

Qy         71 [illegible] 130
Db        680 [illegible] 739

Qy        131 [illegible] 190
Db        740 [illegible] 799

Qy        191 [illegible] 196
Db        800 [illegible] 805


RESULT 15
US-10-023-529-48
; Sequence 48, Application US/10023529
; Patent No. US20020129388A1
; GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT:  Lees, Robert S.
;  APPLICANT:  Law, Simon W.
;  APPLICANT:  Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION:  PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION:  ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/10/023,529
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: 09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-10-023-529-48

  Query Match             8.2%;  Score 44.4;  DB 12;  Length 2561;
  Best Local Similarity   55.9%;  Pred. No. 0.13;
  Matches  104;  Conservative    0;  Mismatches   81;  Indels    1;  Gaps    1;

Qy         11 [illegible] 70
Db        620 [illegible] 679

Qy         71 [illegible] 130
Db        680 [illegible] 739

Qy        131 [illegible] 190
Db        740 [illegible] 799

Qy        191 GGACGC 196
Db        800 GCCCGC 805


RESULT 16
US-10-023-528-48
; Sequence 48, Application US/10023528
; Patent No. US20020127485A1
; GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT:  Lees, Robert S.
;  APPLICANT:  Law, Simon W.
;  APPLICANT:  Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION:  PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION:  ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/10/023,528
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: US/09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-10-023-528-48

  Query Match             8.2%;  Score 44.4;  DB 12;  Length 2561;
  Best Local Similarity   55.9%;  Pred. No. 0.13;
  Matches  104;  Conservative    0;  Mismatches   81;  Indels    1;  Gaps    1;

Qy         11 [illegible] 70
Db        620 [illegible] 679

Qy         71 [illegible] 130
Db        680 [illegible] 739

Qy        131 [illegible] 190
Db        740 [illegible] 799
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[illegible]

[illegible]


RESULT [illegible]
[illegible]
[illegible] APPLICATION [illegible]
[illegible]
GENERAL INFORMATION:
  APPLICANT: Thomas Buchler, [illegible] Andreas [illegible]
  TITLE OF INVENTION: [illegible] and its uses
  FILE REFERENCE: [illegible]
  CURRENT APPLICATION NUMBER: [illegible]
  CURRENT FILING DATE: [illegible]
  NUMBER OF SEQ ID NOS: [illegible]
  SOFTWARE: PatentIn [illegible]
 SEQ ID NO [illegible]
   LENGTH: [illegible]
   TYPE: DNA
   ORGANISM: [illegible]
   FEATURE:
   NAME/KEY: [illegible]
   LOCATION: ([illegible])..([illegible])
[illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible]

[illegible]

[illegible]

[illegible]

[illegible]

Search completed: February [illegible], 2003, [illegible]
Job time : [illegible] secs
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           Copyright (c) 199[illegible] - 200[illegible] Compugen Ltd.

 [illegible] nucleic search, using [illegible] model

Run on:        February 24, 200[illegible] [illegible]
                                          ([illegible])
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Title:         US [illegible]
Perfect score: 1[illegible]
Sequence:      1 atatcc[illegible] [illegible]

Scoring table: IDENTITY_NUC
               Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters:      [illegible]

Minimum DB seq length: [illegible]
Maximum DB seq length: [illegible]

Post-processing: Minimum Match [illegible]
                 Maximum Match 1[illegible]%
                 Listing first 45 summaries

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                 2:  [illegible]_COMB.seq:*
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                 5:  [illegible]_COMB.seq:*
                 6:  [illegible]_COMB.seq:*
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                 8:  [illegible]_COMB.seq:*
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                 14: [illegible]_COMB.seq:*
                 15: [illegible]_COMB.seq:*
                 16: [illegible]_COMB.seq:*
                 17: [illegible]/US0[illegible]_COMB.seq:*
                 18: [illegible]/US0[illegible]_COMB.seq:*
                 19: [illegible]/US095A_COMB.seq:*
                 20: [illegible]_COMB.seq:*
                 21: [illegible]_COMB.seq:*
                 22: [illegible]/US095[illegible]_COMB.seq:*
                 23: [illegible]_COMB.seq:*
                 24: [illegible]_COMB.seq:*
                 25: [illegible]_COMB.seq:*
                 26: [illegible]_COMB.seq:*
                 27: [illegible]/US06[illegible]_COMB.seq:*
                 28: [illegible]_COMB.seq:*
                 29: [illegible]_COMB.seq:*
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                 34: [illegible]_COMB.seq:*
                 35: [illegible]_COMB.seq:*
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                 55: [illegible]_COMB.seq:*
                 56: [illegible]_COMB.seq:*
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                 66: [illegible]_COMB.seq:*
                 67: /cgn2_[illegible]/ptodata/2/pna/US0[illegible]_COMB.seq:*
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                 69: [illegible]_COMB.seq:*
                 70: [illegible]_COMB.seq:*
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                 78: [illegible]_COMB.seq:*
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                 85: [illegible]_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES
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   3    1[illegible] 1[illegible] [illegible] [illegible] [illegible]-18   Sequence [illegible] App
   4    1[illegible] 99.2  18[illegible] [illegible] US [illegible]-181-[illegible]   Sequence [illegible] App
   5    1[illegible] 99.2  18[illegible] [illegible] US [illegible]-988-7   Sequence [illegible] App
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   7    1285  93.1   2110  21  US 09-540-216-1175   Sequence 11[illegible], Ap
   8    1285  93.1   2110  2[illegible]  US 09-[illegible]-1175   Sequence 11[illegible], Ap
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  21    [illegible] [illegible] [illegible] [illegible] US [illegible]-524-[illegible]   Sequence [illegible] App
  26    721.2   52.5     733  17  US-09-[illegible]548A-27        Sequence 27, Appl
  27    [illegible]  52.5  733  [illegible]  US-09-[illegible]   Sequence [illegible], Appl
  28    [illegible]  45.[illegible]  1174  [illegible]  US-09-[illegible]   Sequence [illegible], Ap
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  37      442   42.0     455  [illegible]  US-09-543-143-28521   Sequence 28521, A
  38    [illegible]  41.8  [illegible]  [illegible]  US-60-252-833-32572   Sequence 32572, A
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ALIGNMENTS

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RESULT 1
[illegible]
; Sequence [illegible], Application US/[illegible]
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY D.
;  APPLICANT: MARTINEZ, RICARDO
;  APPLICANT: WHYTE, DAVID
;  APPLICANT: MANNING, GERARD
;  APPLICANT: [illegible]ARGANAM, [illegible]
;  APPLICANT: CAENEPEEL, SEAN
;  APPLICANT: HILL, [illegible]N
;  APPLICANT: FLANAGAN, PETER
;  TITLE OF INVENTION: MAMMALIAN [illegible]
;  FILE REFERENCE: [illegible]/[illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.[illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;     OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;     OTHER INFORMATION: phosphothioate nucleotide
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Db          1 [illegible]

Qy         61 [illegible]
Db         61 [illegible]

Qy        121 [illegible]
Db        121 [illegible]

Qy        181 [illegible] 240
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Qy        241 [illegible] 300
Db        241 [illegible] 300

Qy        301 [illegible] 360
Db        301 [illegible] 360

Qy        361 [illegible] 420
Db        361 [illegible] 420

Qy        421 [illegible] 480
Db        421 [illegible] 480

Qy        481 [illegible] 540
Db        481 [illegible] 540

Qy        541 [illegible] 600
Db        541 [illegible] 600

Qy        601 [illegible] 660
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Qy        661 [illegible] 720
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Qy        721 [illegible] 780
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Qy        781 [illegible] 840
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Qy        841 [illegible] 900
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Qy       1081 [illegible] 1140
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Qy       1201 [illegible] 1260
Db       1201 [illegible] 1260
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Db       1261 ATACACAGTAGACAGGGAAAGGAAGACAGTCTCACAGAGGAAGGGCAGGTGTCCTACGAT 1320

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RESULT 2
PCT-US02-30474-316
; Sequence 316, Application PCT/US0230474
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  [illegible]
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Ghosh, Malabika
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Wang, Zezhi
;  APPLICANT:  Batey-Vicente, Dana
;  APPLICANT:  Drmanac, Radoje T
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 81011 PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/30474
;  CURRENT FILING DATE:  2002-09-24
;  PRIOR APPLICATION NUMBER: US 09/324,631
;  PRIOR FILING DATE: 2000-04-24
;  PRIOR APPLICATION NUMBER: US 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: PCT/US00/35017
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/491,404
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: PCT/US01/02623
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: US 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: PCT/US01/03800
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: US 09/515,126
;  PRIOR FILING DATE: 2000-02-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3476
;  SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 316
;   LENGTH: 2054
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (156)..(1535)
PCT-US02-30474-316

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Db        276 AGCTCCAG[illegible] 335

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Db        336 [illegible] 395

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Db        456 [illegible] 515

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Db        516 [illegible] 575

Qy        421 [illegible] 480
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Db        576 [illegible] 635

Qy        481 [illegible] 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 [illegible] 695

Qy        541 [illegible] 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        696 [illegible] 755

Qy        601 [illegible] 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        756 [illegible] 815

Qy        661 [illegible] 720
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Db        816 [illegible] 875

Qy        721 [illegible] 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        876 [illegible] 935

Qy        781 [illegible] 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        936 [illegible] 995

Qy        841 [illegible] 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        996 [illegible] 1055

Qy        901 [illegible] 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1056 [illegible] 1115

Qy        961 [illegible] 1020
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Db       1116 [illegible] 1175

Qy       1021 [illegible] 1080
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Db       1176 [illegible] 1235

Qy       1081 [illegible] 1140
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Db       1236 [illegible] 1295
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Qy       1141 [illegible] 1200
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Db       1296 [illegible] 1355

Qy       1201 [illegible] 1260
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Qy       1261 [illegible] 1320
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RESULT 5
US-60-324-631-318
; Sequence 318, Application US/60324631
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Jian Rui
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Ghosh, Malabika
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Weng, Gezhi
;  APPLICANT:  Haley Vicente, Dana
;  APPLICANT:  Drmanac, Radoje T
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 810
;  CURRENT APPLICATION NUMBER: US/60/[illegible]
;  CURRENT FILING DATE:  2001-[illegible]
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: PCT/[illegible]
;  PRIOR FILING DATE: 2000-12-[illegible]
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-02-[illegible]
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-03-07
;  PRIOR APPLICATION NUMBER: US 09/574,454
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-03-[illegible]
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-08-23
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: US 09/552,929
;  PRIOR FILING DATE: 2000-04-18
;  PRIOR APPLICATION NUMBER: US 09/770,160
;  PRIOR FILING DATE: 2001-01-26
;  PRIOR APPLICATION NUMBER: PCT/US01/08656
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: US 09/577,408
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: PCT/US01/14827
;  PRIOR FILING DATE: 2001-05-16
;  NUMBER OF SEQ ID NOS: 3334
;  SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 318
;   LENGTH: 2054
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (156)..(1535)
US-60-324-631-318

  Query Match             100.0%;  Score 1380;  DB 76;  Length 2054;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-273;
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Db        156 [illegible] 215

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 CCGCCTGGGCCGCATGCCAGCCCCGTGCCCTACCGACGGCCCCGCTTCCTTCGCGGCTCC 275

Qy        121 AGCTCCAGCCCCGGGGCGGCCGACGCCTCGCGCCGCCCAGACTCCCGGCCCGTGCGCAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 AGCTCCAGCCCCGGGGCGGCCGACGCCTCGCGCCGCCCAGACTCCCGGCCCGTGCGCAGC 335

Qy        181 [illegible] 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 [illegible] 395

Qy        241 [illegible] 300
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Db        396 [illegible] 455

Qy        301 [illegible] 360
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Db        456 [illegible] 515

Qy        361 [illegible] 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 [illegible] 575

Qy        421 [illegible] 480
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Db        576 [illegible] 635

Qy        481 [illegible] 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 [illegible] 695

Qy        541 [illegible] 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        696 [illegible] 755

Qy        601 [illegible] 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        756 [illegible] 815

Qy        661 [illegible] 720
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       816 GCTGTGTCTCTTCAGGGAAAGTTGTACATCGCCAATGCTGGGGATAGCAGGGCCATCTTG 875

Qy       721 GTGCGGACAGATCAGATATGCCCACTGAGCTTCCAGTTGACCCTAGAGACTGAGCGGCAG 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       876 GTGCGGACAGATCAGATATGCCCACTGAGCTTCCAGTTGACCCTAGAGACTGAGCGGCAG 935

Qy       781 GGGATCCAGCAGCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTG 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       936 GGGATCCAGCAGCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTG 995

Qy       841 GAGTTCCCTCGGCGGCTGAAGGGGGATGACTTGGACAGAAGGTTTTGTTCAGGGATCAC 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       996 GAGTTCCCTCGGCGGCTGAACGGGGATGACTTGGACAGAAGGTTTTGTTCAGGGATCAC 1055

Qy       901 CACATGAGTGGCTGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATC 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1056 CACATGAGTGGCTGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATC 1115

Qy       961 CATGGACAGGGTAGGCAGGCTCGGTTACTAGGAACACTGGCTGTCTCCCGGGGCCTGGGA 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1116 CATGGACAGGGTAGGCAGGCTCGGTTACTAGGAACACTGGCTGTCTCCCGGGGCCTGGGA 1175

Qy      1021 GACCATCAGCTCAGAGTCCTGGACACAAACATCCAGCTCAAGCCCTTCTTGCTCTCTGTG 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1176 GACCATCAGCTCAGAGTCCTGGACACAAACATCCAGCTCAAGCCCTTCTTGCTCTCTGTG 1235

Qy      1081 CCACAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1236 CCACAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTC 1295

Qy      1141 ATGGCAACTGATGGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGG 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1296 ATGGCAACTGATGGACTCTGGGATGTACTGTCCAACCAGCACCTGCCATGGCTGGTCCCC 1355

Qy      1201 AGCTTCCTCCCTGGGAACCAAGAGGACCCACACAGGTTCTCAAAGCTGGCCCAGATCCTC 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1356 AGCTTCCTCCCTGGGAACCAAGAGGACCCACACAGGTTCTCAAAGCTGGCCCAGATGCTG 1415

Qy      1261 ATACACAGCACACAGGGAAAGGAAGACAGTCTCACAGAGGAAGGGCAGGTGTCCTACGAT 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1416 ATACACAGCACACAGGGAAAGGAAGACAGTCTCACAGAGGAAGGGCAGGTGTCCTACGAT 1475

Qy      1321 GACGTCTCTGTGTTCGTGATTCCCTTGCACAGTCAGGGCCAAGAGAGCAGTGACCACTGA 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1476 GACGTCTCTGTGTTCGTGATTCCCTTGCACAGTCAGGGCCAAGAGAGCAGTGACCACTGA 1535


RESULT 4
US-10-181-590-13
; Sequence 13, Application US/10181590
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  BANDMAN, Olga
;  APPLICANT:  MATHUR, Preete
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  AZIMZAI, Yalda
;  APPLICANT:  YUE, Henry
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  HILLMAN, Jennifer L.
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  WANG, Eureka
;  APPLICANT:  GANDHI, Ameena R.
;  APPLICANT:  POLICKY, Jennifer L.
;  TITLE OF INVENTION: PHOSPHATASES
;  FILE REFERENCE: PI-0018 PCT
;  CURRENT APPLICATION NUMBER: US/10/181,590
;  CURRENT FILING DATE:  2002-07-19
;  PRIOR APPLICATION NUMBER: 60/177,714; 60/178,[illegible]; 60/181,575; 60/[illegible]
;  PRIOR FILING DATE: 2000-01-21; 2000-01-28; 2000-02-25; 2000-03-17
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: PERL Program
; SEQ ID NO 13
;   LENGTH: 1837
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 1723447CB1
US-10-181-590-13

  Query Match             99.2%;  Score 1366;  DB 41;  Length 1837;
  Best Local Similarity   99.9%;  Pred. No. 6.3e-271;
  Matches 1380;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         1 ATGTCCGCCGGCTGGTTCCGGCGGCGCTTCCTGCCTGGGGAGCCGCTGCCCGGGCCCCGG 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGTCCGCCGGCTGGTTCCGGCGGCGCTTCCTGCCTGGGGAGCCGCTGCCCGGGCCCCGG 60

Qy        61 CCGCCTGGGCCGCATGCCAGCCCCGTGCCCTACCGACGGCCCCGCTTCGCTTCGGGCTCC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CCGCCTGGGCCGCATGCCAGCCCCGTGCCCTACCGACGGCCCCGCTTCGCTTCGGGCTCC 120

Qy       121 AGCTCCAGCCCCGGGGCGGCCGACGCCTCGCCGCCCAGACTCCTCGCCCCGTGCGCAGC 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 AGCTCCAGCCCCGGGGCGGCCGACGCCTCGCCGCCCAGACTCCTCGCCCCGTGCGCAGC 180

Qy       181 CCCGCACGAGGACGCACCCTACCCTGGAATGCAGGCTACGCCGAGATTATCAATGCAGAG 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CCCGCACGAGGACGCACCCTACCCTGGAATGCAGGCTACGCCGAGATTATCAATGCAGAG 240

Qy       241 AAATCTGAATTCAATGAGGATCAAGCCGCCTGTGGGAAGCTGTGCATCCGGAGATGTGAG 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 AAATCTGAATTCAATGAGGATCAAGCCGCCTGTGGGAAGCTGTGCATCCGGAGATGTGAG 300

Qy       301 TTTGGGGCTGAAGAAGAGTGGCTGACCCTGTGCCCAGAGGAGTTCCTGACAGGCCATTAC 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 TTTGGGGCTGAAGAAGAGTGGCTGACCCTGTGCCCAGAGGAGTTCCTGACAGGCCATTAC 360

Qy       361 TGGGCACTGTTCGATGGGCACGGCGGTCCTGCAGCAGCCATCTTGGCTGCCAACACCCTG 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 TGGGCACTGTTCGATGGGCACGGCGGTCCTGCAGCAGCCATCTTGGCTGCCAACACCCTG 420

Qy       421 CACTCCTGCTTGCGCCGGCAGCTGGAGGCCGTGGTGGAAGGCTTGGTGGCCACTCAGGCC 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 CACTCCTGCTTGCGCCGGCAGCTGGAGGCCGTGGTGGAAGGCTTGGTGGCCACTCAGGCC 480

Qy       481 CCCATGCACTTCAATCCCCCGGCATCTGCCCCACTGACCCCACTTTGTCCACCAAAAG 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 CCCATGCACTTCAATCCCCCGGCATCTGCCCCACTGACCCCACTTTGTCCACCAAAAG 540

Qy       541 GGCATCAGGGTAGAAGATTGGTTGATGGGGGCATTGGAGAGTGGCTTTCAGGAATGTGAT 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GGCATCAGGGTAGAAGATTGGTTGATGGGGGCATTGGAGAGTGGCTTTCAGGAATGTGAT 600

Qy       601 GAGGTGATCGGGCGGGAGCTGGAGGGCTCAGGCCAGATGGGCGGCTCCACAGCCCTGGTG 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 GAGGTGATCGGGCGGGAGCTGGAGGGCTCAGGCCAGATGGGCGGCTCCACAGCCCTGGTG 660

Qy       661 GCTGTGTCCCTGCAGGGAAAGCTGTACATCGCCAATGCTGGGGATAGCAGGGCCATCTTG 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 GCTGTGTCCCTGCAGGGAAAGCTGTACATCGCCAATGCTGGGGATAGCAGGGCCATCTTG 720

Qy       721 GTGCGGACAGATCAGATATGCCCACTGAGCTTCCAGTTGACCCTAGAGACTGAGCGGCAG 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 GTGCGGACAGATCAGATATGCCCACTGAGCTTCCAGTTGACCCTAGAGACTGAGCGGCAG 780

Qy       781 GGGATCCAGCAGCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTG 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 GGGATCCAGCAGCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTG 840

Qy       841 GAGTTCCCTCGGCGGCTGAAGGGGGATGACTTGGACAGAAGGTTTTGTTCAGGGATCAC 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 GAGTTCCCTCGGCGGCTGAAGGGGGATGACTTGGACAGAAGGTTTTGTTCAGGGATCAC 900

Qy       901 CACATGAGTGGCTGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATC 960
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; Sequence 7, Application US/0[illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PERL Program
; SEQ ID NO 7
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: [illegible]

  Query Match [illegible]  Score [illegible]  DB [illegible]  Length [illegible]
  Best Local Similarity [illegible]  Pred. No. [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

[illegible]
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Qy       [illegible] [illegible]
                     [illegible]
Db       [illegible] [illegible]

Qy       1320 [illegible] 1379
                     [illegible]
Db       [illegible] [illegible]

Qy       1380 A 1380

Db       1381 A 1381


RESULT 6
US-09-526-996-1047/c
; Sequence 1047, Application US/09526996
; GENERAL INFORMATION:
;  APPLICANT: Shyjan, Andrew W.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM
;  TITLE OF INVENTION: HUMAN PROSTATE AND BREAST LIBRARIES
;  FILE REFERENCE: 1000,1098-001
;  CURRENT APPLICATION NUMBER: US/09/526,996
;  CURRENT FILING DATE: 2000-03-15
;  EARLIER APPLICATION NUMBER: 60/125,469
;  EARLIER FILING DATE: 1999-03-22
;  EARLIER APPLICATION NUMBER: 60/125,560
;  EARLIER FILING DATE: 1999-03-22
;  NUMBER OF SEQ ID NOS: 1296
;  SOFTWARE: FastSEQ for Windows Version 4
; SEQ ID NO 1047
;   LENGTH: 2110
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-526-996-1047

  Query Match             93.1%;  Score 1285;  DB 19;  Length 2110;
  Best Local Similarity   99.9%;  Pred. No. 1.2e-29[illegible];
  Matches 1296;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         85 [illegible] 144
              [illegible]
Db       2110 [illegible] 2051

Qy        145 [illegible] 204
              [illegible]
Db       [illegible] [illegible] 1991

Qy        205 [illegible] 263
              [illegible]
Db       1990 [illegible] 1931

Qy        264 [illegible] 323
              [illegible]
Db       [illegible] [illegible] 1871

Qy        324 [illegible] 383
              [illegible]
Db       [illegible] [illegible] 1811

Qy        384 [illegible] 443
              [illegible]
Db       [illegible] [illegible] 1751

Qy        444 [illegible] 503
              [illegible]
Db       [illegible] [illegible] 1691

Qy        504 [illegible] [illegible]
              [illegible]
Db       [illegible] [illegible] [illegible]

Qy        564 [illegible] 623
              [illegible]
Db       [illegible] [illegible] [illegible]

Qy       [illegible] [illegible]
                     [illegible]
Db       [illegible] [illegible]

Qy        624 [illegible] [illegible]
              [illegible]
Db       [illegible] [illegible] [illegible]

Qy       [illegible] [illegible] [illegible]
              [illegible]
Db       1510 [illegible] [illegible]

Qy        744 [illegible] [illegible]
              [illegible]
Db       1450 [illegible] 1391

Qy        804 [illegible] 863
              [illegible]
Db       [illegible] [illegible] [illegible]

Qy        864 [illegible] [illegible]
              [illegible]
Db       [illegible] [illegible] [illegible]

Qy        924 [illegible] [illegible]
              [illegible]
Db       1270 [illegible] [illegible]

Qy        984 [illegible] [illegible]
              [illegible]
Db       [illegible] [illegible] [illegible]

Qy       1044 [illegible] [illegible]
              [illegible]
Db       1150 [illegible] [illegible]

Qy       1104 [illegible] [illegible]
              [illegible]
Db       1090 [illegible] [illegible]

Qy       1164 [illegible] [illegible]
              [illegible]
Db       1030 [illegible] [illegible]

Qy       1224 [illegible] [illegible]
              [illegible]
Db        970 [illegible] [illegible]

Qy       1284 [illegible] [illegible]
              [illegible]
Db        910 [illegible] [illegible]

Qy       1344 [illegible] 1380
              [illegible]
Db        850 [illegible] 814


RESULT 7
US-09-540-216-1175/c
; Sequence 1175, Application US/09540216
; GENERAL INFORMATION:
;  APPLICANT: Gearing, David P.
;  APPLICANT: Kingsbury, Gillian A.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM
;  TITLE OF INVENTION: HUMAN BONE MARROW AND T CELL LIBRARIES
;  FILE REFERENCE: 1000,1166-001
;  CURRENT APPLICATION NUMBER: US/09/540,216
;  CURRENT FILING DATE: 2000-03-31
;  EARLIER APPLICATION NUMBER: 60/126,[illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 1284
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1175
;   LENGTH: 2110
;   TYPE: DNA
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[illegible]

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RESULT 8
US-09-617-[illegible]-1175/c
; Sequence 1175, Application US/[illegible]
; GENERAL INFORMATION:
;  APPLICANT: Gearing, David P.
;  APPLICANT: Kingsbury, Gillian A.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM
;  TITLE OF INVENTION: HUMAN BONE MARROW AND T CELL LIBRARIES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/617,[illegible]
;  CURRENT FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: 60/126,971
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 1284
;  SOFTWARE: FastSEQ for Windows Version [illegible]
; SEQ ID NO 1175
;   LENGTH: 211[illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-617-[illegible]-1175

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];
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[illegible]

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Db       1750 [illegible] 1691

Qy        504 [illegible] 563
Db       1690 [illegible] 1631

Qy        564 [illegible] 623
Db       1630 [illegible] 1571

Qy        624 [illegible] 683
Db       1570 [illegible] 1511

Qy        684 [illegible] 743
Db       1510 [illegible] 1451

Qy        744 [illegible] 803
Db       1450 [illegible] 1391

Qy        804 [illegible] 863
Db       1390 [illegible] 1331

Qy        864 [illegible] 923
Db       1330 [illegible] 1271

Qy        924 [illegible] 983
Db       1270 [illegible] 1211

Qy        984 [illegible] 1043
Db       1210 [illegible] 1151

Qy       1044 [illegible] 1103
Db       1150 [illegible] 1091

Qy       1104 [illegible] 1163
Db       1090 GGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGATGGACTCTGGGA 1031

Qy       1164 [illegible] 1223
Db       1030 [illegible] 971

Qy       1224 [illegible] 1283
Db        970 [illegible] 911

Qy       1284 [illegible] 1343
Db        910 [illegible] 851

Qy       1344 [illegible] 1383
Db        850 [illegible] 814


RESULT 9
US-09-760-475-724
; Sequence 724, Application US/09760475
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PZ049
;  CURRENT APPLICATION NUMBER: US/09/760,475
;  CURRENT FILING DATE: 2001-01-16
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 724
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (65)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (73)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (83)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (2088)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-760-475-724

  Query Match             [illegible];  Score 127[illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative    0;  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy         75 [illegible] 134
Db          1 [illegible] 60

Qy        135 [illegible] 194
Db         61 [illegible] 120

Qy        195 [illegible] 254
Db        121 [illegible] 179

Qy        255 [illegible] 314
Db        180 [illegible] 239

Qy        315 [illegible] 374
Db        240 [illegible] 299

Qy        375 [illegible] 434
Db        300 [illegible] 359

Qy        435 [illegible] 494
Db        360 [illegible] 419

Qy        495 [illegible] 554
Db        420 [illegible] 479

Qy        555 [illegible] 614
Db        480 [illegible] 539

Qy        615 [illegible] 674
Db        540 [illegible] 598

Qy        675 [illegible] 734
Db        599 [illegible] 658

Qy        735 [illegible] 794
Db        659 [illegible] 718
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Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

[illegible]
[illegible]
; Sequence 2217, Application PCT/US02/30474
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: Zhang, Qing A.
;  APPLICANT: Wang, [illegible]
;  APPLICANT: Weitzman, [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: Ma, Yunqing
;  APPLICANT: [illegible]
;  APPLICANT: Wang, Zhiwei
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION: Polypeptides
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]
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;  PRIOR APPLICATION NUMBER: PCT/US00/[illegible]
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: PCT/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: pt FL genes Version 6.0
; SEQ ID NO 2217
;   LENGTH: 2124
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US02-30474-2217

  Query Match             [illegible];  Score 1239.4;  DB 1;  Length 2124;
  Best Local Similarity   [illegible];  Pred. No. 2.7e-244;
  Matches [illegible];  Conservative    [illegible];  Mismatches    [illegible];  Indels   [illegible];  Gaps    [illegible];

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Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        121 [illegible] 180

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
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Db        661 GAGATACGGGCACTGAGCTTCGAGTTCACCCCAGAGACTGAGCGGCAGCGGATCCAGCAG 720

Qy        793 CTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCCCTCGG 852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCCCTCGG 780

Qy        853 CGGCTGAAGGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCACCACATGAGTGGC 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGCTGAAGGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCACCACATGAGTGGC 840

Qy        913 TGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGACAGGGT 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGACAGGGT 900

Qy        973 AGGCAGGCTCGGTTACTAGGAACACTGGCTGTCTCCGGGGCCTGGGAGACCATCAGCTC 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 [illegible] 960

Qy       1033 [illegible] 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 [illegible] 1020

Qy       1093 [illegible] 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 [illegible] 1080

Qy       1153 GGACTCTGGGATGTACTGTCCAAGGAGCAGGTGGCATGGCTGGTGCGGAGCTTCCTCCCT 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGACTCTGGGATGTACTGTCCAAGGAGCAGGTGGCATGGCTGGTGCGGAGCTTCCTCCCT 1140

Qy       1213 [illegible] 1247
              |||||||||||||||||                          |||||||||||||||||
Db       1141 [illegible] 1200

Qy       1248 GCCCCAGATGCTGATACACAGCACACAGCAAAGGAAGACAGTCTTCACAGAGGAAGGGGA 1307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GCCCCAGATGCTGATACACAGCACACAGCAAAGGAAGACAGTCTTCACAGAGGAAGGGGA 1260

Qy       1308 [illegible] 1367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 [illegible] 1320

Qy       1368 CACTCACCACTGA 1380
              |||||||||||||
Db       1321 CACTCACCACTGA 1333


RESULT 11
PCT-US02-30474-2218
; Sequence 2218, Application PC/TUS0230474
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Jian Rui
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Ghosh, Malabika
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  W[illegible]
;  APPLICANT:  Haley Vicente, Dana
;  APPLICANT:  Drmanac, Radoje T
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 810CIP PCT
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE:  2002-09-24
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: US 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: [illegible]5017
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: PCT/US01/02623
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: US 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]800
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: US 09/515,126
;  PRIOR FILING DATE: 2000-02-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3476
;  SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 2218
;   LENGTH: 2124
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US02-30474-2218

  Query Match             89.8%;  Score 1239.4;  DB 1;  Length 2124;
  Best Local Similarity   97.5%;  Pred. No. 2.7e-244;
  Matches 1.36; [illegible]

Qy         75 [illegible] 134
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db          1 TGGCAGCCCCGTGGTCTACCGACGGGCCCGCTTCCTTCGGCGGCTCCAGCTCCAGCCCGG 60

Qy        135 [illegible] 193
              |||| || ||||  |||||||| |||||||||||||||||||||||||| ||||||||||
Db         61 [illegible] 120

Qy        194 [illegible] 252
              |||||||||||| ||||||||||||||   | |||||||||||||||||| |||||||||
Db        121 [illegible] 180

Qy        253 [illegible] 312
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        181 AATGAGGATCAAGTCACTGTGGGAAGCTGTGCATCCGGAGATGTGAGTTTGGGGTTGAA 240

Qy        313 [illegible] 372
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        241 GAAGACTGACTGACCCTGTGCCCAGAGGAGTTCCTGACAGGCCATTACTGGGCACTGTTC 300

Qy        373 GATGGGCACGGCGGTCCTGCAGCAGCCATCTTGGCTGCCAACACCCTGCACTCCTGCTTG 432
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        301 [illegible] 360

Qy        433 [illegible] 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 [illegible] 420

Qy        493 [illegible] 552
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |
Db        421 [illegible] 480

Qy        553 [illegible] 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 [illegible] 540

Qy        613 [illegible] 672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 [illegible] 600

Qy        673 [illegible] 732
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```
Db        601 [illegible] 660

Qy        733 [illegible] 792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 [illegible] 720

Qy        793 [illegible] 852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 [illegible] 780

Qy        853 [illegible] 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 [illegible] 840

Qy        913 [illegible] 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 [illegible] 900

Qy        973 [illegible] 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 [illegible] 960

Qy       1033 [illegible] 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 [illegible] 1020

Qy       1093 [illegible] 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 [illegible] 1080

Qy       1153 [illegible] 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGGGGAGCTTCCTCCCT 1140

Qy       1213 GGGAACCAAGAGGACCCA     ------ --       -    -CACAGGTTCTCAAAGCT 1247
              ||||||||||||||||||                        |||||||||||||||||
Db       1141 GGGAACCAAGAGGACCCACACAGTCTATCTGCAGGATGGCCTTCACAGGTTCTCAAAGCT 1200

Qy       1248 [illegible] 1307
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 [illegible] 1260

Qy       1308 [illegible] 1367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 [illegible] 1320

Qy       1368 CAGTGACCACTGA 1380
               |||||||||||
Db       1321 CAGTGACCACTGA 1333


RESULT 12
US-09-471-275-7040
; Sequence 7040, Application US/09471275
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: Novel Contigs Obtained
;  TITLE OF INVENTION: From Various Libraries
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/471,275
;  CURRENT FILING DATE: 1999-12-23
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: 1999-03-18
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: 1999-04-15
;  EARLIER APPLICATION NUMBER: US 09/274,861
;  EARLIER FILING DATE: 1999-03-23
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: 1999-03-19
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: 1999-03-26
;  EARLIER APPLICATION NUMBER: US 09/306,[illegible]
;  EARLIER FILING DATE: 1999-05-07
;  EARLIER APPLICATION NUMBER: US 09/399,720
;  EARLIER FILING DATE: 1999-09-21
;  EARLIER APPLICATION NUMBER: [illegible],404,284
;  EARLIER FILING DATE: 1999-09-21
;  EARLIER APPLICATION NUMBER:
;  EARLIER FILING DATE: 1999-12-16
;  NUMBER OF SEQ ID NOS: 10451
;  SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 7040
;   LENGTH: 2124
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (280)...(1504)
;   OTHER INFORMATION: similar to gi2804429 in the genpept database release 114,
;   [illegible] with [illegible] 3.3t00, default parameters
US-09-471-275-7040

  Query Match             89.8%;  Score 1239.4;  DB 18;  Length 2124;
  Best Local Similarity   97.5%;  Pred. No. 2.7e-244;
  Matches 1300;  Conservative    0;  Mismatches    6;  Indels   27;  Gaps    [illegible];

Qy         75 TGCCAGCCCGGTGCCCTACCGACGGCCCCGCTTCCTTCGCGGCTCCAGCTCCAGCCCCGG 134
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCCAGCCCCGTGCCCTACCGACGGCCCCGCTTCCTTCGCGGCTCCAGCTCCAGCCCCGG 60

Qy        135 GGCGGCC-GACGCCTCGGCCGCCCAGACTCCCGGCCCGTGCGCAGCCCCGCACGAGGAC 193
              |||| || ||||| |||||||||| ||||||||||||||||||||||||||||||||||
Db         61 [illegible] 120

Qy        194 [illegible] 252
              ||||||||||||||||||||||||||||     | ||||||||||||||||||||||||
Db        121 [illegible] 180

Qy        253 [illegible] 312
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 [illegible] 240

Qy        313 [illegible] 372
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 [illegible] 300

Qy        373 [illegible] 432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 [illegible] 360

Qy        433 [illegible] 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 [illegible] 420

Qy        493 [illegible] 552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 [illegible] 480

Qy        553 [illegible] 612
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 [illegible] 540

Qy        613 [illegible] 672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 [illegible] 600

Qy        673 [illegible] 732
```

```
Db     601 [illegible]

Qy     733 GAGATAC[illegible] 792
Db     661 GAGATAC[illegible]CCAGAGA[illegible] 720

Qy     793 [illegible]GGCTGGTGAG[illegible] 852
Db     721 [illegible]GGCTGGTGA[illegible] 780

Qy     853 [illegible]AGAAGGTTTTG[illegible] 912
Db     781 [illegible]AGAAGGTTTTG[illegible] 84[illegible]

Qy     913 TGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTAC[illegible]TGAT[illegible]ATGGACA[illegible] 972
Db     841 [illegible]AAATCGGATCTCAAGTA[illegible] 900

Qy     973 AGG[illegible]TAGGAACA[illegible]GGCTG[illegible] 1032
Db     901 AGG[illegible] 960

Qy    1033 [illegible] 1092
Db     961 [illegible]AAA[illegible]GAAG[illegible] 1020

Qy    1093 [illegible]ACAGGAGGATGAT[illegible]AT[illegible]AACTGAT 1152
Db    1021 [illegible]TACAGGAGGATGAT[illegible]AT[illegible]AACTGAT 1080

Qy    1153 [illegible]CAA[illegible]AGGTGG[illegible] 1212
Db    1081 [illegible] 1140

Qy    1213 [illegible]A------------------------A[illegible]AA[illegible] 1247
Db    1141 [illegible]TATTTCCAGCA[illegible]AA[illegible] 1200

Qy    1248 [illegible]AAAG[illegible] 1307
Db    1201 [illegible]GGGAAAGGAAGA[illegible] 1260

Qy    1308 GGTGTCCTACGATGACGTCTCTGTGTTCGTGATTCCCTGCACAGTCACGGGCAAGAGAG 1367
Db    1261 GGTGTCCTACGATGACGTCTCTGTGTTCGTGATTCCCTGCACAGTCACGGGCAAGAGAG 1320

Qy    1368 CAG[illegible]GACCACTGA 1380
Db    1321 CAG[illegible]GA[illegible]A 1333


RESULT 14
US-60-324-631-2198
; Sequence 2198, Application US/60324631
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Jian Rui
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Ghosh, Malabika
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Wang, Gezhi
;  APPLICANT:  [illegible]
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION: Polypeptides
;  FILE REFERENCE: 81[illegible]
;  CURRENT APPLICATION NUMBER: US/60/324,631
;  CURRENT FILING DATE: 20[illegible]-24
;  PRIOR APPLICATION NUMBER: US [illegible]/486,72[illegible]
;  PRIOR FILING DATE: 2[illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]/[illegible]2,[illegible]7
;  PRIOR FILING DATE: 2000-04-2[illegible]
;  PRIOR APPLICATION NUMBER: PCT/US[illegible]/[illegible]
;  PRIOR FILING DATE: 20[illegible]-12-22
;  PRIOR APPLICATION NUMBER: US [illegible]/4[illegible]1,4[illegible]4
;  PRIOR FILING DATE: 2000-0[illegible]-25
;  PRIOR APPLICATION NUMBER: PCT/US01/02623
;  PRIOR FILING DATE: 2001-0[illegible]-25
;  PRIOR APPLICATION NUMBER: US 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: US 09/[illegible],875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: PCT/US01/0[illegible]
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: US 09/515,126
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: US [illegible]/577,409
;  PRIOR FILING DATE: 2000-[illegible]
;  PRIOR APPLICATION NUMBER: PCT/US[illegible]/[illegible]4927
;  PRIOR FILING DATE: 2001-02-2[illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]/[illegible]
;  PRIOR FILING DATE: 2000-0[illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]/[illegible]4,454
;  PRIOR FILING DATE: 2000-0[illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 20[illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]/54[illegible]
;  PRIOR FILING DATE: 20[illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]/[illegible]4[illegible],167
;  PRIOR FILING DATE: 2000-0[illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-[illegible]-30
;  PRIOR APPLICATION NUMBER: US 09/552,929
;  PRIOR FILING DATE: 20[illegible]-13
;  PRIOR APPLICATION NUMBER: US 09/770,160
;  PRIOR FILING DATE: 2001-01-26
;  PRIOR APPLICATION NUMBER: PCT/US01/03656
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: US 09/577,408
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: PCT/US01/14827
;  PRIOR FILING DATE: 2001-05-16
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: pt FL genes Version [illegible]
; SEQ ID NO 2198
;   LENGTH: 2124
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-324-631-2198

  Query Match             [illegible];  Score 12[illegible].4;  DB [illegible];  Length 2124;
  Best Local Similarity   [illegible];  Pred. No. 2.7e-244;
  Matches [illegible];  Conservative  [illegible];  Mismatches  6[illegible];  Indels  [illegible];  Gaps  [illegible];

Qy      75 [illegible]
Db       [illegible]

Qy     135 [illegible]
Db      6[illegible] [illegible]

Qy     1[illegible] [illegible] 25[illegible]
Db     12[illegible] [illegible] 18[illegible]

Qy     2[illegible] [illegible] 312
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[illegible]
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Db      1261 [illegible]

Qy      1308 [illegible]

Db      1321 [illegible]


RESULT 14
US-60-324-631-2199
; Sequence 2199, Application US/60324631
; GENERAL INFORMATION:
;   APPLICANT: Tang, Y. Tom
;   APPLICANT: Zhang, Jie
;   APPLICANT: Ren, Feiyan
;   APPLICANT: Xue, Aidong J.
;   APPLICANT: Zhao, Qing A.
;   APPLICANT: Wang, Jian Rui
;   APPLICANT: Wehrman, Tom
;   APPLICANT: Zhou, Ping
;   APPLICANT: Ghosh, Malabika
;   APPLICANT: Wang, Dunrui
;   APPLICANT: Ma, Yunqing
;   APPLICANT: Asundi, Vinod
;   APPLICANT: Wang, Zhiwei
;   APPLICANT: Weng, Gezhi
;   APPLICANT: Haley Vicente, Dana
;   APPLICANT: Drmanac, Radoje T
;   TITLE OF INVENTION: Novel Nucleic Acids and
;   TITLE OF INVENTION: Polypeptides
;   FILE REFERENCE: 810
;   CURRENT APPLICATION NUMBER: US/60/324,631
;   CURRENT FILING DATE: 2001-09-24
;   PRIOR APPLICATION NUMBER: US 09/488,725
;   PRIOR FILING DATE: 2000-01-21
;   PRIOR APPLICATION NUMBER: US 09/552,317
;   PRIOR FILING DATE: 2000-04-25
;   PRIOR APPLICATION NUMBER: PCT/US00/35017
;   PRIOR FILING DATE: 2000-12-22
;   PRIOR APPLICATION NUMBER: US 09/[illegible]
;   PRIOR FILING DATE: [illegible]
;   PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;   PRIOR FILING DATE: [illegible]
;   PRIOR APPLICATION NUMBER: US 09/[illegible]
;   PRIOR FILING DATE: 2000-02-03
;   PRIOR APPLICATION NUMBER: US 09/560,875
;   PRIOR FILING DATE: 2000-04-27
;   PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;   PRIOR FILING DATE: [illegible]
;   PRIOR APPLICATION NUMBER: US 09/[illegible]
;   PRIOR FILING DATE: [illegible]-28
;   PRIOR APPLICATION NUMBER: US 09/577,409
;   PRIOR FILING DATE: 2000-05-18
;   PRIOR APPLICATION NUMBER: PCT/US01/04927
;   PRIOR FILING DATE: 2001-02-26
;   PRIOR APPLICATION NUMBER: US 09/[illegible]
;   PRIOR FILING DATE: [illegible]
;   PRIOR APPLICATION NUMBER: US 09/574,454
;   PRIOR FILING DATE: 2000-05-19
;   PRIOR APPLICATION NUMBER: PCT/US01/04941
;   PRIOR FILING DATE: [illegible]
;   PRIOR APPLICATION NUMBER: US 09/540,217
;   PRIOR FILING DATE: 2000-03-31
;   PRIOR APPLICATION NUMBER: US 09/649,167
;   PRIOR FILING DATE: 2000-08-23
;   PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;   PRIOR FILING DATE: [illegible]
;   PRIOR APPLICATION NUMBER: US 09/[illegible]
;   PRIOR FILING DATE: [illegible]-04-18
;   PRIOR APPLICATION NUMBER: US 09/770,160
;   PRIOR FILING DATE: 2001-01-26
;   PRIOR APPLICATION NUMBER: PCT/US01/08656
;   PRIOR FILING DATE: 2001-04-18
;   PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/14827
;  PRIOR FILING DATE: 2001-05-16
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: pt_FL_genes Version [illegible]
; SEQ ID NO 2199
;   LENGTH: 2124
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-324-631-2199

  Query Match             89.8%;  Score 1259.4;  DB 76;  Length 2124;
  Best Local Similarity   97.5%;  Pred. No. [illegible];
  Matches [illegible];  Conservative    0;  Mismatches    6;  Indels   27;  Gaps    [illegible];

Qy         75 TGCCAGCCCCGTGCCCTACCGACGGCCCCGGCTTCCTTCGGGGCTCCAGCTCCAGCCCCGG 134
Db          1 TGCCAGCCCCGTGCCCTACCGACGGCCCCGGCTTCCTTCGGGGCTCCAGCTCCAGCCCCGG 60

Qy        135 [illegible]
Db         61 [illegible] 120

Qy        194 [illegible] 252
Db        121 [illegible] 180

Qy        253 [illegible]
Db        181 [illegible] 240

Qy        313 [illegible]
Db        241 [illegible] 300

Qy        373 [illegible]
Db        301 [illegible]

Qy        433 [illegible]
Db        361 [illegible] 420

Qy        493 [illegible]
Db        421 [illegible]

Qy        553 [illegible]
Db        481 [illegible]

Qy        613 [illegible]
Db        541 [illegible]

Qy        673 [illegible]
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Qy        733 [illegible]
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Qy        [illegible]
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Qy        853 [illegible]
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Qy        [illegible]

Db        [illegible]

Qy        [illegible]
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Db        [illegible]

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Qy        [illegible] 1247
Db        [illegible]

Qy        [illegible]
Db        [illegible] 1260

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Db        [illegible]

Qy        [illegible] CAGTGACCACTGA [illegible]
Db        [illegible] CAGTGACCACTGA [illegible]


RESULT [illegible]
US-60-[illegible]
; Sequence [illegible], Application US/[illegible]
; GENERAL INFORMATION:
;  APPLICANT: Hodgson, David M.                     Jones, Anissa L.
;  APPLICANT: Lincoln, Stephen E.            Yu, Jimmy Y.
;  APPLICANT: Russo, Frank D.                       Groenawalt, [illegible]
;  APPLICANT: Spiro, Peter A.                       Panzer, Scott R.
;  APPLICANT: [illegible]                    [illegible], Ann M.
;  APPLICANT: Bratcher, Shawn R.             Wright, Rachel J.
;  APPLICANT: [illegible]                           Chen, [illegible]
;  APPLICANT: [illegible]                           [illegible]
;  APPLICANT: Rosen, [illegible]             Yap, Pierre E.
;  APPLICANT: Shah, Purvi                           [illegible]
;  APPLICANT: [illegible]                    Amshey, [illegible]
;  APPLICANT: Hillman, Jennifer L.                  Fong, Willy [illegible]
;  TITLE OF INVENTION: [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PERL Program
; SEQ ID NO [illegible]
;   LENGTH: 2084
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: [illegible]
US-60-[illegible]

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches 1156;  Conservative    0;  Mismatches    0;  Indels   26;  Gaps    [illegible];

Qy        [illegible]
Db        [illegible]
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Db        173 [illegible] 232

Qy        345 [illegible] 404
Db        233 [illegible] 292

Qy        405 [illegible] 464
Db        293 [illegible] 352

Qy        465 [illegible] 524
Db        353 [illegible] 412

Qy        525 [illegible] 584
Db        413 [illegible] 472

Qy        585 [illegible] 644
Db        473 [illegible] 532

Qy        645 [illegible] 704
Db        533 [illegible] 592

Qy        705 [illegible] 764
Db        593 [illegible] 652

Qy        765 [illegible] 824
Db        653 [illegible] 712

Qy        825 [illegible] 884
Db        713 [illegible] 772

Qy        885 [illegible] 944
Db        773 [illegible] 832

Qy        945 [illegible] 1004
Db        833 [illegible] 892

Qy       1005 [illegible] 1064
Db        893 [illegible] 952

Qy       1065 [illegible] 1124
Db        953 [illegible] 1012

Qy       1125 [illegible] 1184
Db       1013 [illegible] 1072

Qy       1185 [illegible] 1230
Db       1073 [illegible] 1132

Qy       1231 [illegible] 1279
Db       1133 [illegible] 1192

Qy       1280 [illegible] 1339
Db       1193 [illegible] 1252

Qy       1340 [illegible] 1380
Db       1253 [illegible] 1294

Search completed: February 23, 2003, 04:45:48
Job time : 3616 secs
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                    GenCore version 5.1.3
          Copyright (c) 1993 - 2003  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 23, 2003, 03:34:38 , Search time 298 Seconds
                                              (without alignments)
                                              7203.021 Million cell updates/sec

Title:           US-09-866-987-3
Perfect score:   1380
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2856587 seqs, 777717511 residues

Total number of hits satisfying chosen parameters:      5701174

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Database :        Pending_Patents_NA_New:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result           Query
  No.    Score   Match Length DB  ID                           Description
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    1     1346    97.5   2185  6  US-10-072-012-197            Sequence 197, App
    2    843.6    61.1   1285  6  US-10-144-771-11494          Sequence 11494, A
    3      826    59.9   1920  6  US-10-072-012-199            Sequence 199, App
    4    367.2    26.6    476  6  US-10-349-781-54167          Sequence 54167, A
    5    264.8    19.2   2519  6  US-10-212-897-212            Sequence 212, App
    6    263.2    19.1   1180  1  PCT-US02-39126-65            Sequence 65, Appl
    7    262.8    19.0   1691  6  US-10-144-771-12171          Sequence 12171, A
    8      256    18.6    271  6  US-10-349-781-22954          Sequence 22954, A
    9    252.6    18.3   2462  6  US-10-144-771-6858           Sequence 6858, Ap
   10      248    18.0   1481  1  PCT-US02-39126-63            Sequence 63, Appl
   11    243.4    17.6   1887  5  US-09-620-312D-42            Sequence 42, Appl
   12    223.6    16.2    241  6  US-10-349-781-23365          Sequence 23365, A
   13    192.6    14.0   1421  1  PCT-US02-39126-62            Sequence 62, Appl
   14    168.8    12.2   1472  1  PCT-US02-39126-64            Sequence 64, Appl
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   17       51     3.7   1511  7  US-60-427-552-19             Sequence 19, Appl
   18       51     3.7   1511  7  US-60-427-579-19             Sequence 19, Appl
c  19     49.8     3.6   6714  6  US-10-267-117-6              Sequence 6, Appli
c  20     49.8     3.6   6714  6  US-10-340-112-6              Sequence 6, Appli
c  21     49.8     3.6   6924  6  US-10-267-117-9              Sequence 9, Appli
c  22     49.8     3.6   6924  6  US-10-267-117-10             Sequence 10, Appl
c  23     49.8     3.6   6924  6  US-10-267-117-11             Sequence 11, Appl
c  24     49.8     3.6   6921  6  US-10-340-112-9              Sequence 9, Appli
c  25     49.8     3.6   6924  6  US-10-340-112-10             Sequence 10, Appl
c  26     49.8     3.6   6924  6  US-10-340-112-11             Sequence 11, Appl
c  27     49.4     3.6   1477  5  US-09-724-676-19511          Sequence 19511, A
c  28     49.4     3.6   1477  5  US-09-724-676A-19511         Sequence 19511, A
c  29     49.4     3.6   1483  5  US-09-724-676-19546          Sequence 19546, A
c  30     49.4     3.6   1483  5  US-09-724-676A-19546         Sequence 19546, A
c  31     49.4     3.6   1505  5  US-09-724-676-19539          Sequence 19539, A
c  32     49.4     3.6   1505  5  US-09-724-676A-19539         Sequence 19539, A
c  33     49.4     3.6   1511  5  US-09-724-676-19543          Sequence 19543, A
c  34     49.4     3.6   1511  5  US-09-724-676A-19543         Sequence 19543, A
c  35     49.4     3.6   1512  5  US-09-724-676-19521          Sequence 19521, A
c  36     49.4     3.6   1512  5  US-09-724-676A-19521         Sequence 19521, A
c  37     49.4     3.6   1518  5  US-09-724-676-19525          Sequence 19525, A
c  38     49.4     3.6   1518  5  US-09-724-676A-19525         Sequence 19525, A
c  39     49.4     3.6   1525  5  US-09-724-676-19531          Sequence 19531, A
c  40     49.4     3.6   1525  5  US-09-724-676A-19531         Sequence 19531, A
c  41     49.4     3.6   1531  5  US-09-724-676-19535          Sequence 19535, A
c  42     49.4     3.6   1531  5  US-09-724-676A-19535         Sequence 19535, A
c  43     49.4     3.6   1650  5  US-09-724-676-19538          Sequence 19538, A
c  44     49.4     3.6   1650  5  US-09-724-676A-19538         Sequence 19538, A
c  45     49.4     3.6   1678  5  US-09-724-676-19542          Sequence 19542, A

                              ALIGNMENTS

RESULT 1
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; Sequence 197, Application US/10072012
; GENERAL INFORMATION:
;  APPLICANT: Tchernev, Velizar
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Li, Li
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Taupier Jr, Raymond J.
;  APPLICANT:  Gusev, Vladimir Y.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Wolenc, Adam R.
;  APPLICANT:  Pena, Carol E. A
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Grosse, William M.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-258
;  CURRENT APPLICATION NUMBER: US/10/072,012
;  CURRENT FILING DATE:  2002-01-31
;  PRIOR APPLICATION NUMBER: 60/265,102
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/265,514
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,517
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,412
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,395
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/266,406
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 60/266,767
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: 60/267,057
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/266,975
;  PRIOR FILING DATE: 2001-02-07
; [illegible]
; PRIOR FILING DATE: 2001-02-08
; [illegible]
; NUMBER OF SEQ ID NOS: 1301
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 167
; LENGTH: 2185
; TYPE: DNA
; ORGANISM: Homo sapiens
US-[illegible]-167

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  Best Local Similarity   98.3%;  Pred. No. [illegible]e-295;
  Matches 1380;  Conservative    0;  Mismatches    0;  Indels   24;  Gaps    1;

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Db          1 [illegible] 60

Qy         61 [illegible] 120
Db         61 [illegible] 120

Qy        121 [illegible] 180
Db        121 [illegible] 180

Qy        181 [illegible] 240
Db        181 [illegible] 240

Qy        241 [illegible] 300
Db        241 [illegible] 300

Qy        301 [illegible] 360
Db        301 [illegible] 360

Qy        361 [illegible] 420
Db        361 [illegible] 420

Qy        421 [illegible] 480
Db        421 [illegible] 480

Qy        481 [illegible] 540
Db        481 [illegible] 540

Qy        541 [illegible] 600
Db        541 [illegible] 600

Qy        601 [illegible] 660
Db        601 [illegible] 660

Qy        661 [illegible] 720
Db        661 [illegible] 720

Qy        721 [illegible] 780
Db        721 [illegible] 780

Qy        781 [illegible] 840
Db        781 [illegible] 840

Qy        841 [illegible] 900
Db        841 [illegible] 900

Qy        901 [illegible] 960
Db        901 [illegible] 960

Qy        961 [illegible] 1020
Db        961 [illegible] 1020

Qy       1021 [illegible] 1080
Db       1021 [illegible] 1080

Qy       1081 CCACAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 CCACAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTC 1140

Qy       1141 ATGGCAACTGATGGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGG 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATGGCAACTGATGGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGG 1200

Qy       1201 AGCTTCCTCCCTGGGAACCAAGAGGACCCA                        CACAGG 1236
              ||||||||||||||||||||||||||||||                        ||||||
Db       1201 [illegible] CACAGG 1260

Qy       1237 [illegible] 1296
Db       1261 [illegible] 1320

Qy       1297 [illegible] 1356
Db       1321 [illegible] 1380

Qy       1357 GGCCAAGAGAGCAGTGACCACTGA 1380
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Db       1361 GGCCAAGAGAGCAGTGACCACTGA 1404


RESULT 2
US-10-144-771-11494
; Sequence 11494, Application US/10144771
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
;  FILE REFERENCE: CL001321
;  CURRENT APPLICATION NUMBER: US/10/144,771
;  CURRENT FILING DATE:  2002-05-15
;  NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 11494
;   LENGTH: 1285
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-144-771-11494

  Query Match             61.1%;  Score 843.6;  DB 6;  Length 1285;
  Best Local Similarity   85.9%;  Pred. No. 5.6e-182;
  Matches  962;  Conservative    0;  Mismatches  149;  Indels    9;  Gaps    2;

Qy        [illegible] 283
Db        [illegible] 172

Qy        [illegible]
Db        [illegible] 232

Qy        [illegible] 398
Db        [illegible] 292

Qy        [illegible] 458
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Db        293 [illegible] 352

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Db        353 [illegible]GA 412

Qy        519 [illegible]TCAGGTCACAAGA[illegible]GA 578
              .|| ||||| ||||||||||||| |||  |||||||||.||||||||||||||  ||||
Db        413 GCCCCAGTTCGTGGAGGAAAATGGATCCAGGCAGAAGATTTCGTGATCGGGGCTCTGGA 472

Qy        579 [illegible] 638
              ||  |||||| ||||||||||||| ||||| ||| | ||||||||||||||||| ||| |
Db        473 [illegible] 532

Qy        639 [illegible] 698
              ||| ||||| ||||||||||||| |||| |||||| || ||||||||  ||||||||||
Db        533 GGGTGGCTGTACAGGCCTGGTGGCGGTGTTCCTGCAAGGGAAGCTGTATGTGGCCAATGC 592

Qy        699 TGGGGA[illegible]AGTT 758
              |||||| |||||||||||||||||||||||| |||||| |||| ||||| |  |||||
Db        593 TGGGG[illegible]AGTT 652

Qy        759 CA[illegible]AGCTTCC 818
              |||||| | || ||||||||||||||||||||||||||.|.| |||  |||||||||||
Db        653 CAGCCAGAAACAGAGGGGCAGGGGATCCAGGCAGCTGGCT[illegible]ACCTACCTGAGCTTC 712

Qy        819 GGCTGGTGAC[illegible] 878
              |||||| |||||||||||||||||||||| ||||||||| ||||.|||||||||| || ||
Db        713 GGCTGGAGAGTTCACCGGATTGGAGTTCCCAGGGGGGTAAAGGGGGATGACTTAGGGCA 772

Qy        879 CAAGTTTTGTTCAGGGATCACCACATGAGTGGCTGGAGCTACAAATCTGTTCAGAAATT 938
              |||||||.||| ||||||||||| |||||||| ||||||||||||||||| ||||| || ||
Db        773 GAAGGTTTTGTTCAGGGATCATCACATGAGAGGCTGGAGCTACAAACGGGTGGAAAAGTC 832

Qy        939 GGATCTCAAGTACCCACTGATCCATGGACAGGGTAGGCAGGCTCGGTTACTAGGAACACT 998
               |||||||||| | |||||||| ||||||||||||||||||||||  |||||||| |||||||
Db        833 TGATCTCAAGTATCCACTGATTCATGGACAGGGTAGGCAGGCGGCTTACTGGGAACACT 892

Qy        999 [illegible]ACCATCAGTTCAGA[illegible]AAACATCCAGCT 1058
              |||||||||| | || ||||| |||||||||| ||||||||||||||  |||||||||
Db        893 GGCTGTCTCCAGAGGGCTGGGCGACCATCAGCTTAGAGTCCTGGACACCGACATCCAGCT 952

Qy       1059 [illegible]CAGTGACTTCT[illegible]GCACCT 1118
               |||||| || | |||||  | ||||||||||||||||||||.|||  |||||||||  |
Db        953 GAA[illegible]ACAGGTGACTCTCCTGGATGTCCACCAGCTGGCACT 1012

Qy       1119 ACAGGAGGATGATGTGGTTGTCATGGCAACTGATGGACTCTGGGATCTACTGTCCAACCA 1178
               ||||||.|  |||||||||||||||||||||||||| |||||||||| ||||||||| ||
Db       1013 GCAGGAGGAGGATGTGGTTGTCATGGCAACTGATGGGCTCTGGGATGTCCTGTCCAATGA 1072

Qy       1179 GCAGGTGG[illegible]GGGAAG.AA     GAGGACGCACACAG 1235
              ||||||||.||  ||| ||||||||||||||| | ||||||||    || ||||||||||
Db       1073 [illegible] 1132

Qy       1236 [illegible]CAGAACTTCAC 1295
              |||||| || ||||| | ||||||||||||| ||| || ||||||||   |  ||   |||
Db       1133 GTTTCAGAGTTGGCCAAAATGCTGATACACAACATTCAAGGAAAGGA[illegible] 1192

Qy       1296 AGAGGAAGGGCAGGTGTCCTACGATGACGTCTCTGTGTTC 1335
               |  || ||| |||    | |         || |||   |    ||
Db       1193 [illegible]
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RESULT 3
US-[illegible]072-012-199
; Sequence 199, Application US/10072012
; GENERAL INFORMATION
; APPLICANT: Tchernev, Velizar
; APPLICANT: [illegible]
; APPLICANT: Zerhusen, Bryan
; APPLICANT: [illegible]
; APPLICANT: Shimkets, Richard
; APPLICANT: [illegible]
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Taupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: [illegible]
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402 298
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: 60/265,192
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1291
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 199
;   LENGTH: 1930
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-072-012-199

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  Matches 1125;  Conservative    0;  Mismatches    0;  Indels  279;  Gaps    2;

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              ||||||||||||||||||||||||||||||||||||||||||||.||||| ||| | ||
Db          1 ATGTCCGCCGGCTGGTTCCGGCGGCGCTTCCTGCCTGGGGAGCCGCT[illegible] 60

Qy         61 CCGGCTGGGCCGCATGCCAGG[illegible]TACCGAGGGCCCCGGC[illegible] 120
              |||||||||||||||||||||||||||||||||||||||||||||| ||||| ||| |||
Db         61 [illegible]CCGCCCCCGG[illegible] 120

Qy        121 AGCTCCAGCCCCGGGGCGG[illegible]CAGACTCC[illegible] 180
              ||||||||||||||||||||||||||||||||||||||||||||.|||| ||.:|.|
Db        121 AGCTCCAGCCCCGGGGCGG[illegible]CAGACTCCCG[illegible] 180

Qy        181 [illegible] 240
              ||||||||||||||||||||||||||||||||||||||||||||| ||| ||| |||
Db        181 [illegible] 240

Qy        241 [illegible]AATGTGAC 300
              ||||||||||||||||||||||||||||||||||||||||||. |||  ||| || |
Db        241 [illegible]AATGTGAC 300
```

```
Qy        [illegible] [illegible]
                [illegible]
Db        [illegible] [illegible]                                   412

Qy        [illegible] [illegible]
                                                                
Db        [illegible]                                               412

Qy        [illegible] [illegible]

Db        [illegible]                                               412

Qy        [illegible] [illegible]

Db        [illegible]                                               412

Qy        [illegible] [illegible]
                                                              |||
Db        [illegible]                                           GAT 415

Qy        [illegible] [illegible]

Db        [illegible] [illegible]

Qy        [illegible] [illegible]

Db        [illegible] [illegible]

Qy        [illegible] [illegible]

Db        [illegible] [illegible]

Qy        [illegible] [illegible]

Db        [illegible] [illegible]

Qy        [illegible] [illegible]

Db        [illegible] [illegible]

Qy        [illegible] [illegible]

Db        [illegible] [illegible]

Qy        [illegible] [illegible]

Db        [illegible] [illegible]

Qy        [illegible] [illegible]

Db        [illegible] [illegible]                                   825

Qy        [illegible] [illegible]

Db        [illegible] [illegible]                                   885

Qy        [illegible] [illegible]

Db        [illegible] [illegible]                                   945

Qy        [illegible] [illegible]

Db        [illegible] [illegible]

Qy        [illegible] [illegible]

Db        [illegible] [illegible]

Qy        [illegible] [illegible]

Db        [illegible] [illegible]

Qy     1357 [illegible] 1380

Db     1126 GGCCAAGAGAGCAGTGACCACTGA 1149


RESULT 4
US-10-349-781-54167
; Sequence 54167, Application US/10349781
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.; Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.; Stuve, Laura L.
;  APPLICANT:  Mullahy, Sara L.; Naughton, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIV
;  FILE REFERENCE: PF-0528 2 CON
;  CURRENT APPLICATION NUMBER: US/10/349,781
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 09/540,764
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 08/992,868
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: 60/032,838
;  PRIOR FILING DATE: 1996-12-13
;  PRIOR APPLICATION NUMBER: 08/734,050
;  PRIOR FILING DATE: 1996-10-18
;  PRIOR APPLICATION NUMBER: 60/006,111
;  PRIOR FILING DATE: 1995-10-24
;  PRIOR APPLICATION NUMBER: 08/733,014
;  PRIOR FILING DATE: 1996-10-18
;  PRIOR APPLICATION NUMBER: 60/005,864
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: 08/763,920
;  PRIOR FILING DATE: 1996-12-11
;  PRIOR APPLICATION NUMBER: 60/008,294
;  PRIOR FILING DATE: 1995-12-14
;  PRIOR APPLICATION NUMBER: 08/772,283
;  PRIOR FILING DATE: [illegible]
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 61458
;  SOFTWARE: PERL Program
; SEQ ID NO 54167
;   LENGTH: 476
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: hn01061679
US-10-349-781-54167

  Query Match             26.6%;  Score 367.2;  DB 6;  Length 476;
  Best Local Similarity   99.2%;  Pred. No. 5.5e-74;
  Matches  366;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        225 [illegible] 284

Db        105 [illegible] 164

Qy        285 [illegible] 344

Db        165 [illegible] 224

Qy        345 [illegible] 404

Db        225 [illegible] 284

Qy        405 [illegible] 464

Db        285 [illegible] 344

Qy        465 [illegible] 524

Db        345 [illegible] 404

Qy        525 [illegible] 584
```

```
Db    405 [illegible] 464

Qy    585 [illegible]AAIG 596

Db    465 [illegible]AGAAIG 476


RESULT 5
US-10-342-887-312
; Sequence 312, Application US/10342887
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT:  He, Yidong
;  APPLICANT:  [illegible], Peter S.
;  APPLICANT:  Mao, Mao
;  APPLICANT:  Roberts, Christopher J.
;  APPLICANT:  Van 't Veer, Laura Johanna
;  APPLICANT:  Van de Vijver, Marc J.
;  APPLICANT:  Bernards, Rene
;  TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
;  FILE REFERENCE: 9301 188-999
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: 2003-01-15
;  PRIOR APPLICATION NUMBER: 60/298,918
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2002-05-14
;  PRIOR APPLICATION NUMBER: 10/172,118
;  PRIOR FILING DATE: 2002-06-14
;  NUMBER OF SEQ ID NOS: [illegible]
; SEQ ID NO 312
;   LENGTH: 2518
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-342-887-312

  Query Match             19.2%;  Score 261.8;  DB [illegible];  Length 2518;
  Best Local Similarity   57.7%;  Pred. No. 1.5e-5[illegible];
  Matches  537;  Conservative    0;  Mismatches  377;  Indels   16;  Gaps    [illegible];

Qy    445 [illegible]
Db   1369 [illegible] 1428

Qy    505 [illegible]
Db   1424 [illegible]

Qy    565 [illegible] 624
Db   1488 [illegible] 1547

Qy    625 [illegible]
Db   1548 [illegible]

Qy    685 [illegible] 744
Db   1608 [illegible]

Qy    745 [illegible]
Db   1668 [illegible]

Qy    805 [illegible]
Db   1728 [illegible]

Qy    865 [illegible]
Db   1788 [illegible]

Qy    925 [illegible] 984
Db   1848 [illegible]

Qy    985 [illegible]
Db   1908 [illegible]

Qy   1045 [illegible]
Db   1968 [illegible]

Qy   1105 [illegible]
Db   2028 [illegible]

Qy   1165 [illegible] 1221
Db   2088 [illegible]

Qy   1222 [illegible]
Db   2147 [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible] 1359
Db   2263 [illegible] 2297


RESULT 6
PCT-US02-39126-65
; Sequence 65, Application PC/TUS0239126
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  KABLE, Amy E.
;  APPLICANT:  CHIEN, David
;  APPLICANT:  WILSON, Amy D.
;  APPLICANT:  [illegible], Anita
;  APPLICANT:  GORVAD, Ann E.
;  APPLICANT:  BAFALIA, April J.A.
;  APPLICANT:  EMERLING, Brooke M.
;  APPLICANT:  RAMKUMAR, [illegible]
;  APPLICANT:  JIN, [illegible]
;  APPLICANT:  GRIFFIN, Jennifer A.
;  APPLICANT:  MARQUIS, Joseph P.
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  CHAWLA, Narinder K.
;  APPLICANT:  LEHR MASON, Patricia M.
;  APPLICANT:  KHARE, Reena
;  APPLICANT:  LEE, Sally
;  APPLICANT:  HAWKINS, Phillip E.
;  APPLICANT:  BECHA, Shanya D.
;  APPLICANT:  LEE, Soo Yeun
;  APPLICANT:  SPRAGUE, William W.
;  APPLICANT:  ZEBARJADIAN, Yeganeh
;  TITLE OF INVENTION: KINASES AND PHOSPHATASES
;  FILE REFERENCE: PF 1315 PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/39126
;  CURRENT FILING DATE: 2002-12-[illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: US 60/343,546
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: [illegible] sapiens
;  FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: [illegible]
[illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]
Db [illegible]

RESULT [illegible]
US-[illegible]
; Sequence [illegible], Application US/[illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: HUMAN [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
```

```
;  NUMBER OF SEQ ID NOS: [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: HUMAN
US-[illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]
Db [illegible]
Db       1121 [illegible] 1180

Qy       1046 [illegible] 1105
              [illegible]
Db       1181 [illegible] 1240

Qy       1106 [illegible] 1165
              [illegible]
Db       1241 [illegible] 1300

Qy       1166 [illegible] 1221
              [illegible]
Db       1301 [illegible] 1360

Qy       1222 [illegible] 12[illegible]
              [illegible]
Db       1361 [illegible] 1419

Qy       12[illegible] [illegible] 1329
              [illegible]
Db       1420 [illegible] 1479

Qy       1330 [illegible] 1359
              [illegible]
Db       1480 [illegible] 1509


RESULT 8
US-[illegible]-349-781-22954
; Sequence 22954, Application US/1[illegible]349781
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.; [illegible], Angelo M.
;  APPLICANT: Stuart, Susan G.; Stuve, Laura L.
;  APPLICANT: Mullahy, Sara J.; Naughton, Robert E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIVE S
;  FILE REFERENCE: PD-1028-2 CON
;  CURRENT APPLICATION NUMBER: US/10/349,781
;  CURRENT FILING DATE: 2003-01-21
;  PRIOR APPLICATION NUMBER: 09/540,764
;  PRIOR FILING DATE: 2000-0[illegible]
;  PRIOR APPLICATION NUMBER: 08/992,368
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: 60/0[illegible]2,338
;  PRIOR FILING DATE: 1996-12-1[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-10-18
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1995-10-24
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-10-18
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-12-11
;  PRIOR APPLICATION NUMBER: [illegible]8,794
;  PRIOR FILING DATE: 1995-12-14
;  PRIOR APPLICATION NUMBER: 08/772,78[illegible]
;  PRIOR FILING DATE: 1996-12-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 61458
;  SOFTWARE: PERL Program
; SEQ ID NO 22954
;   LENGTH: 271
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. ha00078869
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: [illegible]
;   OTHER INFORMATION: a, t, c, g, or other
US-[illegible]-349-781-22954
```

```
  Query Match             18.8%;  Score 259;  DB 6;  Length 271;
  Best Local Similarity   [illegible];  Pred. No. [illegible]-49;
  Matches  270;  Conservative    0;  Mismatches    1;  Indels    1;  Gaps    1;

Qy       1051 ATCCAGCTCAAGCCCTTCTTGCTCTCTGTGCCACAGGTGACTGTGCTGGATGTGGACTAG 1110
              [illegible]
Db          1 ATCCAGCTCAAGCCCTTCTTGCTCTCTGTGCCACAGGTGACTGTGCTGGATGTGGACTAG 60

Qy       1111 CTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGATGGACTCTGGGATCTACTG 1170
              [illegible]
Db         61 CTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGA[illegible]GGACTCTGGGATCTACTG 120

Qy       1171 [illegible] 1230
              [illegible]
Db        121 [illegible] 179

Qy       1231 [illegible] 1290
              [illegible]
Db        180 [illegible] 239

Qy       1291 [illegible] 1322
              [illegible]
Db        240 [illegible] 271


RESULT 9
US-10-144-771-6858
; Sequence 6858, Application US/10144771
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
;  FILE REFERENCE: CL001321
;  CURRENT APPLICATION NUMBER: US/10/144,771
;  CURRENT FILING DATE: 2002-05-15
;  NUMBER OF SEQ ID NOS: [illegible]
; SEQ ID NO 6858
;   LENGTH: 2462
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-144-771-6858

  Query Match             18.3%;  Score 252.6;  DB 6;  Length 2462;
  Best Local Similarity   [illegible];  Pred. No. [illegible]-48;
  Matches  [illegible];  Conservative    0;  Mismatches  209;  Indels  [illegible];  Gaps  [illegible];

Qy        5[illegible] [illegible] 594
              [illegible]
Db        446 [illegible] 505

Qy        595 [illegible] 654
              [illegible]
Db        5[illegible] [illegible] [illegible]

Qy        655 [illegible] 714
              [illegible]
Db        566 [illegible] 62[illegible]

Qy        715 [illegible] 774
              [illegible]
Db        626 [illegible] [illegible]

Qy        775 [illegible] [illegible]
              [illegible]
Db        686 [illegible] 74[illegible]

Qy        [illegible] [illegible] [illegible]4
              [illegible]
Db        746 [illegible] [illegible]

Qy        [illegible] [illegible] [illegible]54
              [illegible]
Db        [illegible] [illegible] [illegible]
```

```
Qy      [illegible]
        [illegible]
Db      [illegible]

Qy      [illegible]
        [illegible]
Db      [illegible]

Qy      [illegible]
        [illegible]
Db      [illegible]

Qy      [illegible]
        [illegible]
Db      [illegible]

Qy      [illegible]
        [illegible]
Db      [illegible]

Qy      [illegible]
        [illegible]
Db      [illegible]

[illegible]
; [illegible]
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT: KABLE, Amy E.
;  APPLICANT: [illegible]
;  APPLICANT: WILSON, Amy [illegible]
;  APPLICANT: SWARNAKAR, Anita
;  APPLICANT: [illegible], Ann E.
;  APPLICANT: [illegible], April J.A.
;  APPLICANT: EMERLING, Brooke M.
;  APPLICANT: RAMKUMAR, Jayalaxmi
;  APPLICANT: [illegible]
;  APPLICANT: GRIFFIN, Jennifer A.
;  APPLICANT: MARQUIS, Joseph P.
;  APPLICANT: [illegible]
;  APPLICANT: CHAWLA, Narinder K.
;  APPLICANT: LEHR-MASON, Patricia M.
;  APPLICANT: KHARE, Reena
;  APPLICANT: LEE, Sally
;  APPLICANT: HAWKINS, Phillip R.
;  APPLICANT: BECHA, Shanya D.
;  APPLICANT: LEE, Soo Yeun
;  APPLICANT: [illegible]
;  APPLICANT: ZEBARJADIAN, Yeganeh
;  TITLE OF INVENTION: KINASES AND PHOSPHATASES
;  FILE REFERENCE: PF-1305 PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/[illegible]
;  CURRENT FILING DATE: 2002-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PERL Program
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: [illegible]
PCT-US02-[illegible]

  Query Match              [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity    [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy      225 [illegible]
            [illegible]
Db      173 [illegible]

Qy      283 [illegible]
            [illegible]
Db      233 [illegible]

Qy      [illegible]
            [illegible]
Db      290 [illegible]

Qy      403 [illegible]
            [illegible]
Db      350 [illegible]

Qy      [illegible]
            [illegible]
Db      411 [illegible]

Qy      [illegible]
            [illegible]
Db      [illegible]

Qy      [illegible]
            [illegible]
Db      [illegible]

Qy      [illegible]
            [illegible]
Db      [illegible]

Qy      [illegible]
            [illegible]
Db      [illegible]

Qy      765 [illegible]
            [illegible]
Db      689 [illegible]

Qy      [illegible]
            [illegible]
Db      [illegible]

Qy      [illegible]
            [illegible]
Db      [illegible]

Qy      [illegible]
            [illegible]
Db      [illegible]

Qy      [illegible]
            [illegible]
Db      [illegible]

Qy      [illegible]
            [illegible]
Db      989 [illegible]

Qy      1125 [illegible]
            [illegible]
Db      1049 [illegible]

Qy      [illegible]
```

```
Db   1109 [illegible] 1168

Qy   1248 [illegible] 1287

Db   1169 [illegible] 1228

Qy   1288 [illegible] 1347

Db   1229 [illegible] 1288

Qy   1348 TATATTTATTTT 1359

Db   1289 TTATTTTTATTTT 1300


RESULT 11
US-09-620-312D-42
; Sequence 42, Application US/09620312D
; GENERAL INFORMATION:
;  APPLICANT: [illegible], Y. Tom
;  APPLICANT: Liu, Chenghua
;  APPLICANT: Asundi, Vinod
;  APPLICANT: Zhang, Jie
;  APPLICANT: Ren, Feiyan
;  APPLICANT: Chen, Rui-hong
;  APPLICANT: Zhao, Qing A.
;  APPLICANT: Wehrman, Tom
;  APPLICANT: [illegible]
;  APPLICANT: Yang, Yonghong
;  APPLICANT: Wang, Jian-Rui
;  APPLICANT: Zhou, Ping
;  APPLICANT: Ma, Yunqing
;  APPLICANT: Wang, Dunrui
;  APPLICANT: Wang, [illegible]
;  APPLICANT: John Tillinghast
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION: Polypeptides
;  FILE REFERENCE: 784CIP2B
;  CURRENT APPLICATION NUMBER: US/09/620,312D
;  CURRENT FILING DATE: 2000-07-19
;  PRIOR APPLICATION NUMBER: 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  NUMBER OF SEQ ID NOS: 1195
;  SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 42
;   LENGTH: 1887
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (55)..(1563)
US-09-620-312D-42

  Query Match             17.6%;  Score 249.1;  DB 5;  Length 1887;
  Best Local Similarity   57.9%;  Pred. No. 9.7e-16;
  Matches  452;  Conservative    0;  Mismatches  329;  Indels    [illegible];  Gaps    [illegible];

Qy    500 [illegible] 559

Db    677 [illegible] 736

Qy    560 [illegible] 619

Db    737 [illegible] 796

Qy    620 TGGAGGCCTCAGGCCAGATGGGGAGGTGGCACAGGCCTGGTGGCTGTGGCCCTGCAGGGAA 679

Db    797 [illegible] 856

Qy    680 [illegible] 739

Db    857 [illegible] 916

Qy    740 [illegible] 799

Db    917 [illegible] 976

Qy    800 [illegible] 859

Db    977 [illegible] 1036

Qy    860 [illegible] 919

Db   1037 [illegible] 1096

Qy    920 [illegible] 979

Db   1097 [illegible] 1156

Qy    980 [illegible] 1039

Db   1157 [illegible] 1216

Qy   1040 [illegible] 1099

Db   1217 [illegible] 1276

Qy   1100 [illegible] 1159

Db   1277 [illegible] 1336

Qy   1160 [illegible] 1219

Db   1337 [illegible] 1396

Qy   1220 [illegible] 1276

Db   1397 [illegible] 1456

Qy   1277 G 1277
          |
Db   1457 G 1457


RESULT 12
US-10-349-781-2885
; Sequence 2885, Application US/10349781
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.; Delegeane, Angelo M.
;  APPLICANT: Stuart, Susan G.; Stowe, Laura L.
;  APPLICANT: Mullaly, Sara J.; Naughton, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIV
;  FILE REFERENCE: PD-1028 2 CON
;  CURRENT APPLICATION NUMBER: US/10/349,781
;  CURRENT FILING DATE: 2003-01-2[illegible]
;  PRIOR APPLICATION NUMBER: 09/[illegible]
;  PRIOR FILING DATE: 2000-0[illegible]
;  PRIOR APPLICATION NUMBER: 08/992,[illegible]
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: 60/[illegible]
;  PRIOR FILING DATE: 1996-12-1[illegible]
;  PRIOR APPLICATION NUMBER: 08/[illegible]
;  PRIOR FILING DATE: 1996-1[illegible]
;  PRIOR APPLICATION NUMBER: 60/[illegible]
;  PRIOR FILING DATE: 1995-1[illegible]-24
;  PRIOR APPLICATION NUMBER: 60/[illegible],814
;  PRIOR FILING DATE: 1996-1[illegible]-18
;  PRIOR APPLICATION NUMBER: 60/005,864
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: 08/[illegible]
;  PRIOR FILING DATE: 1996-12-11
;  PRIOR APPLICATION NUMBER: 60/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PERL Program
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: [illegible]
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: [illegible]
;   OTHER INFORMATION: [illegible] or other
US-[illegible]

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy   [illegible] [illegible] 944

Db   [illegible] [illegible]

Qy   [illegible] [illegible] 1004

Db   [illegible] [illegible] 120

Qy   1005 [illegible] 1064

Db    121 [illegible] 180

Qy   1065 [illegible] 1124

Db    181 [illegible] 240

Qy   [illegible]

Db   [illegible]


RESULT [illegible]
US-[illegible]
; Sequence [illegible], Application US/[illegible]
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT: KABLE, Amy E.
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: SWARNAKAR, Anita
;  APPLICANT: [illegible]
;  APPLICANT: HAFALIA, April J. A.
;  APPLICANT: EMERLING, Brooke M.
;  APPLICANT: RAMKUMAR, Jayalaxmi
;  APPLICANT: [illegible]
;  APPLICANT: GRIFFIN, Jennifer A.
;  APPLICANT: MARQUIS, Joseph P.
;  APPLICANT: BAUGHN, Mariah R.
;  APPLICANT: CHAWLA, Narinder K.
;  APPLICANT: [illegible]
;  APPLICANT: KHARE, Reena
;  APPLICANT: LEE, Sally
;  APPLICANT: HAWKINS, Phillip R.
;  APPLICANT: [illegible]
;  APPLICANT: LEE, [illegible]
;  APPLICANT: SPRAGUE, William W.
;  APPLICANT: ZEBARJADIAN, Yeganeh
;  TITLE OF INVENTION: KINASES AND PHOSPHATASES
;  FILE REFERENCE: [illegible] PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PERL Program
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: [illegible]
PCT-US02-[illegible]

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy    710 [illegible]

Db    577 [illegible]

Qy    770 [illegible] 829

Db    637 [illegible] 696

Qy    830 [illegible] 889

Db    697 [illegible] 756

Qy    890 [illegible]

Db    757 [illegible]

Qy    [illegible]

Db    [illegible]

Qy    [illegible]

Db    [illegible]

Qy    [illegible]

Db    [illegible]

Qy    [illegible]

Db    [illegible]

Qy    [illegible]

Db    [illegible]

Qy    1241 [illegible]

Db    1117 [illegible]

Qy    [illegible]

Db    1177 [illegible]

Qy    [illegible]

Db    1237 [illegible] 1241
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PCT-US02-39126-64
; Sequence 64, Application PC/TUS0239126
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  KABLE, Amy E.
;  APPLICANT:  [illegible], David
;  APPLICANT:  WILSON, Amy D.
;  APPLICANT:  SWARNAKAR, Anita
;  APPLICANT:  GORVAD, Ann E.
;  APPLICANT:  HAFALIA, April J.A.
;  APPLICANT:  EMERLING, Brooke M.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  JIN, Pei
;  APPLICANT:  GRIFFIN, Jennifer A.
;  APPLICANT:  MARQUIS, Joseph P.
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  CHAWLA, Narinder K.
;  APPLICANT:  LEHR-MASON, Patricia M.
;  APPLICANT:  KHARE, Reena
;  APPLICANT:  LEE, Sally
;  APPLICANT:  HAWKINS, Phillip R.
;  APPLICANT:  BECHA, Shanya D.
;  APPLICANT:  LEE, Soo Youn
;  APPLICANT:  SPRAGUE, William W.
;  APPLICANT:  ZEBARJADIAN, Yeganeh
;  TITLE OF INVENTION: KINASES AND PHOSPHATASES
;  FILE REFERENCE: PF-1315 PCT
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE:  2002-12-06
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2001-12-07
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: US 60/354,[illegible]
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: 2002-02-15
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PERL Program
; SEQ ID NO 64
;   LENGTH: 1472
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 7[illegible]
PCT-US02-39126-64

  Query Match             12.2%;  Score 168.8;  DB 1;  Length 1472;
  Best Local Similarity   65.3%;  Pred. No. 7.7e-29;
  Matches  248;  Conservative    0;  Mismatches  132;  Indels    0;  Gaps    0;

Qy        536 [illegible] 595
              [illegible]
Db        516 [illegible] 575

Qy        596 [illegible] 655
              [illegible]
Db        576 [illegible] 635

Qy        656 [illegible] 715
              [illegible]
Db        636 [illegible] 695

Qy        716 [illegible] 775
              [illegible]
Db        696 [illegible] 755

Qy        776 [illegible] 835
              [illegible]
Db        756 [illegible] 815

Qy        [illegible] 895
              [illegible]
Db        [illegible] 875

Qy        [illegible] 911
              [illegible]
Db        876 [illegible] 891


RESULT 15
US-10-349-781-46051/c
; Sequence 46051, Application US/10349781
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.; Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.; Stowe, Laura L.
;  APPLICANT:  Mulfahy, Sara [illegible]; Nickitan, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIV
;  FILE REFERENCE: PD-[illegible]028 [illegible]N
;  CURRENT APPLICATION NUMBER: US/10/349,781
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 09/540,764
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 08/992,868
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: 60/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1995-10-24
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-10-[illegible]
;  PRIOR APPLICATION NUMBER: 60/[illegible]
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-12-11
;  PRIOR APPLICATION NUMBER: 60/008,794
;  PRIOR FILING DATE: 1995-12-14
;  PRIOR APPLICATION NUMBER: 08/772,783
;  PRIOR FILING DATE: 1996-12-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 61458
;  SOFTWARE: PERL Program
; SEQ ID NO 46051
;   LENGTH: 183
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: [illegible]
US-10-349-781-46051

  Query Match             4.[illegible]%;  Score [illegible];  DB 6;  Length 183;
  Best Local Similarity   74.5%;  Pred. No. 4.7e-05;
  Matches   79;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy        738 [illegible]
              [illegible]
Db        183 [illegible] 124

Qy        798 [illegible]
              [illegible]
Db        123 [illegible]


Search completed: February [illegible], 2003, [illegible]:47:48
Job time : [illegible]82 secs
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                    GenCore version 5.1.3
          Copyright (c) 1993 - 2003 Compugen Ltd.

 OM nucleic - nucleic search, using sw model

Run on:          February 24, 2003, 03:45:54 ; Search time [illegible] Seconds
                                            (without alignments)
                                            9999.848 Million cell updates/sec

Title:           US-09-866-987-3
Perfect score:   1380
Sequence:        1 atgtccgccggctggttccg..........aagagagcagtgaccactga 1380

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        1[illegible] seqs, 8[illegible] residues

Total number of hits satisfying chosen parameters:      [illegible]

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        EST:*
                1:   em_estba:*
                2:   em_esthum:*
                3:   em_estin:*
                4:   em_estmu:*
                5:   em_estov:*
                6:   em_estpl:*
                7:   em_estro:*
                8:   em_htc:*
                9:   gb_est1:*
                10:   gb_est2:*
                11:   gb_htc:*
                12:   gb_est3:*
                13:   gb_est4:*
                14:   gb_est5:*
                15:   em_estfun:*
                16:   em_estom:*
                17:   gb_gss:*
                18:   em_gss_hum:*
                19:   em_gss_inv:*
                20:   em_gss_pln:*
                21:   em_gss_vrt:*
                22:   em_gss_fun:*
                23:   em_gss_mam:*
                24:   em_gss_mus:*
                25:   em_gss_other:*
                26:   em_gss_pro:*
                27:   em_gss_rod:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                   %
Result           Query
   No.   Score   Match Length DB  ID                          Description
-------------------------------------------------      ----------------
     1    1027    74.4   1737  11  AK013149                    AK013149 Mus muscu
     2   [illegible].2    [illegible]    [illegible]8  13  BI911268                    BI911268 6030662811
     3     732    [illegible]    796  1[illegible]  AW560759                    AW560759 EST172830
     4   591.6    42.9   1182  11  AK017245                    AK017245 Mus muscu
     5   556.2    40.3    760  13  BI909341                    BI909341 603065418
c    6     547    39.6    547  14  BM719494                    BM719494 UI-E-EJ1
     7     [illegible]    38.8    517   9  AA292266                    AA292266 [illegible]
     8   520.6    37.7    631  12  BG079112                    BG079112 [illegible]
     9     498    36.1    997  13  BM563697                    BM563697 AGENCOURI
    10     498    36.1   1018  13  BM563742                    BM563742 AGENCOURI
    11   496.6    36.0    639   1  AW742365                    AW742365 [illegible]
    12     [illegible]    [illegible]    [illegible]  1[illegible]  [illegible]                    [illegible]
    13   488.6    35.4    [illegible]  1[illegible]  BI344[illegible]                    BI344[illegible] MA
    14   485.4    35.[illegible]    [illegible]  1[illegible]  BI347[illegible]                    BI347[illegible] MA
    15   478.2    34.7    [illegible]  12  BF415112                    BF415112 UI-R-BJ2-
    16   476.4    34.5    [illegible]  1[illegible]  AW654[illegible]                    AW654[illegible] [illegible] MA
    17     473    34.3    473   9  AI924511                    AI924511 wn[illegible]
    18     473    34.3    474  12  BF515449                    BF515449 UI-H-BW1-
    19     468    33.9    600  10  BB308316                    BB308316 BB308316
    20   451.4    32.7    675  10  BB645012                    BB645012 BB645012
    21     447    32.4    447   9  AI924333                    AI924333 wn55009.x
    22   446.2    32.3    757  10  BE613822                    BE613822 [illegible]
    23     433    31.4    581  12  BF419191                    BF419191 UI-R-BJ2
    24     431    31.2   1[illegible]  12  BE31[illegible]                    [illegible]
    25   426.4    30.9    [illegible]  12  BG754[illegible]                    [illegible]
c   26   425.2    [illegible]    372  12  [illegible]                    [illegible]
    27   413.4    30.0    [illegible]4  1[illegible]  AW434[illegible]                    AW434[illegible] UI-R-BJ
    28   409.2    29.7    445   9  AA[illegible]                    AA[illegible]
    29   407.2    29.5    [illegible]1  10  AW434[illegible]                    AW434[illegible] UI-R-BJ
c   30   405.8    29.4    409  13  BM153[illegible]                    BM153[illegible]
    31   397.6    28.8    492   9  AI430626                    AI430626 mr[illegible]
    32   390.4    28.3    667  12  BF509035                    BF509035 UI-H-BI4
    33   387.2    28.1    519   9  AA116600                    AA116600 mn[illegible]
    34     379    27.5    4[illegible]  12  BF[illegible]                    [illegible]
    35     37[illegible]    27.[illegible]    4[illegible]  1[illegible]  AW6[illegible]                    AW6[illegible]
    36   372.2    27.0    6[illegible]7   9  AI2[illegible]                    AI2[illegible] EST2[illegible]
    37   369.2    26.8    4[illegible]  12  BF415064                    BF415064 UI-R-BJ2
    38     367    26.6    4[illegible]  14  W5[illegible]                    W5[illegible]
    39     367    26.6    [illegible]  1[illegible]  BG[illegible]                    [illegible]
    40   363.4    26.3    625  1[illegible]  BB6[illegible]                    BB6[illegible]
    41   360.8    26.1    364  12  BF195641                    BF195641 [illegible]
    42   35[illegible].8    25.9    472   9  AI090672                    AI090672 [illegible]
c   43     356    25.8    626   9  AI011509                    AI011509 EST205964
    44     355    25.7    516  10  AW6[illegible]                    AW6[illegible] MA
    45   351.2    25.4    356  10  BE486088                    BE486088 [illegible] BA

                              ALIGNMENTS

RESULT 1
AK013149
LOCUS       AK013149                  1737 bp    mRNA    linear   HTC [illegible]-JAN-2002
DEFINITION  Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
            enriched library, clone:2810423O19:Protein phosphatase 2C
            containing protein, full insert sequence.
ACCESSION   AK013149
VERSION     AK013149.1  GI:[illegible]
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) 10, 11 days embryo cDNA to mRNA
            clone_lib:RIKEN full-length enriched mouse cDNA library
            clone:2810423O19
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzym. [illegible], 19-44 ([illegible])
  MEDLINE   9927[illegible]
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
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```
REFERENCE   2
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., [illegible] Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   [illegible]
   PUBMED   11076861
REFERENCE   3
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   [illegible]
   PUBMED   11217851
REFERENCE   4  (bases 1 to 1737)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arai,A.,
            Arakawa,T., [illegible], Bono,H., [illegible]
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., [illegible]
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa [illegible], Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-[illegible],
            Fax:81-45-503-[illegible])
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [illegible]AGAGAGAGAAAAGAGAGAGA[illegible]TTTTTTTTTTTTTTTTVN-3', cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. cDNA went
            through one round of normalization to Rot = [illegible] and subtraction to
            Rot = [illegible]. Second strand cDNA was prepared with the primer adapter
            of sequence [illegible]
            [illegible]AGAGAGA[illegible]TTAAATAAATAAAT[illegible] cDNA was cleaved
            with XhoI and SstI. Cloning sites: [illegible] and XhoI [illegible]
            Host: [illegible]
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                     /strain="C57BL/6J"
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                     /db_xref="MGD:MGI:[illegible]"
                     /db_xref="taxon:10090"
                     /clone="2410[illegible]"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="10, 11 days embryo"
     CDS             <1..1362
                     /note="Protein phosphatase 2C containing protein
                     data source:Pfam, source key:PF00481, evidence:ISS
                     putative"
                     /codon_start=1
                     /protein_id="BAB2[illegible].1"
                     /db_xref="GI:128[illegible]"
                     /db_xref="MGD:MGI:[illegible]"
                     /translation="VLPGGPLPEPRLAGPRSSPVPYHRPRRLGSGSSPGAIPASRKP
                     FALEVESAP[illegible]
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                     CVCPSDPQFVEEKGIQAEDLVIGALENAFQECDEVIGRELEASGQVGGCTALVAVFLQ
                     GKLYVANAGDSRAILVRRHEIRQLSSEFTPETERQRIQQLAFIYPELLAGEFIRLEFP
                     [illegible]
                     [illegible]
                     [illegible]
                     SIR"
BASE COUNT      [illegible] a    477 c    [illegible] g    [illegible] t
ORIGIN

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  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
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Qy         [illegible] [illegible]
Db          2 [illegible]

Qy         89 [illegible] 148
Db         62 [illegible] 121

Qy        149 [illegible]
Db        122 [illegible] 181

Qy        209 [illegible] 268
Db        182 [illegible] 241

Qy        269 [illegible]
Db        242 [illegible]

Qy        [illegible] [illegible]
Db        302 [illegible] 361

Qy        [illegible] [illegible]
Db        362 [illegible] 421

Qy        [illegible] [illegible]
Db        422 [illegible] 481

Qy        [illegible] [illegible]
Db        482 [illegible] 541
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Qy        563 [illegible] 622
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Db        542 [illegible] 601

Qy        623 [illegible] 682
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Db        602 [illegible] 661

Qy        683 [illegible] 742
              [illegible]
Db        662 [illegible] 721

Qy        743 [illegible] 802
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Db        722 [illegible] 781

Qy        803 [illegible] 862
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Db        782 [illegible] 841

Qy        863 [illegible] 922
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Db        842 [illegible] 901

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Qy        983 [illegible] 1042
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Db        962 [illegible] 1021

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Db       1022 [illegible] 1081

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Db       1082 [illegible] 1141

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              [illegible]
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              [illegible]
Db       1202 [illegible]

Qy       1283 [illegible]
              [illegible]
Db       1262 [illegible]

Qy       1343 [illegible]
              [illegible]
Db       1322 [illegible]


RESULT 2
BI61126
LOCUS       BI61126                  908 bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible] NIH_MGC_[illegible] Homo sapiens cDNA [illegible] IMAGE:5212[illegible]
            mRNA sequence.
ACCESSION   BI61126[illegible]
VERSION     BI611266.1  GI:1617490[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 908)
  AUTHORS   NIH MGC [illegible]
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11532  row: c  column: 04
            High quality sequence start: 35
            High quality sequence stop: 831.
FEATURES             Location/Qualifiers
     source          1..908
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5212[illegible]"
                     /clone_lib="NIH_MGC_[illegible]"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from [illegible]
                     non-activated adult donors. Library is oligo dT primed
                     and directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb. Library is normalized and enriched for
                     full length clones and was constructed by [illegible]
                     (Invitrogen). Research Genetics tracking code [illegible]. Note:
                     this is a NIH_MGC Library."
BASE COUNT      178 a    252 c    307 g    171 t
ORIGIN

  Query Match             57.5%;  Score 753.2;  DB 13;  Length 908;
  Best Local Similarity   97.8%;  Pred. No. 3.8e-170;
  Matches  857;  Conservative    0;  Mismatches   13;  Indels    [illegible];  Gaps    7;

Qy         83 [illegible] 142
              [illegible]
Db         35 [illegible]

Qy        143 [illegible] 202
              [illegible]
Db         95 [illegible]

Qy        203 [illegible] 262
              [illegible]
Db        155 [illegible] 214

Qy        263 [illegible] 322
              [illegible]
Db        215 [illegible] 274

Qy        323 [illegible] 382
              [illegible]
Db        275 [illegible] 334

Qy        383 [illegible] 442
              [illegible]
Db        335 [illegible] 394

Qy        443 [illegible] 502
              [illegible]
Db        395 [illegible] 454

Qy        503 [illegible] 562
              [illegible]
Db        455 [illegible] 514

Qy        563 [illegible] 622
              [illegible]
Db        515 [illegible] 574

Qy        623 [illegible] 682
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Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      860 [illegible] 919
Db      [illegible]

Qy      [illegible]
Db      [illegible]


RESULT 3
AW[illegible]
LOCUS       AW[illegible]                [illegible] bp    mRNA    linear   EST [illegible]
DEFINITION  EST[illegible] MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW[illegible]
VERSION     AW[illegible]  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   [illegible], Abernathy,K., [illegible], Gaspard,R., [illegible]
            [illegible], [illegible], [illegible],V., [illegible],N.H., Yeatman,[illegible] and
            [illegible]
  TITLE     Assessment of gene expression patterns in [illegible]
            [illegible] using a [illegible] element cDNA [illegible]
  JOURNAL   Unpublished (2000)
COMMENT     Contact: [illegible]
            [illegible] Institute for Genomic Research
            [illegible] Medical Center Dr., Rockville, MD [illegible], USA
            [illegible]
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FEATURES             Location/Qualifiers
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ORIGIN

  Query Match          [illegible]
  Best Local Similarity [illegible]
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Qy      [illegible]
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Qy      [illegible]
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Qy      [illegible]
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Qy      665 [illegible]
Db      421 [illegible]

Qy      725 [illegible]
Db      481 [illegible]

Qy      785 [illegible] 844
Db      541 [illegible] 600

Qy      845 [illegible]
Db      601 [illegible]

Qy      905 [illegible]
Db      661 [illegible]

Qy      965 [illegible]
Db      721 [illegible]

Qy      1023 [illegible]
Db      781 [illegible]


RESULT 4
AK017245
LOCUS       AK017245               [illegible] bp    mRNA    linear   HTC [illegible]
DEFINITION  Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched
            library, clone:[illegible]:Protein phosphatase 2C containing
            protein, full insert sequence.
ACCESSION   AK017245
VERSION     AK017245.1  GI:[illegible]
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) 6 days neonate head cDNA to mRNA,
            clone_lib:RIKEN full-length enriched mouse cDNA library
            [illegible]
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. [illegible], [illegible]-44 (1999)
  MEDLINE   [illegible]
   PUBMED   [illegible]
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            [illegible],M., Konno,H., [illegible],Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., [illegible]
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., [illegible], Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., [illegible]
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., [illegible]
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5  (bases 1 to 1182)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., [illegible]
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            [illegible]
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., [illegible]
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (1?-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN [illegible]
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan ([illegible])
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216
  COMMENT   [illegible] for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5'-GAGAGAGAGAACTAGTCTCGAGTTTTTTTTTTTTTTTTVN-3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. cDNA went
            through one round of normalization to Rot = [illegible] and subtraction to
            Rot = [illegible]. Second strand cDNA was prepared with the primer
            adapter of sequence [5'
            GAGAGAGAGA[illegible]-3'], cDNA was cleaved
            with BamHI and XhoI. Vector: a modified pBluescript KS(+) after
            bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'
            end: BamHI. Host: DH10B.
FEATURES             Location/Qualifiers
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                     /clone="5430400J23"
                     /tissue_type="head"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="6 days neonate"
     CDS             <1..766
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                     data source:Pfam, source key:PF00481, evidence:ISS
                     putative"
                     /codon_start=2
                     /protein_id="BAB30649.1"
                     /db_xref="GI:12856386"
                     /db_xref="MGD:MGI:1919160"
                     /translation="[illegible]
                     [illegible]
                     [illegible]
                     [illegible]
                     [illegible]GSVSYIDVSVFVIPLHSQAQEGSGH"
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ORIGIN

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  Matches  664;  Conservative    0;  Mismatches   99;  Indels    3;  Gaps    1;

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Db         61 [illegible] 120

Qy        738 [illegible] 797
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Db        121 [illegible] 180

Qy        798 [illegible] 857
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Db        181 [illegible] 240

Qy        858 [illegible] 917
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Db        241 [illegible] 300

Qy        918 [illegible] 977
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Db        301 [illegible] 360

Qy        978 [illegible] 1037
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Qy       1038 [illegible] 1097
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Qy       [illegible] 1274
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Qy       [illegible] 1334
Db       [illegible]

Qy       [illegible]
Db       [illegible]


RESULT [illegible]
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LOCUS       [illegible]                  bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible] NIH MGC [illegible] Homo sapiens cDNA clone IMAGE:[illegible],
            mRNA sequence.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; [illegible]
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   NIH MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished ([illegible])
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: [illegible]
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: [illegible]
            High quality sequence stop: [illegible]4.
FEATURES             Location/qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:[illegible]"
                     /clone_lib="NIH_MGC_[illegible]"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; [illegible]
                     (destroyed); RNA source: leukocytes from anonymous pool [illegible]
                     [illegible] adult donors. Library is oligo-dT primed
                     and directionally cloned ([illegible] site is destroyed upon
                     cloning). Average insert size [illegible] kb, insert size range
                     [illegible] kb. Library is normalized and enriched for
                     full length clones and was constructed by [illegible]
                     ([illegible]). Research Genetics tracking code [illegible]. Note:
                     this is a NIH MGC Library."
BASE COUNT  [illegible]
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];
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Qy       [illegible]
Db         1 [illegible]

Qy       [illegible]
Db        61 [illegible]

Qy       [illegible]
Db       120 [illegible]

Qy       968 [illegible] 1027
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Qy      1028 [illegible]
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Qy      [illegible]
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Qy      [illegible]
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Qy      [illegible]
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Qy      [illegible]
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Qy      [illegible] 1571
Db       540 [illegible] AAGAGAGCAGT 584


RESULT [illegible]
BM719494/c
LOCUS       BM719494                 547 bp    mRNA    linear   EST [illegible] MAR 2002
DEFINITION  UI-E-EJ1-ajt-m-24-0-UI.r1 UI-E-EJ1 Homo sapiens cDNA clone
            UI-E-EJ1-ajt-m-24-0-UI 5', mRNA sequence.
ACCESSION   BM719494
VERSION     BM719494.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 547)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. [illegible] ([illegible]), [illegible] ([illegible])
  MEDLINE   [illegible]44[illegible]
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA [illegible], USA
            Tel: [illegible]
            Fax: [illegible]
            Email: msoares@blue.weeg.uiowa.edu
            Tissue Procurement: Dr. Teresa Bateman
             cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
```

```
FEATURES             Location/Qualifiers
     source          1..547
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "UI-E-EJ1-ajt-m-24-0-UI"
                     /clone_lib "UI-E-EJ1"
                     /tissue_type "fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     Choroid"
                     /dev_stage "fetal and adult"
                     /lab_host "DH10B (Life Technologies) (T1 phage resistant)"
                     /note "Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EJ1 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tags for this library are: fetal eyes, AGAATCAAGA
                     ; lens, CGATTAGCGA; eye anterior segment, AATGCGCTAT;
                     optic nerve, CCATTAACTC; retina, [illegible]; Retina Foveal and
                     Macular, CTCC; RPE and Choroid, ATTA. This library was
                     created for the program, Gene Discovery in the Visual
                     System, supported by National Eye Institute (NEI)."
BASE COUNT      117 a    179 c    134 g    117 t
ORIGIN

  Query Match             39.6%;  Score 547;  DB 14;  Length 547;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-114;
  Matches  547;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        672 GCAGGGAAAGCTGTACATGGCCAATGCTGGGATAGCAGGGCATCTTCCTCCCGACAGA 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GCAGGGAAAGCTGTACATGGCCAATGCTGGGATAGCAGGGCATCTTCCTCCCGACAGA 488

Qy        732 TGAGATAGGGGTCCCTGAGTTTAGATTTAAGGTTAGAGGCCAGGTGCATCTTAGTCAGCA 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 TGAGATAGGGGTCCCTGAGTTTAGATTTAAGGTTAGAGGCCAGGTGCATCTTAGTCAGCA 428

Qy        792 GCTGGCTTTTGTCTATCTGAGTTTCTGGCTGGTAGTTCAGCTCAGTGGAGTTCCTCCT 851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 GCTGGCTTTTGTCTATCTGAGTTTCTGGCTGGTAGTTCAGCTCAGTGGAGTTCCTCCT 368

Qy        852 GCGGCTGAAGGGGATGACTTGGGACAGAAGCTTTTGTTTACGCATCACCATATCACTGC 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 GCGGCTGAAGGGGATGACTTGGGACAGAAGCTTTTGTTTACGCATCACCATATCACTGC 308

Qy        912 CTGGAGCTACAAAGTGTGGAGAAATCGGATCTCAAGTAGCTATGATCCATGGACAGCC 971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGGAGCTACAAAGTGTGGAGAAATCGGATCTCAAGTAGCTATGATCCATGGACAGCC 248

Qy        972 TAGGCAGGCTGGTTACTAGGAACATTGGTGTCTCCTGGGGCTGGGAGATCATCAGCT 1031
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 TAGGCAGGCTGGTTACTAGGAACATTGGTGTCTCCTGGGGCTGGGAGATCATCAGCT 188

Qy       1032 CAGAGTCCTGGACACAAAGATCCAGCTCAAGCGCTTCTTGCTCCTGTGGCACAGGTGAC 1091
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CAGAGTCCTGGACACAAAGATCCAGCTCAAGCGCTTCTTGCTCCTGTGGCACAGGTGAC 128

Qy       1092 TGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGA 1151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGA 68

Qy       1152 TGGACTCTGGGATGTACTGGTCTAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTCCTCCC 1211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TGGACTCTGGGATGTACTGGTCTAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTCCTCCC 8

Qy       1212 TGGGAAT 1218
              ||||||
Db          7 TGGGAAC 1


RESULT 7
AA292266
LOCUS       AA292266                 547 bp    mRNA    linear   EST 8 AUG 1997
DEFINITION  zt50f12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGE:725807 5' similar to SW:PZ02_ARATH P49596 PROTEIN PHOSPHATASE
            2C ;, mRNA sequence.
ACCESSION   AA292266
VERSION     AA292266.1  GI:1940249
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 547)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
            ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
            ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
            Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
            Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1457   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 474.
FEATURES             Location/Qualifiers
     source          1..547
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "IMAGE:725807"
                     /clone_lib "Soares ovary tumor NbHOT"
                     /sex "female"
                     /tissue_type "ovarian tumor"
                     /lab_host "DH10B (ampicillin resistant)"
                     /note "Organ: ovary; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     [illegible]GCGGCCGCTTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. "
BASE COUNT      125 a    135 c    171 g    116 t
ORIGIN

  Query Match             38.8%;  Score 536;  DB 9;  Length 547;
  Best Local Similarity   99.8%;  Pred. No. 1.1e-111;
  Matches  547;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy        792 GCTGGCTTTTGTCTATCTGAGTTTCTGGCTGGTAGTTCAGCTCAGTGGAGTTCCTCCT 851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTGGCTTTTGTCTATCTGAGTTTCTGGCTGGTAGTTCAGCTCAGTGGAGTTCCTCCT 60

Qy        852 GCGGCTGAAGGGGATGACTTGGGACAGAAGCTTTTGTTTACGCATCACCATATCACTGC 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGGCTGAAGGGGATGACTTGGGACAGAAGCTTTTGTTTACGCATCACCATATCACTGC 120

Qy        912 CTGGAGCTACAAAGTGTGGAGAAATCGGATCTCAAGTAGCTATGATCCATGGACAGCC 971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGGAGCTACAAAGTGTGGAGAAATCGGATCTCAAGTAGCTATGATCCATGGACAGCC 180
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Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]


RESULT 8
B[illegible]
LOCUS       B[illegible]                  [illegible] bp    mRNA    linear   EST [illegible] JAN [illegible]
DEFINITION  [illegible] NIA Mouse [illegible]K cDNA Clone Set Mus musculus cDNA clone
            [illegible] mRNA sequence.
ACCESSION   [illegible]
VERSION     [illegible]  GI:[illegible]
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   [illegible], [illegible], [illegible], [illegible], Tanaka
            [illegible], Carter,M.G. and Ko,M.S.H.
  TITLE     Verification and initial annotation of NIA mouse 15K cDNA clone set
  JOURNAL   Unpublished (2001)
COMMENT     Other ESTs: [illegible]
            Contact: Geeorge [illegible] Kargul
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            [illegible] Eastern Avenue, Suite [illegible], Baltimore, MD 21224-[illegible], USA
            Email: [illegible]
            This clone set has been freely distributed to the community. Please
            visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
            Plate: [illegible] row: [illegible] column: [illegible]
            Seq primer: [illegible]
            High quality sequence stop: [illegible]
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="Mus musculus"
                     /strain="[illegible]"
                     /db_xref="[illegible]"
                     /db_xref="taxon:10090"
                     /tissue_type="[illegible]"
                     /clone_lib="NIA Mouse 15K cDNA Clone Set"
                     /sex="Clones arrayed from a variety of cDNA libraries"
                     /dev_stage="Clones arrayed from a variety of cDNA
                     libraries"
                     /lab_host="[illegible]"
                     /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
                     clone is [illegible] rearrayed set [illegible]
                     cDNA libraries (including preimplantation stage
                     embryos from unfertilized egg to blastocyst, embryonic
                     part of E7.5 embryos, extraembryonic part of E7.5 embryos
                     , and E12.5 female mesonephros/gonad) and one newborn
                     ovary cDNA library. Average insert size 1.5 kb. All
                     source libraries are cloned unidirectionally with oligo(dT
                     ) Not primers. References include: (1) Genome-wide
                     expression profiling of mid-gestation placenta and embryo
                     using a 15,000 mouse developmental cDNA microarray. 2000,
                     Proc. Natl. Acad. Sci. U.S.A, 97: 9127-9132; (2)
                     Large-scale cDNA analysis reveals phased gene expression
                     patterns during preimplantation mouse development. 2000,
                     Development, 127: 1737-1749; (3) Genome-wide mapping of
                     unselected transcripts from extraembryonic tissue of
                     7.5-day mouse embryos reveals enrichment in the t-complex
                     and under-representation on the X chromosome. 1998, Hum
                     Mol Genet 7: 1967-1978."
BASE COUNT      138 a    154 c    214 g    125 t
ORIGIN

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  56[illegible];  Conservative    [illegible];  Mismatches   [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]


RESULT 9
BM5[illegible]
LOCUS       BM5[illegible]                  [illegible] bp    mRNA    linear   EST [illegible] FEB [illegible]
DEFINITION  AGEN[illegible] NIH_MGC_[illegible] Homo sapiens cDNA clone IMAGE:[illegible]
```

```
            5', mRNA sequence.
ACCESSION   BM563[illegible]
VERSION     BM5636[illegible]7.1  GI:18810842
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   NIH MGC http://[illegible]
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1916  row: I  column: 12
            High quality sequence stop: 6[illegible]7.
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5441819"
                     /clone_lib="NIH_MGC_98"
                     /tissue_type="astrocytoma grade IV, cell line"
                     /lab_host="DH10B (phage resistant)"
                     /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Library constructed by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC library."
BASE COUNT      245 a    274 c    271 g    207 t
ORIGIN

  Query Match             36.1%;  Score 498;  DB 15;  Length 997;
  Best Local Similarity   [illegible];  Pred. No. 6.[illegible];
  Matches  498;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        8[illegible] [illegible] 942
              [illegible]
Db          1 [illegible]

Qy        943 [illegible]
              [illegible]
Db         61 [illegible] 120

Qy       1003 [illegible] 1062
              [illegible]
Db        121 GTCTCCCGGGGCCTGGAGACCATCAGCTCAGAG[illegible] 180

Qy       1063 CCCTTCTTGCTCTCTGTGCCACAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAG 1122
              [illegible]
Db        181 [illegible] 240

Qy       1123 [illegible]
              [illegible]
Db        241 [illegible]

Qy       1183 [illegible] 1242
              [illegible]
Db        301 [illegible]

Qy       1243 [illegible]
              [illegible]
Db        361 [illegible] 420

Qy       1[illegible] [illegible]
              [illegible]
Db        421 [illegible] 48[illegible]

Qy       1[illegible] GAGA[illegible]ACTTGA 1[illegible]
              [illegible]
Db        481 GAGA[illegible]A 4[illegible]


RESULT 1[illegible]
BM563742
LOCUS       BM563742              1018 bp    mRNA    linear   EST 2[illegible]-FEB-2002
DEFINITION  AGENCOURT_6[illegible] NIH_MGC_98 Homo sapiens cDNA clone IMAGE:[illegible]
            5', mRNA sequence.
ACCESSION   BM563742
VERSION     BM563742.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   NIH MGC http://[illegible]
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1[illegible]  row: [illegible]  column: 14
            High quality sequence stop: [illegible]7.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:5441845"
                     /clone_lib="NIH_MGC_98"
                     /tissue_type="astrocytoma grade IV, cell line"
                     /lab_host="DH10B (phage resistant)"
                     /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Library constructed by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC library."
BASE COUNT      25[illegible] a    2[illegible] c    26[illegible] g    214 t
ORIGIN

  Query Match             [illegible];  Score 4[illegible];  DB 13;  Length 1[illegible];
  Best Local Similarity   100.0%;  Pred. No. 6.3e-103;
  Matches  498;  Conservative    0;  Mismatches    0;  Indels    [illegible];  Gaps    [illegible];

Qy        88[illegible] [illegible]
              [illegible]
Db          1 [illegible] 60

Qy        94[illegible] [illegible]
              [illegible]
Db         61 [illegible] 12[illegible]

Qy       1003 [illegible]
              [illegible]
Db        121 [illegible] 1[illegible]

Qy       1063 [illegible]
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             [illegible]
Db        [illegible] [illegible]

Qy      1223 [illegible] 1282
             [illegible]
Db       241 [illegible] 300

Qy      1283 [illegible] 1342
             [illegible]
Db       301 [illegible] 360

Qy      1343 AA[illegible]AGA[illegible]GATACACAGCACACAG[illegible]AAAGAAGACA[illegible]CAGAGGAA 1402
             [illegible]
Db       361 AA[illegible]AGA[illegible]GATACACAGCACA[illegible]AAA[illegible]AAGAC[illegible]CAGAGGAA 420

Qy      1403 [illegible] 1462
             [illegible]
Db       421 [illegible] 480

Qy      1463 [illegible]
             [illegible]
Db       481 [illegible]


RESULT 11
AW1[illegible]
LOCUS       AW1[illegible]              [illegible] bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible] Soares mouse NMIE Mus musculus cDNA clone IMAGE:[illegible]
            similar to WP:[illegible] CE[illegible] PROTEIN [illegible] ;, mRNA
            sequence.
ACCESSION   AW1[illegible]
VERSION     AW1[illegible]  GI:[illegible]
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 699)
  AUTHORS   NCI-CGAP http://www.[illegible]
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (199[illegible])
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40RP from Gibco
            High quality sequence stop: [illegible].
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="Mus musculus"
                     /strain="[illegible]"
                     /db_xref="taxon:[illegible]"
                     /clone="IMAGE:[illegible]"
                     /clone_lib="Soares mouse NMIE"
                     /sex="male"
                     /dev_stage="newborn"
                     /lab_host="DH10B"
                     /note="Organ: [illegible]; Vector: pT7T3D [illegible];
                     Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed
                     with a Not I - oligo(dT) primer [illegible]
                     [illegible]
                     [illegible] double-stranded cDNA [illegible]
                     (Pharmacia), digested with Not I and cloned into the Not
                     I and Eco RI sites of the modified pT7T3 vector. Library
                     is normalized and was constructed and [illegible] by Bento
                     Soares and M.Fatima Bonaldo (University of Iowa) and [illegible]
                     [illegible], A. Varela-Carver, [illegible] and [illegible] (MRC
                     UK Mouse Genome Centre and Mammalian Genetics Unit,
                     Harwell [illegible])."
BASE COUNT      [illegible] a    [illegible] c    [illegible] g    [illegible] t
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  [illegible];  Conservative    [illegible];  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy       562 [illegible] 621
             [illegible]
Db         1 [illegible] 60

Qy       622 [illegible] 681
             [illegible]
Db        61 [illegible] 120

Qy       682 [illegible] 741
             [illegible]
Db       121 [illegible] 180

Qy       742 [illegible] 801
             [illegible]
Db       181 [illegible] 240

Qy       802 [illegible] 861
             [illegible]
Db       241 [illegible] 300

Qy       862 [illegible] 921
             [illegible]
Db       301 [illegible] 360

Qy       922 [illegible] 981
             [illegible]
Db       361 [illegible] 420

Qy       982 [illegible] 1041
             [illegible]
Db       421 [illegible] 480

Qy      1042 [illegible]AGGTGACTGTGCTGGAT 1101
             [illegible]
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Qy      1102 [illegible] 1161
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Db       541 [illegible]

Qy      1162 [illegible] 1200
             [illegible]
Db       601 [illegible]


RESULT 12
BF[illegible]21
LOCUS       BF[illegible]21              494 bp    mRNA    linear   EST [illegible]
DEFINITION  7k[illegible].x1 NCI_CGAP_[illegible] Homo sapiens cDNA clone IMAGE:[illegible]
            similar to TR:Q9ULE[illegible] Q9ULE[illegible] KIAA1[illegible] PROTEIN ;, mRNA sequence.
ACCESSION   BF[illegible]21
VERSION     BF[illegible]21.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 494)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (199[illegible])
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., M.D.,
            R. Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 467.
FEATURES             Location/Qualifiers
     source          1..494
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3480060"
                     /clone_lib="NCI_CGAP_GC6"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                     from the normalized library NCI_CGAP_GC4 was prepared, and
                     ss circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     1257396-1258631, 1469064-1470983, and 1475592-1476743).
                     Subtraction by Bento Soares and M. Fatima Bonaldo."
BASE COUNT       [illegible] a    [illegible] c    [illegible] g     [illegible] t      1 others
ORIGIN

  Query Match             85.7%;  Score 493;  DB 12;  Length 494;
  Best Local Similarity   99.8%;  Pred. No. [illegible];
  Matches  493;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         75 [illegible] 134
Db          1 [illegible] 60

Qy        135 [illegible] 194
Db         61 [illegible] 120

Qy        195 [illegible] 254
Db        121 [illegible] 180

Qy        255 [illegible] 314
Db        181 [illegible] 240

Qy        315 [illegible] 374
Db        241 [illegible] 300

Qy        375 [illegible] 434
Db        301 [illegible] 360

Qy        435 [illegible] 494
Db        361 [illegible] 420

Qy        495 [illegible] 554
Db        421 [illegible] 480

Qy        555 AGACTTGGTGATCG 568
Db        481 AGACTTGGTGATCG 494


RESULT 1[illegible]
BI344[illegible]
LOCUS       BI344[illegible]             [illegible]7 bp    mRNA    linear   EST [illegible]-JUL-200[illegible]
DEFINITION  [illegible]7244 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BI344[illegible]
VERSION     BI344[illegible].1  GI:150[illegible]
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.L., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (200[illegible])
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE [illegible], USA
            Tel: 4[illegible]2 762 4[illegible]
            Fax: 402 762 4[illegible]
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            [illegible]. Vector identified by cross_match with the [illegible]
            and -minmatch 1. options.
            PCR PRimers
            FORWARD: [illegible]
            BACKWARD: [illegible]
            Plate: 11[illegible]  row: L  column: 22
            Seq primer: [illegible].
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
                     /clone_lib="MARC 2PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: Not I; Site_2: Sal I;
                     library made from pooled tissue from testis, ovary,
                     endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT      1[illegible]4 a    14[illegible] c    2[illegible] g    1[illegible] t
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB 1[illegible];  Length [illegible]7;
  Best Local Similarity   [illegible];  Pred. No. 7.2e-101;
  Matches  537;  Conservative    [illegible];  Mismatches   54;  Indels    [illegible];  Gaps    [illegible];

Qy        2[illegible]7 [illegible]
Db          1 [illegible]

Qy        2[illegible]7 [illegible]
Db         61 [illegible]

Qy        351 [illegible]
Db        121 [illegible]

Qy        411 [illegible]
Db        181 [illegible]

Qy        471 [illegible]
Db        241 [illegible]

Qy        531 [illegible]
Db        301 [illegible]

Qy        591 [illegible]
Db        361 [illegible]

Qy        651 [illegible]
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Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]


RESULT 14
[illegible]
LOCUS       [illegible]                    5[illegible] bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible] MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 5[illegible])
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rexroad,C.A., Smith,T.P.L., [illegible]
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished ([illegible])
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and qual trimmed with phred
            [illegible]. Vector identified by cross match with the minscore 18
            and minmatch 12 options.
            PCR PRIMERS
            FORWARD: [illegible]
            BACKWARD: [illegible]
            Plate: [illegible]  row: A  column: [illegible]
            Seq primer: [illegible]
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                     /db_xref="taxon:9823"
                     /clone_lib="MARC 2PIG"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from testis, ovary,
                     endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT   [illegible]
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length 5[illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative    [illegible];  Mismatches   41;  Indels    [illegible];  Gaps    [illegible];

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
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Db       181 [illegible]

Qy       708 [illegible]
Db       241 [illegible]

Qy       768 [illegible] 827
Db       301 [illegible]

Qy       828 [illegible] 887
Db       361 [illegible] 420

Qy       888 [illegible] 947
Db       421 [illegible] 480

Qy       948 [illegible]
Db       481 [illegible]

Qy      1008 [illegible]
Db       541 [illegible]


RESULT 15
BF415112
LOCUS       BF415112                  589 bp    mRNA    linear   EST 28-NOV-2000
DEFINITION  UI-R-BJ2-[illegible] UI.s1 UI-R-BJ2 Rattus norvegicus cDNA clone
            UI-R-BJ2-[illegible] 3', mRNA sequence.
ACCESSION   BF415112
VERSION     BF415112.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   [illegible]
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            [illegible] Eckstein Medical Research Building Iowa City, IA [illegible] USA
            Tel: 319 335 8250
            Fax: 319 335 [illegible]
            Email: msoares@[illegible].uiowa.edu
            Insert Length: [illegible] Std Error: [illegible]
            Plate: [illegible]
            [illegible] Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: M.B.
            Soares Lab. Clone distribution: clones will be available through
            Research Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA No.
FEATURES             Location/Qualifiers
     source          1..589
                     /organism="Rattus norvegicus"
                     /strain="Sprague Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-BJ2-[illegible]"
                     /clone_lib="UI-R-BJ2"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ2
                     library is a subtracted library derived from the following
                     tissues: heart - atrium at 15 dpc, ventricle at [illegible] dpc,
                     atrium at [illegible] dpc, ventricle at 18 dpc, ventricle at 19
```

```
                    dpc, AV canal at 15 dpc.  For a detailed description of
                    the library from which this clone was derived, please
                    visit our web site at ratest.eng.uiowa.edu. The
                    subtraction has been previously described in (Bonaldo,
                    Lennon and Soares, Genome Research 6:791-806, 1996)
                    TAG_SEQ=None found"
BASE COUNT      131 a     140 c     196 g     122 t
ORIGIN

  Query Match             34.7%;  Score 478.2;  DB 12;  Length 589;
  Best Local Similarity   88.4%;  Pred. No. 1.7e-98;
  Matches  519;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy        496 [illegible] 555
              [illegible]
Db          3 [illegible] 62

Qy        556 [illegible] 615
              [illegible]
Db         63 [illegible] 122

Qy        616 [illegible] 675
              [illegible]
Db        123 [illegible] 182

Qy        676 [illegible] 735
              [illegible]
Db        183 [illegible] 242

Qy        736 [illegible] 795
              [illegible]
Db        243 [illegible] 302

Qy        796 [illegible] 855
              [illegible]
Db        303 [illegible] 362

Qy        856 [illegible] 915
              [illegible]
Db        363 [illegible] 422

Qy        916 [illegible] 975
              [illegible]
Db        423 [illegible] 482

Qy        976 [illegible] 1035
              [illegible]
Db        483 [illegible] 542

Qy       1036 [illegible] 1082
              [illegible]
Db        543 [illegible] 589

Search completed: February 23, 2003, 07:31:57
Job time : 2259 secs
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                    GenCore version 5.1.3
           Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 23, 2003, 08:33:39 ; Search time 1786 Seconds
                                              (without alignments)
                                              1919.458 Million cell updates/sec

Title:           US-09-866-987-3
Perfect score:   1380
Sequence:        1 atgtcccccgggtggttccg..........aaaaaggcaatgaacactga 1380

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters:       4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        GenEmbl:*
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                 30:  em_htg_hum:*
                 31:  em_htg_inv:*
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                 41:  em_htgo_other:*

      Pred. No. is the number of results predicted by chance to have a
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      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                 SUMMARIES
                   %
Result           Query
  No.    Score  Match Length DB  ID                          Description
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    1     1380  100.0   1380  6  AX352514                    AX352514 Sequence
    2     1369   99.2   1867  6  AX352534                    AX352534 Sequence
    3   1076.4   78.0   2121  9  AK0[illegible]              AK0[illegible] Homo sapi
    4     1049   76.0   2134  9  HSM80[illegible]7?2         AL832494 Homo sapi
    5   1014.4   73.5   2429  9  AK056894                    AK056894 Homo sapi
    6      783   56.7   1820  9  BC009644                    BC009644 Homo sapi
    7    281.8   20.4   1667  9  AK0[illegible]27            AK0[illegible]27 Homo sapi
    8    281.8   20.4   1665  9  BC0[illegible]8[illegible]  BC0[illegible] Homo sapi
    9    264.8   19.2   2518  6  AX413118                    AX413118 Sequence
   10    264.8   19.2   2518  9  HSM801407                   AL133644 Homo sapi
   11    264.4   19.2    903  6  AX119116                    AX119116 Sequence
   12    262.6   19.0   [illegible]  6  AX1[illegible]71     AX4[illegible]71 Sequence
c  13    260.2   18.9  8[illegible]  9  AC0[illegible]252   AC0[illegible]252 Homo sapi
c  14    260.2   18.9  17[illegible]  9  AC0[illegible]245  AC0[illegible]245 Homo sapi
   15    260.2   18.9 214160  9  AC004[illegible]21           AC004[illegible]21 Homo sapi
c  16    260.2   18.9 240294  2  AC044892                    AC044892 Homo sapi
   17    243.4   17.6   5791  6  AX397499                    AX397499 Sequence
   18    243.4   17.6   5791  9  AB0[illegible]2[illegible]83   AB0[illegible] Homo sapi
   19    242.4   17.6   [illegible]  9  AK0[illegible]815     AK0[illegible]815 Homo sapi
   20    167.4   12.1    657  9  HSA336006                   AJ336006 Homo sapi
   21    162.6   11.8    688  9  HSA332762                   AJ332762 Homo sapi
   22    159.4   11.6    852  9  HSA336051                   AJ336051 Homo sapi
   23      157   11.4    872  9  HSNL[illegible]04R           X875[illegible] H.sapiens a
   24    154.4   11.2  24[illegible]4  2  AC044892           AC044892 Homo sapi
   25    129.2    9.4    731  9  HSA33[illegible]82[illegible]   AJ33[illegible] Homo sapi
   26    101.2    7.3   [illegible]  3  AY0[illegible]51     AY0[illegible]51 Drosophil
   27    101.2    7.3  18700  2  AC017946                    AC017946 Drosophil
c  28    101.2    7.3 141716  3  AC130649                    AC130649 Drosophil
   29    101.2    7.3  17[illegible]  4  AC1[illegible]4515  AC1[illegible] Drosophil
c  30    101.2    7.3  20[illegible]19  2  AC[illegible]1176  AC[illegible] Drosophil
c  31    101.2    7.3  2[illegible]  3  AE0[illegible]3574   AE0[illegible] Drosophil
c  32     68.6    5.0 125020  9  AF429315                    AF429315 Homo sapi
   33     66.2    4.8 125020  9  AF429315                    AF429315 Homo sapi
c  34     64.8    4.7 157347  2  AC115403                    AC115403 Rattus no
c  35     62.6    4.5  44686  3  AF043695                    AF043695 [illegible]
c  36     61.2    4.4 135733  2  AC128114                    AC128114 Rattus no
   37     58.6    4.2 141747  2  AC129604                    AC129604 Rattus no
c  38     58.2    4.2 129000  2  AC127988                    AC127988 Rattus no
   39     58.2    4.2 158897  2  AC121439                    AC121439 Rattus no
c  40     58.2    4.2 208129  2  AC094216                    AC094216 Rattus no
   41     58.2    4.2 277339  2  AC09[illegible]41[illegible]   AC09[illegible] Rattus no
c  42       58    4.2 161257  2  AC1[illegible]6111          AC1[illegible]6111 Rattus no
c  43       58    4.2 162820  2  AC097338                    AC097338 Rattus no
c  44     57.8    4.2  55035  2  AC093944                    AC093944 Rattus no
   45     57.8    4.2 211[illegible]  2  AC1[illegible]656   AC1[illegible] Rattus no

                                 ALIGNMENTS

RESULT 1
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LOCUS       AX352514              1380 bp    DNA     linear   PAT [illegible]
DEFINITION  Sequence 3 from Patent WO0192491.
ACCESSION   AX352514
VERSION     AX352514.1  GI:18617749
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Plowman,G.D., Whyte,D., Sudarsanam,S., Manning,G., Caenepeel,S.,
            Martinez,R., Hunter,T. and Fhaheran,P.
  TITLE     Mammalian protein phosphatases
  JOURNAL   Patent: WO 0192491-A 3 06-DEC-2001;
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            [illegible] Inc. (US)
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="[illegible]"
                     /db_xref="[illegible]"
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BASE COUNT   [illegible]
ORIGIN

  Query Match             100.0%;  Score 1080;  DB 6;  Length 1080;
  Best Local Similarity   100.0%;  Pred. No. [illegible];
  Matches 1080;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         61 [illegible]

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Db        121 [illegible]

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Qy        661 [illegible]
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Qy        721 [illegible]
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Qy        781 [illegible]
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Qy        841 [illegible]
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Qy        901 [illegible]
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Qy        961 [illegible]
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Qy       1021 [illegible] 1080
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Qy       1081 [illegible]
Db       1081 [illegible]

Qy       1141 [illegible]
Db       1141 [illegible]

Qy       1201 [illegible]
Db       1201 [illegible]

Qy       1261 [illegible]
Db       1261 [illegible] 1320

Qy       1321 [illegible]
Db       1321 [illegible]


RESULT 2
AX202234
LOCUS       AX202234               1837 bp    DNA     linear   PAT [illegible]-AUG-2001
DEFINITION  Sequence 15 from Patent WO0153469.
ACCESSION   AX202234
VERSION     AX202234.1  GI:[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1837)
  AUTHORS   Baughman,[illegible], Tang,Y.T., Azimzai,Y., Yue,H., Baughn,M.R.,
            Hillman,J.L., [illegible], Walia,N., Gandhi,A.R., Policky,J.L. and
            Mathur,[illegible]
  TITLE     Phosphatases
  JOURNAL   Patent: WO [illegible]
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1837
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /note="Incyte ID No: [illegible]"
BASE COUNT   [illegible]
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB 6;  Length 1837;
  Best Local Similarity   99.9%;  Pred. No. [illegible];
  Matches 1080;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 [illegible]
Db          1 [illegible]

Qy         61 [illegible]
Db         61 [illegible]

Qy        121 [illegible]
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Db    121 AGTCCAGCCCGGGGCGGTGAGGCCTCGCGCCGCCCAGATCCCGGCCCGTGCGCAGC 180

Qy    181 [illegible] 240

Db    181 [illegible] 240

Qy    241 AAATCTGAATTCAATGAGGATCAAGCTGCCTGTGGGAAGCTGTGTATCTGGAGATGTGAG 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AAATCTGAATTCAATGAGGATCAAGCGGCCTGTGGGAAGCTGTGTATCTGGAGATGTGAG 300

Qy    301 [illegible] 360

Db    301 [illegible] 360

Qy    361 [illegible] 420

Db    361 [illegible] 420

Qy    421 [illegible] 480

Db    421 [illegible] 480

Qy    481 [illegible] 540

Db    481 [illegible] 540

Qy    541 GGCATCAGGGCAGAAGACTTGGTGATGGGGCATTGGAGAGTGCCTTTCAGGAATGTGAT 600
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 [illegible] 600

Qy    601 [illegible] 660

Db    601 [illegible] 660

Qy    661 [illegible] 720

Db    661 [illegible] 720

Qy    721 GTGCGGAGAGATGAGATAGGGGACTGAGCTTGAGTTGACCCAGAGACTGAGGGGCAG 780

Db    721 [illegible] 780

Qy    781 [illegible] 840

Db    781 CGGATCCAGCAGCTGGCTTTGTCTATCCTGAGCTTCTCCTTGGTGACTTCACCGACTG 840

Qy    841 [illegible] 900

Db    841 [illegible] 900

Qy    901 [illegible] 960

Db    901 [illegible] 960

Qy    961 [illegible] 1020
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 [illegible] 1020

Qy   1021 [illegible] 1080

Db   1021 [illegible] 1080

Qy   1081 GCAGAGGTGACTGTGCTGGATGCGACCAGCTGGAGGTACAGGAGGATGATGTGGTTGTC 1140

Db   1081 GCAGAGGTGACTGTGCTGGATGCGACCAGCTGGAGGTACAGGAGGATGATGTGGTTGTC 1140

Qy   1141 ATGGCAACTGATGCACTCTGGATGTACTGTCAACGACCACC[illegible] 1200

Db   1141 [illegible] 1200

Qy   1201 [illegible] 1259

Db   1201 [illegible] 1260

Qy   1260 [illegible] 1319

Db   1261 [illegible] 1320

Qy   1320 [illegible] 1379

Db   1321 [illegible] 1380

Qy   1380 A 1380
          |
Db   1381 A 1381


RESULT 3
AK096681
LOCUS       AK096681                2121 bp    mRNA    linear   HTC 13-JUL-2002
DEFINITION  Homo sapiens cDNA FLJ39362 fis, clone PEBLM2005282, weakly similar
            to [illegible] HOMOLOG 3 (EC 3.1.3.16).
ACCESSION   AK096681
VERSION     AK096681.1  GI:21756226
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens peripheral blood mononuclear cells (PBMC [illegible]) cDNA
            mRNA, clone_lib:PEBLM2 clone:PEBLM2005282.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   [illegible],A., Takahashi F.,[illegible],A., Tanase,T., Imose,N., Takeuchi,K.,
            Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
            Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
            Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
            Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
            Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B.,
            Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and
            Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2121)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
            Kazusa Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
FEATURES             Location/Qualifiers
     source          1..2121
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="PEBLM2005282"
                     /cell_type="peripheral blood mononuclear cells
                     (PBMC [illegible])"
                     /clone_lib="PEBLM2"
                     /note="cloning vector: pME18SFL3; primary culture
                     peripheral blood mononuclear cells"
     CDS             111..782
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="BAC04839.1"
                     /db_xref="GI:21756227"
                     /translation="MHLNGRCIC[illegible]SDP[illegible]EVPEKC[illegible]EALCVL[illegible]A[illegible]SAL[illegible]
                     [illegible]MANA[illegible]SRAL[illegible]VEK[illegible]
                     QLVSALISMEAVK[illegible]LLDGRGF"
BASE COUNT      457 a    597 c    619 g    448 t
ORIGIN
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  Query Match             [illegible]  Score [illegible]  DB [illegible]  Length [illegible]
  Best Local Similarity   [illegible]  Pred. No. [illegible]
  Matches [illegible]  Conservative  [illegible]  Mismatches  [illegible]  Indels  [illegible]  Gaps  [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]

Db    1019 [illegible]

Qy    1119 [illegible]
Db    1079 [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    1199 CTCAAA[illegible]AGATGCTGATACACAGCACACAGGGAAAGGAAGACAGT[illegible]ACAGA 1258

Qy    1299 GGAA[illegible]  1358
Db    1259 GGAA[illegible]AGATGAC[illegible]GATTCC[illegible]GCACAGTCAGGG 1318

Qy    [illegible]
Db    [illegible]


RESULT 4
HSM8[illegible]
LOCUS       HSM8[illegible]              [illegible] bp    mRNA    linear   PRI [illegible]
DEFINITION  Homo sapiens mRNA; cDNA DKFZp686N2219 (from clone DKFZp686N2219).
ACCESSION   AL832484
VERSION     AL832484.1  GI:[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2134)
  AUTHORS   [illegible], Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible] JUL 2002) [illegible] 69120 Heidelberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by DKFZ (German Cancer Research Center,
            Heidelberg/Germany) within the cDNA sequencing consortium of the
            German Genome Project.
            This clone (DKFZp686N2219) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://[illegible].
FEATURES             Location/Qualifiers
     source          1..2134
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="DKFZp686N2219"
                     /tissue_type="cDNA correction"
                     /clone_lib="[illegible] (synonym: hlcc3). Vector pSport1 Sfi; host
                     DH10B; sites SfiIA + SfiIB"
                     /dev_stage="adult"
     polyA_signal    [illegible]
     polyA_site      [illegible]
BASE COUNT     [illegible]
ORIGIN

  Query Match             [illegible]  Score [illegible]  DB [illegible]  Length [illegible]
  Best Local Similarity   [illegible]  Pred. No. 4e-197;
  Matches [illegible]  Conservative    0;  Mismatches    0;  Indels   [illegible]  Gaps    1;

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
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Db        128 CATCGGAGATGTGAGTTTGGGCTGAAGAAGAGTGGCTGACCGTGTGCCCAGAGGAGTT 187

Qy        345 [illegible]GGACAGG[illegible]ATTACTGGGTAC[illegible]TTCGATGGG[illegible]TAGCAGCCATCTT 404
              |||||||| |||||||||||||||.|||||||||||||||||.|. |||||||||||.|||.
Db        188 [illegible]GGACAGG[illegible]ATTACTGGGACTGTTCGATGGGTACGG[illegible]GGAGCAGCCATCTT 247

Qy        405 [illegible]CAA[illegible]CCTG[illegible]AGC[illegible]GAAGG[illegible] 464
              ||||||| ||||.|||||||||||||||||||||||||||||.:.||||||||||||| |||
Db        248 [illegible] 307

Qy        465 GGTGGCCACTCAGCCCCCCATGCACCTCAATGGCCGCTGCATCTGCCCCAGTCACCCTCA 524
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        308 GGTGGCCACTCAGCCCCCCATGCACCTCAATGGCCGCTGCATCTGCCCCAGTCACCCTCA 367

Qy        525 GTTTGTGGAGGAAAA[illegible]CATCA[illegible]AGAAGA[illegible]ATGGAGAG[illegible] 584
              ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        368 GTTTGTGGA[illegible] 427

Qy        585 [illegible]TTCAGGAA[illegible]GGAT[illegible]GGAG[illegible]GGA[illegible]CAGATCCCCCC 644
              ||||||.||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        428 [illegible]TTCAGGAA[illegible]GGAT[illegible]GGAG[illegible]GGA[illegible]CAGATCCC[illegible] 487

Qy        645 CTGCATAG[illegible]TGGCTGGT[illegible]AGGGAAAG[illegible]CAATG[illegible]TGGGA 704
              |||||| ||.|.|||.||||.|||||.||||.||.||||.|||| | |||||||||||
Db        488 CTGCA[illegible]AG[illegible]TGGCTGGT[illegible]GCAGGGAAAG[illegible]CAAT[illegible]TGGGA 547

Qy        705 TAGTAG[illegible]TCA[illegible] 764
               ||||| | .  ||  | |||||| |||||  |  ||||.....|||| |||| | ||||
Db        548 TA[illegible] 607

Qy        765 AGA[illegible]AGCAGCT---- ------------ ---   ------- 794
              |||||||||||||||||||||||||||||
Db        608 AGA[illegible]AGCAG[illegible]TGG[illegible]AGCTCC[illegible] 667

Qy        795 ------------ ----------------------------    ---------------- 794

Db        668 GAAGTCCAACTCCTGGTCCAGGGCCATAAGAAGTACTATCATCCAGCCACCCTCCC 727

Qy        795 --------GGCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCC 847
                      ||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        728 CACCCAGCCCTTTCTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCC 787

Qy        848 CTCGGCGGCTGAAGGGGGATGACTTGGGACAGAA[illegible]CATCA 907
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        788 CTCGGCGGCTGAAGGGGGATGACTTGGGACAGAA[illegible]CATCA 847

Qy        908 GTG[illegible]TGGA[illegible]ACAAAG[illegible]GAGAAAT[illegible]GAA[illegible]AT[illegible]CA[illegible]ATGCAT 967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 [illegible] 907

Qy        968 [illegible]AA[illegible]AT 1027
              ||||||||| ||||||||| |||||||||||||||||||||||||| ||||||||||| ||
Db        908 AG[illegible]TAG[illegible]A[illegible]AG[illegible]ACAC[illegible]AT 967

Qy       1028 [illegible]AGAG[illegible]GGAC[illegible]AAATATCCAG[illegible]CAA[illegible]CACAG 1087
              |||||||| ||||||| | |||||||||||||||||||||||| |||||||| ||||||||
Db        968 AG[illegible]AGA[illegible]A AAA AT[illegible]CAA[illegible]A[illegible] 1027

Qy       1088 TGA[illegible]AT[illegible]TGGA[illegible] 1147
              | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 TGA[illegible]A[illegible] 1087

Qy       1148 CTGATG[illegible]AG[illegible]AA[illegible] 1207
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1088 CTGA[illegible]CCTTCC 1147

Qy       1208 [illegible]GGAA[illegible]AAGA[illegible]ACAGA[illegible]AAAG[illegible]ATCA[illegible]A 1267
              ||||| |||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1148 TCCCTGGCA[illegible]ACAGA[illegible]AAAG[illegible]A 1207

Qy       1268 [illegible] 1327
              ||||||||||||||||||||||||||||||||||| | ||||||||||||||||||||||
Db       1208 [illegible] 1267
```

```
Qy       1328 [illegible]
              ||||||||||||||||||||||||||||||||||||
Db       1268 CTGT[illegible]GA[illegible]AAGA[illegible]AGCAGTGA[illegible]A[illegible]
```

```
RESULT 5
AK056894
LOCUS       AK056894                2425 bp    mRNA    linear   [illegible]
DEFINITION  Homo sapiens cDNA FLJ32332 fis, clone PROST2[illegible], weakly similar
            to PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 ([illegible]).
ACCESSION   AK056894
VERSION     AK056894.1  GI:16552415
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens prostate cDNA to mRNA, clone_lib:PROST2
            clone:PROST2005121.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ishibashi,T., Kanehori,K., Yoshida,M., Watanabe,S., [illegible]
            [illegible]ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S.,
            Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
            Yamashita,H., Ohira,Y., Sugiyama,T., Irie,R., Otsuki,T., Sat[illegible],
            Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai[illegible],Y.,
            Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y.,
            Sekine,M., Kikuchi,H., Kanda,K., Wakatsuki,M., Takahashi[illegible],A.,
            [illegible]shima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., [illegible],S.,
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2425)
  AUTHORS   Isogai,T., Otsuki,T. and Sugiyama,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24 [illegible] 2001) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; [illegible] Yana, Kisarazu, Chiba [illegible], Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: RAB and
            HRI.
FEATURES             Location/Qualifiers
     source          1..2425
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "PROST2005121"
                     /tissue type "prostate"
                     /clone lib "PROST2"
                     /note "cloning vector: pME18SFL3"
     CDS             405..1217
                     /note "unnamed protein product"
                     /codon_start 1
                     /protein_id "BAB71[illegible].1"
                     /db_xref "GI:16552416"
                     /translation "[illegible]VLD[illegible]SAF[illegible]EVI[illegible]
                     [illegible]FAS[illegible]TALVAVS[illegible]KLYMANAGDSRAILVRR[illegible]SE[illegible]
                     [illegible]APVT[illegible]KRVL[illegible]VEKS[illegible]KY[illegible]
                     GGRQARI[illegible]LAVSRGDCDHQLRVLDTNIQLKPFLLSVPQVIVLDVD[illegible]EDDVV
                     [illegible]VASSK[illegible]K"
BASE COUNT      [illegible] a     [illegible] c     [illegible] g     [illegible] t
ORIGIN

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length 2425;
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches 1015;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        [illegible] 264
              |||||||||||| | |.||||||||||| | ||||||||||||||||| |.|||| ||
Db        [illegible] 204
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[illegible]

RESULT [illegible]
[illegible]
LOCUS       [illegible]            mRNA    linear   [illegible]
DEFINITION  Homo sapiens [illegible] MGC [illegible] IMAGE:[illegible] mRNA, complete cds.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 182[illegible])
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site: http://www-shgc.stanford.edu
            Contact: (Dickson, Mark) mwd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 14 Row: p Column: 20.
FEATURES             Location/Qualifiers
     source          1..182[illegible]
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="MGC:17869 IMAGE:[illegible]"
                     /tissue_type="Uterus, leiomyosarcoma"
                     /clone_lib="NIH_MGC_71"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             [illegible]
                     /codon_start=1
                     /product="Unknown (protein for MGC:17869)"
                     /protein_id="AAH[illegible]44.1"
                     /db_xref="GI:[illegible]"
                     /translation="[illegible]IALVAV[illegible]KI[illegible]MANA[illegible]ATLVEEEEIRPLSEEFIEE
                     IERQRIQQLAFVYPELLAGEFIRLEEPRRLKGDDLGQKVLERDHHMSGWSYKRVEKSD
                     [illegible]
                     [illegible]VVVMA[illegible]VLSNE[illegible]VAWLVRSE[illegible]NQEDRREFSKLA[illegible]
                     [illegible]QVSYDDVSVEVIPLHSQ[illegible]QESSDH"
BASE COUNT      415 a    469 c    515 g    391 t
ORIGIN

  Query Match             [illegible]%;  Score 7[illegible];  DB [illegible];  Length 182[illegible];
  Best Local Similarity   100.0%;  Pred. No. 1.4e-144;
  Matches  7[illegible];  Conservative    [illegible];  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

[illegible]
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Qy        898 [illegible] 957
              [illegible]
Db        525 [illegible] 584

Qy        958 [illegible] 1017
              [illegible]
Db        585 [illegible] 644

Qy       1018 [illegible] 1077
              [illegible]
Db        645 [illegible] 704

Qy       1078 [illegible] 1137
              [illegible]
Db        705 [illegible] 764

Qy       1138 [illegible] 1197
              [illegible]
Db        765 [illegible] 824

Qy       1198 [illegible] 1257
              [illegible]
Db        825 [illegible] 884

Qy       1258 [illegible] 1317
              [illegible]
Db        885 [illegible] 944

Qy       1318 [illegible] 1377
              [illegible]
Db        945 [illegible] 1004

Qy       1378 [illegible]CA 1380
              [illegible]
Db       1005 [illegible]CA 1007


RESULT 7
AK093270
LOCUS       AK093270                1687 bp    mRNA    linear   PRI 15-JUL-2002
DEFINITION  Homo sapiens cDNA [illegible], highly similar
            to PROBABLE PROTEIN PHOSPHATASE 2C [illegible] (EC 3.1.3.16).
ACCESSION   AK093270
VERSION     AK093270.1  GI:21752092
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens testis cDNA to mRNA, clone lib:TESTI2
            clone:TESTI2012[illegible]4.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.,
            Ono,Y., Hotuta,T., Hiraoka,S., [illegible]
            Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
            Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., [illegible]
            Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
            Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y.,
            Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A.,
            Oshima,A., [illegible]
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1687)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); [illegible]
            Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /clone_lib="TESTI2"
                     /note="cloning vector: pME18SFL3"
BASE COUNT      336 a    512 c    513 g    326 t
ORIGIN

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  Matches  725;  Conservative    0;  Mismatches  547;  Indels [illegible];  Gaps [illegible];

Qy         87 [illegible]
              [illegible]
Db        193 [illegible]

Qy        147 [illegible]
              [illegible]
Db        253 [illegible]

Qy        207 [illegible] 264
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Db        313 [illegible]

Qy        267 [illegible] 324
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Db        374 [illegible]

Qy        325 [illegible] 384
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Db        431 [illegible] 490

Qy        385 [illegible] 444
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Qy        445 [illegible]
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Db        551 [illegible]

Qy        494 [illegible]
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Db        611 [illegible]

Qy        545 [illegible]
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Qy        592 [illegible]
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Qy        652 [illegible]
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Db        791 [illegible]

Qy        712 [illegible]
              [illegible]
Db        851 [illegible]

Qy        772 [illegible]
              [illegible]
Db        911 [illegible]

Qy        832 [illegible]
              [illegible]
Db        971 [illegible]
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Db      [illegible]

Qy      [illegible]

Db      [illegible]

Qy      [illegible]

Db      [illegible]

Qy      [illegible]

Db      [illegible]

Qy      [illegible]

Db      [illegible]

Qy      [illegible]

Db      [illegible]

Qy      [illegible]

Db      [illegible]

Qy      [illegible]

Db      [illegible]


RESULT [illegible]
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LOCUS       [illegible]                 1606 bp    mRNA    linear   PRI [illegible] 2001
DEFINITION  Homo sapiens, Similar to RIKEN cDNA [illegible] gene, clone
            MGC:[illegible] IMAGE:[illegible], mRNA, complete cds.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1606)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible] 2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD [illegible],
            USA
  REMARK    NIH-MGC Project URL: http://[illegible]
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis Staudt
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC)
            Gaithersburg, Maryland;
            Web site: http://[illegible]
            Contact: [illegible]
            Chu,[illegible] Wetherby,K., Beckstrom-Sternberg,S.M.,
            [illegible] Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
            [illegible] Gupta,J., [illegible] Karlins,E., Legaspi,R.,
            Lim,M., Maduro,[illegible] Masiello,C., Maskeri,B., McDowell,[illegible]
            McDowell,J., Peterson,K., Snyder,B., Stantripop,S., Thomas,P.J.,
            Thomas,R.F., Touchman,J.W., [illegible] Vogt,J.L., Walker,M.A.,
            Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 27 Row: p Column: 16
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: [illegible]
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="MGC:[illegible] IMAGE:[illegible]"
                     /tissue_type="Primary B-Cells from Tonsils"
                     /clone_lib="NIH_MGC_48"
                     /lab_host="DH10B"
                     /note="Vector: pOTB7"
     CDS             46..1478
                     /codon_start=1
                     /product="Similar to RIKEN cDNA [illegible] gene"
                     /protein_id="AAH11803.1"
                     /db_xref="GI:[illegible]"
                     /translation="MASKLLHHHIRE[illegible]
                     [illegible]
                     GKVYVANAG[illegible]KATIVRNGEIIPMSREFIPETERQKLQLLGFLKPELLGSFFIHLEFF
                     [illegible]
                     [illegible]
                     [illegible]
                     [illegible]YS"
BASE COUNT     [illegible]
ORIGIN

  Query Match             [illegible];  Score 261.8;  DB [illegible];  Length 1606;
  Best Local Similarity   54.[illegible];  Pred. No. 1.3e-45;
  Matches  [illegible];  Conservative    [illegible];  Mismatches  147;  Indels  [illegible];  Gaps  [illegible];

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Db        147 [illegible]

Qy        147 [illegible]

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Qy        [illegible]

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Qy        [illegible]

Db        [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible] 444

Db        444 [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible]
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Db        684 [illegible] 743

Qy        652 [illegible]GGCAGGAAA[illegible]GTA[illegible]AATAGCAGG 711

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Qy        712 [illegible] 771

Db        804 [illegible] 863

Qy        772 [illegible] 831

Db        864 [illegible]TCAGTTGCTTGGCTTCCTGAAA[illegible]AG[illegible]GAATTC 923

Qy        832 [illegible] 891

Db        924 [illegible] 983

Qy        892 [illegible] 951

Db        984 [illegible] 1043

Qy        952 [illegible] 1011

Db       1044 [illegible]

Qy       1012 GGCCTGGGAGACCAT[illegible] 1071

Db       1104 [illegible]

Qy       1072 CTCTCTGTGCCACAGC[illegible]CTGT[illegible]GATCT[illegible] 1131

Db       1164 [illegible] 1223

Qy       1132 CTGCTT[illegible]CAACTCATG[illegible]ATCTA[illegible] 1191

Db       1224 [illegible]

Qy       1192 CTGGTGCGGAGCTTCCTCCCTG---GGAACCAAGA[illegible]TCAAA[illegible] 1248

Db       1284 ACTGTGGACA[illegible] 1343

Qy       1249 GCCCA[illegible] 1296

Db       1344 GCCCAA[illegible] 1403

Qy       1297 GAGGAAG[illegible]GCAGTCAG 1356

Db       1404 [illegible]

Qy       1357 [illegible] 1359

Db       1464 GGC 1466


RESULT 9
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LOCUS       AX4[illegible]          2518 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence 3 from Patent WO0218565.
ACCESSION   AX4[illegible]
VERSION     AX4[illegible].1  GI:[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human protein phosphatase IIc like enzyme
  JOURNAL   Patent: WO 0218565-A 3 07-MAR-2002;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1..2518
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                     /db_xref="GI:[illegible]"
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                     [illegible]
                     [illegible]
                     [illegible]SSTLPIKH[illegible]LSC[illegible]EVKVYL[illegible]YEH[illegible]LVLV
                     LGTDGLWDVITDCEVAATV[illegible]VLSATE[illegible]NDHSKYIALAQALVLSAR[illegible]PRR[illegible]WRLPN
                     NKLGSGD[illegible]ISVFVIFL[illegible]G[illegible]SYS"
BASE COUNT      [illegible] a    [illegible] c    [illegible] g    184 t
ORIGIN

  Query Match             [illegible]%;  Score [illegible];  DB 6;  Length 2518;
  Best Local Similarity   [illegible]%;  Pred. No. 2.7e-42;
  Matches  537;  Conservative    [illegible];  Mismatches  377;  Indels  [illegible];  Gaps  [illegible];

Qy        447 [illegible]

Db       1368 [illegible] 1428

Qy        [illegible]

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Qy        [illegible]

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Qy        627 [illegible]

Db       1548 [illegible]AGATCTA[illegible] 1607

Qy        [illegible]

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Qy         74[illegible]

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Qy        807 [illegible]GAA[illegible] 864

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Qy        [illegible]A[illegible]TAAA [illegible]

Db       17[illegible] AAAGA[illegible]A[illegible]AAA [illegible]

Qy        925 [illegible] 984

Db       1848 AAGAT[illegible]AAAAA[illegible]

Qy        985 [illegible]CAGAGT[illegible]GGAC 1044

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Qy       1045 [illegible] 1104

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Qy       1105 [illegible] 1164

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Db       2088 [illegible]
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LOCUS       HSM[illegible]          [illegible] bp    mRNA    linear   PRI [illegible] FEB 2000
DEFINITION  Homo sapiens mRNA; cDNA DKFZp[illegible] (from clone DKFZp[illegible]);
            partial cds.
ACCESSION   AL[illegible]
VERSION     AL[illegible]  GI:[illegible]
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., [illegible]
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) MIPS, [illegible]
            Martinsried, GERMANY
COMMENT     [illegible] Wiemann, [illegible] German Cancer
            Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;
            sequenced by BMFZ (Biomedical Research Center at the [illegible],
            [illegible]) within the cDNA sequencing consortium of the German
            Genome Project.
            This clone (DKFZp[illegible]) is available at the RZPD in Berlin.
            Please contact the [illegible]
            Berlin, [illegible], GERMANY; Email: [illegible] Further
            information about the clone and the sequencing project is available
            at http://www[illegible]
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     [illegible]WEVE[illegible]VAATV[illegible]
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     polyA_signal    [illegible]
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ORIGIN

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Qy   [illegible]
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DEFINITION  Sequence [illegible] from Patent W[illegible]
ACCESSION   AX[illegible]
VERSION     AX[illegible]  GI:[illegible]
KEYWORDS    .
SOURCE      [illegible]
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human protein phosphatase [illegible]-like enzyme
  JOURNAL   Patent: WO [illegible] A 1 07-MAR-2002;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1..900
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      [illegible] a    247 c    282 g    185 t
ORIGIN

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  Best Local Similarity   58.8%;  Pred. No. [illegible]e-42;
  Matches  [illegible];  Conservative    0;  Mismatches  [illegible];  Indels   15;  Gaps    2;

Qy        522 [illegible] 582
Db         37 [illegible] 96

Qy        583 [illegible] 642
Db         97 [illegible] 156

Qy        643 [illegible] 702
Db        157 [illegible] 216

Qy        703 [illegible] 762
Db        217 [illegible] 276

Qy        763 [illegible] 822
Db        277 [illegible]

Qy        823 [illegible] 882
Db        337 [illegible] 396

Qy        883 [illegible] 942
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Qy        [illegible]
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Qy        [illegible]
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Qy        [illegible]
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Qy        [illegible]
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Qy       1348 CACAGTCAGGGC 1359
Db        [illegible] 888


RESULT 12
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LOCUS       AX400071                [illegible] bp    DNA     linear   PAT [illegible]
DEFINITION  Sequence 242 from Patent WO0218424.
ACCESSION   AX400071
VERSION     AX400071.1  GI:[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Tang,Y.T., Asundi,V., Zhou,P., Xue,A.J., Ren,F., Zhang,J.,
            Wang,J.R., Zhao,Q.A., Wang,D., Liu,C., Drmanac,R.T. and Wehrman,T.
  TITLE     Nucleic acids and polypeptides
  JOURNAL   Patent: WO 0218424-A 242 07-MAR-2002;
            HYSEQ, INC. (US)
FEATURES             Location/Qualifiers
     source          1..1198
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                     [illegible]
                     [illegible]
                     [illegible]SYS"
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ORIGIN

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  Best Local Similarity   59.0%;  Pred. No. 8.3e-42;
  Matches  495;  Conservative    0;  Mismatches  329;  Indels   [illegible];  Gaps    2;

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Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
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[illegible]

RESULT [illegible]
A[illegible]
LOCUS       A[illegible]          [illegible] bp    DNA     linear   [illegible]
DEFINITION  Homo sapiens [illegible] clone RP[illegible] (Roswell Park Cancer
            Institute Human PAC Library) complete sequence.
ACCESSION   A[illegible]
VERSION     A[illegible]
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Muzny,D., Abramson,A.D., Boneck,L., Bonaparte,C., Chen,L., Chen,Z.,
            Culpepper,P., Ding,Y., Dugan,S.P., Durbin,K.J., Forbes,L.,
            [illegible], Garcia,K., [illegible],
            He,X., Hernandez,J., Jackson,L.R., Kandelewski,N., Leal,B.,
            [illegible], Liu,W., Lopez,J., Lu,J., Martinez,E., Moore,S.,
            Morgan,M.B., Nguyen,N., Oswald,C., Pampell,[illegible], Parrish,K.,
            [illegible], Rives,M., Scherer,S.E., Shen,H.,
            [illegible], V[illegible], Wei,Y., Williamson,A., Worley,K.C., [illegible],
            Naylor,J. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to [illegible])
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) Molecular and Human Genetics, Baylor
            College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to [illegible])
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Mar [illegible] this sequence version replaced gi:[illegible].
            INFORMATION: http://www.hgsc.bcm.tmc.edu/ [illegible]
            [illegible]

            CLONE LENGTH: This sequence does not necessarily represent the
            entire insert of this clone. Overlapping clones are [illegible]
            sequenced and [illegible] the sequence for the remainder of
            the insert may be found in the record for the adjacent clones.
            Overlapping clones are noted at the beginning and end of the
            features listing.

            ANNOTATION OF FEATURES:
              STSs are identified using ePCR (Genome Res. 7:541-550) searches
            of a local database that includes entries from dbSTS, GDB, and
            local mapping efforts.
              Repeats are identified using RepeatMasker (A. Smit and P. Green,
            unpublished.) for Human and Mouse sequences.
              Genes and Region of sequence similarity are identified by BLAST
            (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-[illegible]) to the
            EST and cDNA sequences. Genes demonstrate at least two exons
            flanked by consensus splice sites that maintained sequence
            continuity across the splice junctions. Sequences that are not
            identical matches are annotated as similar.

            SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
            standard of double strand coverage with a minimum of 2 clones and 2
            reads with no ambiguities or 2 chemistries with a minimum of 2
            clones and 3 reads with no ambiguities. If the sequence quality for
            a region does not meet this standard, it will be indicated in the
            annotation as low coverage.

            QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality
            standards (estimated error rate less than 1 per 10,000 bases).
            Reports of lowest quality individual bases and measures of base
            quality are listed below. Description of the metrics can be found
            at URL: http://www.hgsc.bcm.tmc.edu/docs/quality/[illegible]
            html.

            QUALSTAT REPORT


                            Summary Statistics
            Contig length:                                          8[illegible]
            Phrap values in estimate:                               [illegible]
            Average error rate (BCM Phrap estimate):                [illegible]
            Fraction of Phrap values less than 40 :                 [illegible]
            Number of consensus changing edits:                     6
            Number of N's in consensus :                            [illegible]


                            Consensus changing edits
            Position        Original-Context           Edited-Context
            5[illegible]    [illegible](n)[illegible]     [illegible](*)[illegible]
            [illegible]     [illegible](n)[illegible]     [illegible](*)[illegible]
            [illegible]     attaaaaaa(n)atacatttt      attaaaaaa(*)atacatttt
            40[illegible]   atgactataa(n)aggatatcta    atgactataa(*)aggatatcta
            47[illegible]   tttatattt(n)atctaatgta     tttatattt(*)atctaatgta
            [illegible]     [illegible](n)[illegible]     [illegible](*)[illegible]


                    Distribution of quality < 40 bases

                      [illegible]                                       *
                      [illegible]                                       *
                      [illegible]                                       *
              #       [illegible]                                       *
            bases     [illegible]                                  *    *
                      [illegible]                                  *    *
                      [illegible]                                  *    *
                      [illegible]                                  *    *
                      [illegible]                             *    *    *
                      [illegible]                   *    *    *    *    *
                      [illegible]  *    *    *      *    *    *    *    *

                              [illegible]
                                      Phrap Value Range


            Version [illegible]
```

```
FEATURES             Location/Qualifiers
     source          1..[illegible]82098
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="[illegible]-1157M2[illegible]"
                     /note="Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
                     Eutheria; Primates; Catarrhini; Hominidae; Homo."
     repeat_region   1..[illegible]
                     /rpt_family="Al[illegible]"
     repeat_region   78..379
                     /rpt_family="AluSx"
     gene            complement(join([illegible]..1542,16[illegible]..20[illegible],2134..2237,
                     2487..255[illegible]..2734..2853))
                     /gene="Unigene cluster containing AI478177, [illegible],
                     AA22759[illegible], T86811, AA72666[illegible], F1243[illegible], and AA292266."
     STS             647..783
                     /standard_name="stSG34682"
                     /db_xref="GDB:456[illegible]425"
     STS             695..86[illegible]
                     /standard_name="[illegible]"
                     /db_xref="dbSTS:32797"
     misc_feature    50[illegible]1..5289
                     /note="Region: Similar to H.sapiens genomic DNA, X8[illegible]."
     repeat_region   5178..5245
                     /rpt_family="GC_rich"
     repeat_region   5290..5532
                     /rpt_family="GC_rich"
     misc_feature    55[illegible]..5[illegible]
                     /note="Region: Similar to H.sapiens genomic DNA, X8[illegible]."
     repeat_region   6319..6602
                     /rpt_family="AluSx"
     repeat_region   complement([illegible]72..7745)
                     /rpt_family="L1M4"
     repeat_region   complement([illegible]47..7[illegible])
                     /rpt_family="AluSp"
     repeat_region   8156..8273
                     /rpt_family="MER4A[illegible]"
     repeat_region   complement(8297..8491)
                     /rpt_family="AluSx"
     repeat_region   complement(8542..8591)
                     /rpt_family="AluSp"
     repeat_region   9144..9[illegible]
                     /rpt_family="MER4[illegible]"
     repeat_region   complement(9421..9582)
                     /rpt_family="FRAM"
     repeat_region   complement(9586..9631)
                     /rpt_family="(TAGA)n"
     repeat_region   complement([illegible]..9894)
                     /rpt_family="Al[illegible]"
     repeat_region   9935..10052
                     /rpt_family="MIR"
     repeat_region   complement(10124..10260)
                     /rpt_family="L2"
     repeat_region   1[illegible]50..11126
                     /rpt_family="L2"
     repeat_region   11[illegible]43..114[illegible]6
                     /rpt_family="AluSp"
     repeat_region   119[illegible]..12[illegible]
                     /rpt_family="GC_rich"
     gene            join(12104..12195,16081..16158,19065..19243,19956..20060,
                     20192..20317,21117..2126[illegible],21[illegible]..21526,21966..22[illegible])
                     /gene="Unigene cluster containing AI18[illegible], AA77[illegible],
                     W8[illegible]22, T6[illegible]51, AA41[illegible], F12[illegible], and AA2[illegible]."
     repeat_region   complement(14187..14295)
                     /rpt_family="MIR"
     repeat_region   complement(14866..15168)
                     /rpt_family="AluSq"
     repeat_region   complement(15623..1572[illegible])
                     /rpt_family="(CA)n"
     repeat_region   complement(17254..17540)
                     /rpt_family="AluY"
     repeat_region   complement(18[illegible]..18451)
                     /rpt_family="AluSp"
     STS             18252..18363
                     /standard_name="[illegible]"
                     /db_xref="dbSTS:[illegible]"
     STS             22[illegible]..22[illegible]
                     /standard_name="stSG[illegible]"
                     /db_xref="GDB:[illegible]"
     repeat_region   complement(228[illegible]..2[illegible])
                     /rpt_family="M[illegible]"
     repeat_region   complement(24[illegible]..24[illegible])
                     /rpt_family="L2"
     repeat_region   complement(25824..26124)
                     /rpt_family="AluSp"
     repeat_region   complement([illegible]..[illegible]71)
                     /rpt_family="(TTTA)n"

  Query Match             18.3%;  Score 260.2;  DB 9;  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. 1.5e-41;
  Matches  262;  Conservative    [illegible];  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy        [illegible]
Db     4222 [illegible]

Qy      394 GCAGCCATCTGGCTGCCAAACACC[illegible] 453
Db     4162 GCAGCCATCTGGCTGCCAAACACCTGCACTCCTGCTTGCGCCGGCAGCTGGAG[illegible] 410[illegible]

Qy      454 [illegible]
Db     4102 GTGGAAG[illegible] 404[illegible]

Qy      514 [illegible]
Db     4042 [illegible]

Qy      574 [illegible] 598
Db     3982 [illegible]


RESULT 11
AC092045/c
LOCUS       AC092045          1[illegible] bp    DNA     linear   [illegible]
DEFINITION  Homo sapiens chromosome [illegible] clone RP11-[illegible], complete sequence.
ACCESSION   AC092045 AC024144
VERSION     AC092045.2  GI:[illegible]281257
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1[illegible])
  AUTHORS   Kaul,R.K., [illegible]son,M.V., Zhou,Y., James,R.A., Raymond,C. and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1[illegible])
  AUTHORS   Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J., [illegible] and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUN-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 1[illegible])
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C. and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (2[illegible]) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
COMMENT     On Aug 23, 2001 this sequence version replaced gi:144[illegible].
              -------  Genome Center
               Center: University of Washington Genome Center
               Center code: UWGC
               Web site: http://www.genome.washington.edu
```

[illegible] Washington [illegible]
[illegible] Vector: [illegible]
Project Information
Vector [illegible] name: [illegible]
Vector [illegible] name: [illegible] ([illegible])
Summary Statistics
Sequencing vector: M13; [illegible] reads
Sequencing vector: plasmid; [illegible] reads
Chemistry: Dye-terminator [illegible] reads
Chemistry: Dye-primer [illegible] reads
Chemistry: Dye-terminator [illegible] reads
Assembly program: Phrap; version [illegible]
Consensus quality: [illegible] bases at least Q40
Consensus quality: [illegible] bases at least Q30
Consensus quality: [illegible] bases at least Q20
Insert size: [illegible]
Insert size: [illegible]; sum of contigs
Quality coverage: [illegible] in [illegible] bases
Quality coverage: [illegible]

[illegible] Sequences:
[illegible] AT [illegible]
[illegible] AT [illegible]

Sequence Quality Assessment:
This entry has been annotated with sequence quality estimates computed by the Phrap assembly program. All manually edited bases have been reduced to quality zero. Quality levels above 40 are expected to have less than 1 error in 10,000 bp. Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

[illegible] all regions were either double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality [illegible]); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

Sequence Validation:
This sequence has been validated by SuperMap fingerprint analysis. Comparison of the experimentally derived digest fragments with sequence predicted fragments is given below. The restriction digested sequence consists of both insert and vector in order to accurately represent the entire clone. [illegible] fragments [illegible] (approximately [illegible] bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Multiple [illegible] fragments are separated by dashed lines.

[illegible]		[illegible]		[illegible]	
SuperMap	Fingerprint	SuperMap	Fingerprint	SuperMap	Fingerprint
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	2[illegible]1	[illegible]	[illegible]
[illegible]	[illegible]	3014	3008	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	24[illegible]4	[illegible]	[illegible]
[illegible]	[illegible]	4567	46[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
2644	[illegible]	[illegible]	6141	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	8744	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]	5268	5277	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
6112	6189	[illegible]	3954	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	26855	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	3954	[illegible]	[illegible]
[illegible]	[illegible]	8435	8744	[illegible]	[illegible]
[illegible]	[illegible]	18224	18042	[illegible]	[illegible]
[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]			[illegible]	[illegible]
[illegible]	[illegible]				
[illegible]	[illegible]				
[illegible]	[illegible]				
[illegible]	[illegible]				
[illegible]	[illegible]				
[illegible]	[illegible]				
[illegible]	[illegible]				

FEATURES Location/Qualifiers

```
     source          1..171348
                     /organism "Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome "3"
                     /clone "RP11 168J18"
                     /clone_lib "RPCI human BAC library 11"
BASE COUNT     [illegible] a  46165 c  4[illegible]178 g  4[illegible]769 t
ORIGIN

  Query Match             38.9%;  Score 26[illegible].2;  DB 9;  Length 171348;
  Best Local Similarity   98.9%;  Pred. No. 1.2e-41;
  Matches  262;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        334 [illegible] 393
              [illegible]
Db     165894 [illegible] 165835

Qy        394 [illegible] 453
              [illegible]
Db     165834 [illegible] 165775

Qy        454 [illegible] 513
              [illegible]
Db     165774 [illegible] 165715

Qy        514 [illegible] 573
              [illegible]
Db     165714 [illegible] 165655

Qy        574 TTGGAGACTGCCTTTCAGGAATGTG 598
              [illegible]
Db     165654 [illegible] 165630


RESULT [illegible]
AC094021
LOCUS       AC094021               214160 bp    DNA     linear   PRI 27-MAR-2002
DEFINITION  Homo sapiens chromosome 3 clone RP11-801L18, complete sequence.
ACCESSION   AC094021 AC069258
VERSION     AC094021.2  GI:19745061
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-2002) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
COMMENT     On Mar 27, 2002 this sequence version replaced gi:15594339.
            ------------ Genome Center
                Center: University of Washington Genome Center
                Center Code: UWGC
                Web site: http://www.genome.washington.edu
                Contact: [illegible]@u.washington.edu
                Drafting Center: BCM
            ------------    Project Information
                Center project name: chr-3
                Center clone name: RP11-801L18 (Dec565)
            ------------ Summary Statistics
                Sequencing vector: M13; L08821; 49% of reads
                Sequencing vector: plasmid; 51% of reads
                Chemistry: Dye-terminator ET; 99% of reads
                Chemistry: Dye-primer Bodipy; 1% of reads
                Chemistry: Dye Terminator Big Dye; 5[illegible]% of reads
                Assembly program: Phrap; version 0.990319
                Consensus quality: 21[illegible] bases at least Q40
                Consensus quality: 214[illegible] bases at least Q30
                Consensus quality: 214157 bases at least Q20
                Insert size: 214160; sum-of-contigs
                Quality coverage: [illegible]x in Q20 bases; sum-of-contigs
            ------------
            Overlapping Sequences:
                5': Mapping in progress
                3': RP11-[illegible] (TWGT[illegible]) AC[illegible]
            ------------
            Sequence Quality Assessment:
             This entry has been annotated with sequence quality
             estimates computed by the Phrap assembly program.
             All manually edited bases have been reduced to quality zero.
             Quality levels above 40 are expected to have less than
             1 error in 10,000 bp.
             Base-by-base quality values are not generally visible from the
             GenBank flat file format but are available as part
             of this entry's ASN.1 file.

            This sequence was finished as follows unless otherwise noted:
            all regions were either double-stranded or sequenced with an
            alternate chemistry or covered by high quality data (i.e., Phred
            quality >= 30); an attempt was made to resolve all sequencing
            problems, such as compressions and repeats; all regions were
            covered by at least one plasmid subclone or more than one M13
            subclone; and the assembly was confirmed by restriction digest.
            ------------
            Sequence Validation:
             This sequence has been validated by Multiple Complete Digest
             fingerprinting. Comparison of the experimentally derived digest
             fragments with sequence predicted fragments is given below.
             The electronically-digested sequence consists of both insert and
             vector, in order to accurately represent the entire circular BAC.
             Small fragments below a variable cutoff (approximately 4 to 800 bp)
             are not resolved in the fingerprint and hence do not appear
             in the table. There are no significant remaining discrepancies
             between the experimental and predicted values. Uniquely ordered
             fragments are separated by dashed lines.
                   BglII                  EcoRI                  HindIII
            ---------------------   ---------------------   ---------------------
            SeqBerMap  FingrPrnt    SeqBerMap  FingrPrnt    SeqBerMap  FingrPrnt
            ---------  ---------    ---------  ---------    ---------  ---------


            -----------             -----
                 3254       3226         8696       8704         489[illegible]      5017
            ----------            -------------           ----------
                 2067       2035            6       [illegible]809       [illegible]      [illegible]44[illegible]
            ----------            -------                 --------
                10266      [illegible]         4672       4541         51[illegible]      [illegible]
            -----  ---            --   -                  ---
                14477      14184         [illegible]2       75[illegible]         41      [illegible]
            ---------  ----                 -                  --
                 6169       [illegible]64         1627       1647      [illegible]      [illegible]
            -     -               ---                      -
                 11235      [illegible]         1167       114[illegible]      14[illegible]      [illegible]
            --       ---          --    --                 --
                 1696       15[illegible]         4966       4941       [illegible]      [illegible]
                 ----             --     -                 --
                 1601       1579         5231       5277       41[illegible]      [illegible]
            ----------            -----    ---             --
                 42[illegible]      [illegible]         6[illegible]2       6041      [illegible]      [illegible]
            -       --            --                       --
                 1426       1399         8037       8002       2[illegible]      [illegible]
            ---      -            -----    ---        -        -
                   [illegible]      [illegible]          [illegible]       [illegible]       7[illegible]      [illegible]
                   --             --
                 5902       [illegible]         8244       8387       2[illegible]      20[illegible]
```

```
[illegible]

FEATURES             Location/Qualifiers
     [illegible]     [illegible]
                     /[illegible] "[illegible]"
                     /db_xref="[illegible]"
                     /[illegible] "[illegible]"
                     /[illegible] "[illegible]"
```

```
                     /[illegible] "[illegible] human BAC library [illegible]"
BASE COUNT    [illegible] a  57[illegible] c  5[illegible]28 g  48[illegible] t
ORIGIN

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length 2[illegible];
  Best Local Similarity   98.[illegible]%;  Pred. No. [illegible]e-41;
  Matches  2[illegible];  Conservative    [illegible];  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy        334 [illegible]
              [illegible]
Db      25941 [illegible]

Qy        394 [illegible]
              [illegible]
Db      26001 [illegible]

Qy        454 [illegible]
              [illegible]
Db      26061 [illegible]

Qy        514 [illegible]
              [illegible]
Db      26121 [illegible]

Qy        574 [illegible] 598
              [illegible]
Db      26181 [illegible]

Search completed: February [illegible], 2003, [illegible]
Job time : 41[illegible] secs
```

```
                         GenCore version 5.1.3
                Copyright (c) 1993 - 2003 Compugen Ltd.

 OM nucleic - nucleic search, using sw model

Run on:           February 22, 2003, 21:44:04 ; Search time 119 Seconds
                                                  (without alignments)
                                                  9742.187 Million cell updates/sec

Title:            US-09-866-987-3
Perfect score:    1380
Sequence:         1 atgtcccgcggctagttccg..........aaaaaagcaatgaccactga 1380

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         2185237 seqs, 1125994159 residues

Total number of hits satisfying chosen parameters:       4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        N_Geneseq_101002:*
                  1: [illegible]:*
                  2: [illegible]:*
                  3: [illegible]:*
                  4: [illegible]:*
                  5: [illegible]:*
                  6: [illegible]:*
                  7: [illegible]:*
                  8: [illegible]:*
                  9: [illegible]:*
                  10: [illegible]:*
                  11: [illegible]:*
                  12: [illegible]:*
                  13: [illegible]:*
                  14: [illegible]:*
                  15: [illegible]:*
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                  18: [illegible]:*
                  19: [illegible]:*
                  20: [illegible]:*
                  21: [illegible]:*
                  22: [illegible]:*
                  23: [illegible]:*
                  24: [illegible]:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                                  SUMMARIES
                          %
Result                  Query
  No.    Score   Match Length  DB  ID                          Description
  ----   -----   ----- ------  --  ---------                   -----------
    1     1369    99.2   1837  22  AAH22961                    Human phosphatase
    2      917    66.4    917  24  ABA94426                    Human protein phos
    3      546    38.8    547  24  ABL79990                    Human ovarian canc
    4    263.8    19.2   2519  21  ABK17152                    DNA encoding human
    5    262.4    19.0   4262  17  AAT38484                    Rat petrin cDNA cl
    6    262.4    19.0   4515  17  AAT38487                    Rat petrin cDNA.
    7    243.4    17.6   1617  23  AAS93640                    DNA encoding novel
    8    243.4    17.6   1887  22  AAI58166                    Human polynucleoti
    9    243.4    17.6   5791  21  ABK16163                    cDNA encoding cl
   10    242.4    17.6   1903  22  AAH17958                    Human cDNA sequenc
   11      178    12.9    47[illegible]  17  AAT38482          Rat petrin cDNA cl
   12    109.2     7.9    7[illegible]  21  AAA[illegible]     Human [illegible] cancer
   13      103     7.5    [illegible]  20  AAZ12841            Human gene express
   14    102.8     7.4    750  20  AAX98454                    Human validated ex
   15    101.2     7.3   2087  23  ABL25549                    Drosophila melanog
   16    101.2     7.3   5107  23  ABL25548                    Drosophila melanog
   17       98     7.1    [illegible]  24  ABL82482            Human ovarian canc
   18       95     6.9    [illegible]  2[illegible]  AAX[illegible]  Human [illegible]
   19     87.6     6.3    794  21  AAA[illegible]7             Human colon cancer
   20     83.6     6.1    294  21  AAA00279                    Human colon cancer
   21     81.2     5.9   2258  23  ABV22179                    Human prostate exp
   22     81.2     5.9   2258  23  ABV2[illegible]             Human prostate exp
   23     81.2     5.9   2258  23  ABV27918                    Human prostate exp
   24     81.2     5.9   2258  23  ABV2[illegible]             Human prostate exp
   25     81.2     5.9   2258  23  ABV2[illegible]             Human prostate exp
c  26     76.8     5.6    582  22  AAH1[illegible]             Human cDNA clone (
   27       68     4.9    431  17  AAT38480                    Rat petrin cDNA cl
   28     5[illegible].4   3.[illegible]   1643  22  AAS[illegible]   Anti-tensin [illegible]
c  29     49.8     3.6   6714  21  AAZ4[illegible]             Nucleotide sequenc
c  30     49.8     3.6   6924  21  AAZ45934                    Nucleotide sequenc
c  31     49.8     3.6   6924  21  AAZ45935                    Nucleotide sequenc
c  32     49.4     3.6   26[illegible]  22  AAK[illegible]     Human [illegible]/[illegible]
   33     49.2     3.6    730  22  AAI59952                    Human polynucleoti
c  34       49     3.6    506  24  ABK4[illegible]             Protein phosphatas
c  35     48.8     3.5   [illegible]  24  AB[illegible]        Histoplasma [illegible]
c  36     48.2     3.5   1491  2[illegible]  AAX15117          Nucleotide sequenc
c  37     48.2     3.5   2887  24  AAD36162                    Human Smad6 DNA.
c  38       48     3.5    [illegible]  24  AB[illegible]14     [illegible]
   39       48     3.5    [illegible]  24  AB[illegible]15     [illegible]
   40     47.6     3.4   [illegible]  22  AAZ[illegible]       EBV 28K gene. Pse
c  41     47.4     3.4   [illegible]  22  AAK[illegible]       Human [illegible]
   42       47     3.4    [illegible]  20  AAZ[illegible]4     Zea mays [illegible]
   43     4[illegible]     3.[illegible]   [illegible]  21  ABN[illegible]  [illegible] used to
c  44     4[illegible]     3.[illegible]   [illegible]  21  ABL64982  Lung cancer relate
c  45     4[illegible]     3.4   13058  24  ABL[illegible]      Lung cancer relate

                                 ALIGNMENTS

RESULT 1
AAH22961
ID   AAH22961 standard; cDNA; 1837 BP.
XX
AC   AAH22961;
XX
DT   17-SEP-2001  (first entry)
XX
DE   Human phosphatase (PP) encoding cDNA (clone ID 1725447CB1).
XX
KW   Phosphatase; PP; Alzheimer's disease; Huntington's disease; human;
KW   immune disorder; cancer; neoplasm; immunomodulator; [illegible]
KW   neuroprotective; anticonvulsant; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1383
FT                   /*tag= a
FT                   /product= "phosphatase"
XX
PN   WO200153469-A2.
XX
PD   26-JUL-2001.
XX
PF   19-JAN-2001; 2001WO-US02[illegible].
XX
PR   21-JAN-2000; 2000US-0177715.
PR   26-JAN-2000; 2000US-0178[illegible].
PR   25-FEB-2000; 2000US-0184959.
PR   17-MAR-2000; 2000US-0190142.
XX
```

```
PA   [illegible]
XX
PI   [illegible] Tang YT, [illegible] Yue H, [illegible] Baughn MR, [illegible]
PI   [illegible] Walia NK, [illegible] Polinsky [illegible] Mathur [illegible]
XX
DR   WPI; [illegible]
DR   N-PSDB; [illegible]
XX
PT   New phosphatases useful for treating diseases associated with
PT   decreased expression of functional phosphatases e.g. Alzheimer's
PT   disease, Huntington's disease, immune disorders, and cancers
XX
PS   Claim [illegible]; Page [illegible]; [illegible] English.
XX
CC   The present invention provides human phosphatases (PP) and polynucleotides
CC   encoding the phosphatases. The polypeptides can be expressed by standard
CC   recombinant methodology. The PP are useful for treating a disease or
CC   condition associated with decreased expression of functional
CC   phosphatases. Compositions containing agonists or antagonists of PP may
CC   be used to treat a disease associated with decreased expression or
CC   overexpression of PP, respectively. Such diseases may include
CC   Alzheimer's disease, Huntington's disease, immune disorders, and
CC   cancers. The present sequence represents a human phosphatase encoding
CC   cDNA.
XX
SQ   Sequence [illegible] BP; [illegible]

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative    [illegible];  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

[illegible]

Db        901 CACATGAGTGGCTGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCATTGATC 960

[illegible]

Qy       1381 A 1381

Db       1381 A 1381


RESULT [illegible]
ABA94426
ID   ABA94426 standard; cDNA; 917 BP.
XX
AC   ABA94426;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human protein phosphatase [illegible] encoding cDNA.
XX
KW   Protein phosphatase; serine threonine phosphatase; [illegible]
KW   cytostatic; immunosuppressive; vasotropic; analgesic; hypertensive;
KW   hypotensive; gastrointestinal; neuroprotective; virucide; antibacterial; [illegible]
KW   fungicide; [illegible]; antiinflammatory; cardiant; [illegible]
KW   antiarthritic; muscular; antiasthmatic; osteopathic; antipsoriatic;
KW   antiarteriosclerotic; antiallergic; antidiabetic; tranquilizer; cancer;
KW   neuroleptic; antiparkinsonian; anorectic; gene therapy; ss.
XX
```

```
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..917
FT                   /*tag= a
FT                   /product= "STP-50"
FT                   /note= "sequence coding for approximately another 154
FT                          amino acid residues in the corresponding protein
FT                          is not printed in the specification."
XX
PN   WO200192491-A2.
XX
PD   06-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US17305.
XX
PR   30-MAY-2000; 2000US-208291P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman GD,  Whyte D,  Sudarsanam S,  Manning G,  Caenepeel S;
PI   Martinez R,  Hill RJ,  Flanagan P;
XX
DR   WPI; 2002-[illegible].
DR   P-PSDB; ABB07304.
XX
PT   New phosphatase polypeptides for treating e.g., cancers, immune related
PT   diseases and disorders, cardiovascular diseases, or brain or
PT   neuronal associated diseases
XX
PS   Claim 28; Fig 1A; 161pp; English.
XX
CC   The invention relates to human protein phosphatase polypeptides and
CC   polynucleotides. The phosphatase polypeptides are useful for diagnosing
CC   and treating various phosphatase-related diseases and conditions, such as
CC   cancers, immune related diseases and disorders, cardiovascular diseases
CC   (e.g., reperfusion restenosis), brain or neuronal-associated diseases,
CC   metabolic disorders (e.g., diabetes or obesity), central or peripheral
CC   nervous system diseases and conditions (e.g., pain, migraine, mood
CC   disorders, hypotension, or hypertension), psychotic and neurological
CC   disorders (e.g., anxiety, schizophrenia), neurodegenerative diseases
CC   (e.g., Alzheimer's or Parkinson's disease), infections caused by viral
CC   (e.g., human immunodeficiency virus (HIV)), bacterial, fungal or prion
CC   agents, ocular diseases, macular degeneration, and inflammatory disorders
CC   (e.g., rheumatoid arthritis, multiple sclerosis, osteoarthritis). The
CC   polypeptides may also be used for screening for small molecule compounds
CC   that inhibit the catalytic activity of the encoded protein phosphatase
CC   with potential use for treating the above mentioned diseases, for
CC   generating antibodies or hybridomas, and as a diagnostic tool for
CC   detecting a disease or disorder. Genetic sequences of phosphatases are
CC   useful in gene therapy. The present sequence represents a cDNA encoding
CC   a novel human serine threonine phosphatase (STP) like phosphatase
CC   polypeptide STP-50.
XX
SQ   Sequence 917 BP; 161 A; 276 C; 310 G; 170 T; 0 other;

  Query Match             66.4%;  Score 917;  DB 24;  Length 917;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-205;
  Matches  917;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 [illegible] 60
              [illegible]
Db          1 [illegible] 60

Qy         61 [illegible] 120
              [illegible]
Db         61 [illegible] 120

Qy        121 [illegible] 180
              [illegible]
Db        121 [illegible] 180

Qy        181 [illegible] 240
              [illegible]
Db        181 [illegible] 240

Qy        241 [illegible] 300
              [illegible]
Db        241 [illegible] 300

Qy        301 [illegible] 360
              [illegible]
Db        301 [illegible] 360

Qy        361 [illegible] 420
              [illegible]
Db        361 [illegible] 420

Qy        421 [illegible] 480
              [illegible]
Db        421 [illegible] 480

Qy        481 [illegible] 540
              [illegible]
Db        481 [illegible] 540

Qy        541 [illegible] 600
              [illegible]
Db        541 [illegible] 600

Qy        601 [illegible] 660
              [illegible]
Db        601 [illegible] 660

Qy        661 [illegible] 720
              [illegible]
Db        661 [illegible] 720

Qy        721 [illegible] 780
              [illegible]
Db        721 [illegible] 780

Qy        781 [illegible] 840
              [illegible]
Db        781 [illegible] 840

Qy        841 [illegible] 900
              [illegible]
Db        841 [illegible] 900

Qy        901 [illegible] 917
              [illegible]
Db        901 [illegible] 917


RESULT 3
ABL79990
ID   ABL79990 standard; cDNA; 547 BP.
XX
AC   ABL79990;
XX
DT   17-MAY-2002  (first entry)
XX
DE   Human ovarian cancer related cDNA clone SEQ ID NO:[illegible].
XX
KW   Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192581-A2.
XX
PD   06-DEC-2001.
XX
PF   29-MAY-2001; 2001WO-US17[illegible].
XX
PR   26-MAY-2000; 2000US-[illegible]184P.
```

```
XX
PA    [illegible] DNA [illegible]
XX
PI    [illegible]
XX
DR    [illegible]
XX
PT    [illegible] for therapy and diagnosis of ovarian cancer comprising
PT    [illegible] polypeptide [illegible]
PT    [illegible] polypeptide [illegible]
PT    polypeptide
XX
PS    [illegible]
XX
CC    The present invention describes a composition (I) comprising carriers
CC    and immunostimulator and a polypeptide (II) of an ovarian tumour
CC    polypeptide encoded by a polynucleotide (III) having a cDNA sequence
CC    (S1) from the [illegible] nucleotide sequences as given in ABK[illegible]
CC    ABK[illegible]. (III) encoding (II) having a sequence (S2), a T cell
CC    population of (II), or antigen presenting cells that express (II).
CC    (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC    (S1) can be used for detecting ovarian cancer in a patient's biological
CC    sample preferably serum or ovarian tissue. The method comprises
CC    contacting a biological sample from a patient with (IV), detecting the
CC    amount of polynucleotide hybridising to (IV) and comparing the amount to
CC    a predetermined cut-off value and thereby detecting ovarian cancer in the
CC    patient, where the amount of polynucleotide hybridising to (IV) is
CC    detected preferably by polymerase chain reaction (PCR). [illegible]
CC    [illegible] (II) is useful for stimulating and/or expanding T cells
CC    specific for an ovarian tumour protein comprising contacting T cells
CC    with (III) or (II). (III) is useful in design and preparation of
CC    [illegible]
CC    [illegible]
CC    [illegible] cDNA library using [illegible]
CC    techniques
XX
SQ    [illegible]

  Query Match             [illegible]
  Best Local Similarity   [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    1272 [illegible]
Db     486 [illegible]

Qy    1332 [illegible]
Db     540 [illegible] 547


RESULT 4
ABK47452
ID    ABK47452 standard; DNA; [illegible] BP.
XX
AC    ABK47452;
XX
DT    [illegible] (first entry)
XX
DE    DNA encoding human protein phosphatase II C like (PPIIC) enzyme.
XX
KW    Protein phosphatase II C like; agonist; antagonist; apoptosis; AIDS;
KW    Acquired immunodeficiency virus; genetic immunodeficiency; PPIIC;
KW    neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW    retinitis pigmentosa; amyotropic lateral sclerosis; myelodysplasia;
KW    aplastic anaemia; ischaemic injury; myocardial infarction; stroke;
KW    reperfusion injury; toxin induced disease; cirrhosis; wasting disease;
KW    cachexia; viral infection; hepatitis; osteoporosis; cancer; diabetes;
KW    central nervous system disorder; CNS disorder; cardiovascular disorder;
KW    inflammatory disorder; chronic obstructive pulmonary disease; [illegible]
KW    gene; ds; human.
XX
OS    Homo sapiens.
XX
FH    Key                 Location/Qualifiers
FT    CDS                 [illegible]
FT                        /*tag= [illegible]
FT                        /product= "PPIIC"
FT                        /note= "Protein phosphatase IIC like enzyme.
FT                                Specifically claimed in claim 1"
FT    misc_binding        [illegible]
FT                        /*tag= b
FT                        /note= "Bound by the antisense oligonucleotide shown
FT                                in ABK47461"
XX
PN    WO200[illegible]-A2.
XX
PD    [illegible]-MAR-200[illegible].
XX
PF    20-AUG-2001; [illegible]
XX
PR    [illegible]
PR    [illegible]-APR-20[illegible]
XX
PA    (FARB ) BAYER AG.
XX
PI    Xia Y;
XX
DR    WPI; [illegible]
DR    P-PSDB; AA[illegible]
XX
PT    New protein phosphatase IIC like enzyme and polynucleotides, useful for
PT    treating a disease associated with an increase or decrease in
PT    apoptosis, e.g. neurodegenerative diseases, viral infections,
PT    myelodysplasia, cancer, diabetes
XX
PS    [illegible] English.
XX
CC    The invention describes an isolated polynucleotide (I) which encodes a
CC    protein phosphatase IIC (PPIIC) like enzyme (II). (I) and (II) can be
CC    used in diagnostic assays for detecting diseases and abnormalities or
CC    susceptibility to diseases and abnormalities related to the presence of
CC    mutations in the nucleic acid sequences encoding the enzyme. (I) and (II)
CC    or its antagonists, agonists, or modulators are useful for treating a
CC   disease or disorder associated with an increase in apoptosis such as AIDS
CC   or other infectious or genetic immunodeficiencies, neurodegenerative
CC   diseases (e.g. Alzheimer's disease or Parkinson's disease, retinitis
CC   pigmentosa, or amyotrophic lateral sclerosis), myelodysplasia (e.g.
CC   aplastic anaemia), ischaemic injuries (e.g. myocardial infarction, stroke
CC   or reperfusion injury), toxin-induced diseases (e.g. alcohol-induced
CC   liver damage or cirrhosis), wasting diseases (e.g. cachexia), viral
CC   infections (e.g. hepatitis B or C), and osteoporosis, or a decrease in
CC   apoptosis such as cancer, diabetes, CNS disorders, cardiovascular
CC   disorders, chronic obstructive pulmonary disease (COPD), and inflammatory
CC   disorders. Regulation of human PP11C-like enzyme can be used to treat
CC   disorders such as diabetes, CNS disorders, cardiovascular disorders,
CC   COPD, and cancers (e.g. leukaemia, lymphoma, or cancers of the organs).
CC   This sequence encodes the novel human protein phosphatase 11C like enzyme
CC   described in the invention.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible]%;  Score [illegible];  DB 24;  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  [illegible];  Conservative    0;  Mismatches  [illegible];  Indels   16;  Gaps    [illegible];

Qy        445 [illegible]
Db       1369 [illegible] 1428

Qy        505 [illegible]
Db       1429 ATC GCCATATCGGAGAGCAGCTAAAGGACCTGAAGGAAGTGAG ACGAGAGCCTGGTA 1487

Qy        565 [illegible] 624
Db       1488 [illegible] 1547

Qy        625 GCCTCAGG CAGATGGGGGGC G ACAGGCCTGGTGG TGTG C TGC AGGGAAAGCTG 684
Db       1548 GGCCACCAAGTGGAGGGGGGCTGCTGTGCACTGGTTGTGATCTAC TGCTAGGCAA GTG 1607

Qy        685 TACATGGCCAATGCTGGGGATAGCAGGGCCATCTTGGTGC GAGAGATGAGATACGGCCA 744
Db       1608 [illegible]

Qy        745 CTGAGCTTCGAGTTCACCCAGACACTGAGGGCAGCGGATCTACCAGCTGCCCTTCGTC 804
Db       1668 [illegible]

Qy        805 [illegible]
Db       1728 [illegible] 1787

Qy        865 [illegible]
Db       1788 [illegible] 1847

Qy        925 [illegible]
Db       1848 AAGATGAGCTGGAGGATCTCAGGTT [illegible] CAAAAAGGCTCGG 1907

Qy        985 [illegible]
Db       1908 [illegible]

Qy       1045 [illegible] 1104
Db       1968 [illegible]

Qy       1105 [illegible]
Db       2028 [illegible]

Qy       1165 GTACTGTCCAACGAGCAGGTGGCATGGCTGG GGGAGCTTC TCCCTG  GGAA CAA 1221
Db       2088 [illegible]
```

```
Qy       1222 [illegible]
Db       2148 [illegible] 2207

Qy       1275 ---------  [illegible]
Db       2208 CCCCGAGACCGTGCCTGCCGTCTCCCAACAACAAGCTGGGTCCGGGATGACATCTCT 2267

Qy       1330 [illegible]
Db       2268 GTCTCGGTCATCCCCTGGGAGGCCAGGC 2297


RESULT 5
AAT38484
ID   AAT38484 standard; cDNA; 4262 BP.
XX
AC   AAT38484;
XX
DT   16-JAN-1997  (first entry)
XX
DE   Rat petrin cDNA clone D1.
XX
KW   Petrin; neurite outgrowth associated protein; CNS;
KW   central nervous system; myelin; protein phosphatase 2C; stroke;
KW   neurodegeneration; gene therapy; ss.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 3825
FT                   /*tag=  a
FT                   /note=  "base 3825 is given as B in the
FT                            specification"
XX
PN   WO9632476-A1.
XX
PD   17-OCT-1996.
XX
PF   12-APR-1996;   96WO-CA00234.
XX
PR   13-APR-1995;   95US-0421701.
XX
PA   (MOUN ) MOUNT SINAI HOSPITAL CORP.
XX
PI   Lubec M, [illegible] A, Roach A, Roder J;
XX
DR   WPI; 1996-477127/47.
DR   P-PSDB; AAW04327.
XX
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, Petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 2; Page 50-52; [illegible]pp; English.
XX
CC   A cDNA sequence (AAT38484) codes for petrin (AAW04327) - a protein
CC   involved in modulating neurite growth inhibition. It was deduced
CC   from fragments of clone D1 (see also AAT38479-83) isolated from an
CC   adult rat brain cDNA library in lambda gt11 by screening with
CC   a monoclonal antibody that blocks the effect on neurons in culture
CC   of CNS myelin inhibitors. The petrin gene is expressed in neurons
CC   in brain tissue, partic. in cerebellum Purkinje cells. It can be
CC   used to produce petrin protein and to prepare probes. Antisense
CC   sequences (see also AAT38485) can be used in gene therapy to enhance
CC   axonal regeneration.
XX
SQ   Sequence 4262 BP; 921 A; 1164 C; 1156 G; 1002 T; 19 other;

  Query Match             [illegible]%;  Score [illegible];  DB 17;  Length 4262;
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  [illegible];  Conservative    0;  Mismatches  306;  Indels    3;  Gaps    3;

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible] AAA[illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible] AT 1262
Db       [illegible]


RESULT [illegible]
AAI38486
ID   AAI38486 standard; cDNA; [illegible]
XX
AC   AAI38486;
XX
DT   [illegible]-JAN-[illegible]  (first entry)
XX
DE   Rat petrin cDNA.
XX
KW   [illegible]
KW   [illegible]
KW   [illegible] gene therapy; ss.
XX
OS   Rattus sp.
XX
FH   Key                 Location/Qualifiers
FT   CDS                 [illegible]
FT                       /*tag=  a
FT                       /product= petrin
FT   misc_difference     [illegible]
FT                       /*tag=  b
FT                       /note= "base [illegible] is given as t in the
FT                              specification"
XX
PN   WO96[illegible]476-A1.
XX
PD   [illegible]-1996.
XX
PF   12-APR-1996;   96WO-CA00234.
XX
PR   1[illegible]-APR-1995;   95US-[illegible].
XX
PA   (MOUN-) MOUNT SINAI HOSPITAL CORP.
XX
PI   Jabes M,  Lozano A,  Roach A,  Roder J;
XX
DR   WPI; 1996-477171/47.
DR   P-PSDB; AAW04527.
XX
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, Petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 4; [illegible]
XX
CC   A nucleotide sequence (AAI38486) codes for petrin (AAW04527), a protein
CC   involved in [illegible] neurite growth inhibition. It was isolated
CC   from an adult rat brain cDNA library in lambda gt11 by screening
CC   with probes based on partial petrin clones (see also AAI38479-84).
CC   The human petrin locus was localised to chromosome 12. The gene
CC   is expressed in neurons in brain tissue, partic. in cerebellum
CC   Purkinje cells. It can be used to produce petrin protein and to
CC   prepare probes. Antisense sequences (see also AAI38485) can be used
CC   in gene therapy to enhance axonal regeneration.
XX
SQ   Sequence 4515 BP; 986 A; 1240 C; 1236 G; 1052 T; 1 other;

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length 4515;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  45[illegible];  Conservative    0;  Mismatches  306;  Indels    3;  Gaps    3;

Qy        498 [illegible]
Db       1091 [illegible] 1150

Qy        558 [illegible]
Db       1151 [illegible]

Qy        618 [illegible]
Db       1211 [illegible]

Qy        678 [illegible]
Db       1271 [illegible]

Qy        738 [illegible]
Db       1331 [illegible]

Qy        798 [illegible]
Db       1391 [illegible]

Qy        858 [illegible]
Db       1451 [illegible]
```

```
Qy     918 [illegible] 977

Db    1511 [illegible] 1570

Qy     978 [illegible] 1037

Db    1571 [illegible] [illegible]

Qy    1038 [illegible] 1097

Db    1631 [illegible] [illegible]

Qy    1098 [illegible] 1157

Db    1691 [illegible] [illegible]

Qy    1158 [illegible] [illegible]

Db    1751 [illegible] [illegible]

Qy    [illegible] [illegible]

Db    1811 [illegible] [illegible]


RESULT 7
AAS[illegible]
ID   AAS93640 standard; cDNA; 1617 BP.
XX
AC   AAS93640;
XX
DT   [illegible]-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #29444.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   [illegible] A2.
XX
PD   11-OCT-2001.
XX
PF   [illegible]-MAR-[illegible]; [illegible].
XX
PR   [illegible]-MAR-2000; [illegible]-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   [illegible] RT, [illegible], Tang YT;
XX
DR   WPI; 2001-[illegible]/7[illegible].
DR   P-PSDB; ABG294[illegible].
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity
XX
PS   Claim 1; SEQ ID No 29444; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS[illegible] AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1617 BP; [illegible] A; 442 C; 467 G; [illegible] T; 0 other;

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   57.[illegible]%;  Pred. No. 6.5e-47;
  Matches  4[illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy     [illegible] [illegible]

Db     [illegible] [illegible] 790

Qy     560 [illegible]

Db     791 [illegible]

Qy     620 [illegible]

Db     851 [illegible] 910

Qy     680 [illegible] 739

Db     911 [illegible]

Qy     740 [illegible]

Db     971 [illegible]

Qy     800 [illegible]

Db    1031 [illegible]

Qy     860 [illegible]

Db    1091 [illegible]

Qy     920 [illegible]

Db    1151 [illegible] 121[illegible]

Qy     980 [illegible]

Db    1211 [illegible] 127[illegible]

Qy    1040 [illegible]

Db    1271 [illegible]

Qy    1100 [illegible]

Db    1331 [illegible] 1390

Qy    1160 [illegible] 121[illegible]

Db    1391 [illegible]

Qy    12[illegible]7 [illegible]

Db    1451 [illegible]

Qy    1277 G 1277

Db    1511 G 1511
```

```
[illegible]
AA[illegible]
ID   AA[illegible] standard; DNA; [illegible] BP.
XX
AC   AA[illegible];
XX
DT   [illegible] (first entry)
XX
DE   Human polynucleotide SEQ ID NO [illegible]
XX
KW   Human; [illegible] immune suppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; [illegible]
KW   [illegible]trophic lateral sclerosis; Shy Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
FN   [illegible]
XX
[illegible]
XX
PN   [illegible]
XX
[illegible]
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   [illegible] Asundi V, [illegible] Ma Y, [illegible]
PI   Wang [illegible] Wang [illegible] Wehrman [illegible] Xu [illegible] Xue A[illegible] Yang Y, Zhang J,
PI   [illegible]
XX
DR   WPI; [illegible]
DR   [illegible] AAM[illegible]
XX
PT   N[illegible] nucleic acids and polypeptides [illegible]
PT   [illegible] nervous system injuries.
XX
PS   [illegible] SEQ ID NO [illegible]
XX
CC   The invention relates to human nucleic acids (AA[illegible]) and
CC   the encoded polypeptides (AAM[illegible] AAM[illegible]) with [illegible]
CC   immune suppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. [illegible]
CC   [illegible] may be used to treat diseases of the peripheral nervous
CC   system such as peripheral nervous injuries, peripheral neuropathy and
CC   [illegible] central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis and Shy Drager Syndrome. Other uses include
CC   [illegible] such as immune system suppression,
CC   [illegible]/inhibitory activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening
CC   [illegible] arthritis and inflammation, leukaemias and
CC   CNS disorders.
CC   N[illegible] sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   [illegible]

  [illegible] Match [illegible] Score [illegible] Length [illegible]
  [illegible] Pred. No. [illegible]
  Matches [illegible] Conservative [illegible] Mismatches [illegible] Indels [illegible] Gaps [illegible]
```

```
Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   620 [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   740 GGCCACTGAGCTTCGAGTTCACCCAGAGACTGAGCGGCAGCGGATCCAGCAGCTGGCC [illegible] 799
Db   [illegible]

Qy   [illegible]
Db   977 [illegible]

Qy   860 [illegible]
Db   [illegible]

Qy   [illegible]
Db   1097 [illegible]

Qy   [illegible]
Db   [illegible]

Qy   1040 [illegible]
Db   1217 [illegible] 1276

Qy   [illegible]
Db   [illegible]

Qy   1160 [illegible]
Db   [illegible]

Qy   1220 [illegible]
Db   [illegible]

Qy   1277 [illegible] 1277
Db   14[illegible]7 [illegible] 14[illegible]7


RESULT 9
ABK4[illegible]
ID   ABK4[illegible] standard; cDNA; [illegible] BP.
XX
AC   ABK4[illegible];
XX
DT   [illegible]-JUN-2002 (first entry)
XX
DE   cDNA encoding colon tumour protein, SEQ ID No 1734.
XX
KW   Human; [illegible] Immunogenic;
KW   immunotherapy; gene; ss.
XX
OS   Homo sapiens.
XX
PN   W[illegible] A[illegible]
```

```
XX
PD   14-FEB-2002.
XX
PF   31-JUL-2001; 2001WO-US24218.
XX
PR   03-AUG-2000; 2000US-223283P.
PR   28-MAR-2001; 2001US-279763P.
PR   29-JUN-2001; 2001US-302651P.
XX
PA   (CORI-) CORIXA CORP.
XX
PI   King GE,  Meagher MJ,  Xu J,  Secrist H;
XX
DR   WPI; 2002-241735/29.
XX
PT   New colon tumor polypeptides and polynucleotides, useful in vaccines,
PT   for diagnosing, preventing, and treating colon cancer, and as markers
PT   for the progression of cancer -
XX
PS   Claim 1; SEQ ID NO 1714; 147pp; English.
XX
CC   The invention relates to polynucleotides encoding colon tumour proteins.
CC   The polynucleotides and encoded polypeptides are useful in pharmaceutical
CC   compositions, such as vaccines, for the diagnosis, prevention, and
CC   treatment of colon cancer. Polynucleotide sequences may be used as
CC   hybridisation probes or primers, and in the design and preparation of
CC   ribozyme molecules for inhibiting expression of tumour polypeptides and
CC   proteins in tumour cells. The compositions are useful for stimulating an
CC   immune response against cancer, particularly for the immunotherapy of
CC   colon cancer, and as markers for the progression of cancer.
CC   ABK44450-ABK46247 represent coding sequences of human colon tumour
CC   proteins of the invention.
CC   Note: With the exception of SEQ ID No 1 and 2, the sequence data
CC   for this patent did not form part of the printed specification but was
CC   supplied by the European Patent Office.
XX
SQ   Sequence 5791 BP; 1436 A; 1312 C; 1595 G; 1448 T; 0 other;

  Query Match             17.6%;  Score 243.4;  DB 24;  Length 5791;
  Best Local Similarity   57.9%;  Pred. No. 5.2e-17;
  Matches  452;  Conservative    0;  Mismatches  326;  Indels    3;  Gaps    1;

Qy        500 [illegible] 559
Db        401 [illegible] 460

Qy        560 [illegible] 619
Db        461 [illegible] 520

Qy        620 [illegible] 679
Db        521 [illegible] 580

Qy        680 [illegible] 739
Db        581 [illegible] 640

Qy        740 [illegible] 799
Db        641 [illegible] 700

Qy        800 [illegible] 859
Db        701 [illegible] 760

Qy        860 [illegible] 919
Db        761 [illegible] 820

Qy        920 [illegible] 979
Db        821 [illegible] 880

Qy        980 [illegible] 1039
Db        881 [illegible] 940

Qy       1040 [illegible]
Db        941 [illegible]

Qy       1100 [illegible]
Db       1001 [illegible]

Qy       1156 [illegible]
Db       1061 [illegible]

Qy       1217 [illegible]
Db       1121 [illegible]

Qy       1277 G 1277
              |
Db       1181 G 1181


RESULT 10
AAH17958
ID   AAH17958 standard; cDNA; 1983 BP.
XX
AC   AAH17958;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:17747.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-[illegible].
XX
PR   29-JUL-1999;   99JP-[illegible].
PR   27-AUG-1999;   [illegible].
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-[illegible].
PR   09-JUN-2000; 2000JP-[illegible].
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J,
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-[illegible].
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5[illegible]
PT   full length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs
XX
PS   Claim 8; SEQ ID 17747; [illegible]pp; [illegible]; English.
XX
CC   The present invention describes primer sets for synthesising 5[illegible]
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5[illegible] nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an [illegible] comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5' end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3' end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5' end sequence/3' end sequence is selected from those detailed in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full length cDNAs. The primers allow obtaining of the full length
CC   cDNA easily without any specialised methods. AAH[illegible] to AAH[illegible] and
CC   AAH[illegible] to AAH[illegible] represent human cDNA sequences; AAK[illegible] to
CC   AAK[illegible] represent human mRNA sequences; and AAH[illegible] to AAH[illegible]
CC   represent oligonucleotides [illegible] which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  [illegible];  Conservative    [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]

Qy   [illegible]
Db   [illegible]
```

```
RESULT 11
AAI88482
ID   AAI88482 standard; cDNA; [illegible] BP.
XX
AC   AAI88482;
XX
DT   16-JAN-[illegible]  (first entry)
XX
DE   Rat petrin cDNA clone [illegible].
XX
KW   Petrin; neurite outgrowth associated protein; CNS;
KW   central nervous system; myelin; protein phosphatase 2C; stroke;
KW   neurodegeneration; gene therapy; ss.
XX
OS   Rattus sp.
XX
PN   WO[illegible]-A1.
XX
PD   [illegible].
XX
PF   12-APR-[illegible];   [illegible].
XX
PR   1[illegible]-APR-[illegible];   [illegible].
XX
PA   ([illegible]) [illegible].
XX
PI   [illegible] M,  [illegible] A,  [illegible] A,  [illegible] J;
XX
DR   WPI; [illegible].
XX
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, Petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 2; Page 4[illegible]; [illegible]pp; English.
XX
CC   A cDNA clone (AAI88482), designated DI 4F3, is a fragment of clone
CC   DI (see also AAI[illegible] and AAI[illegible]) that codes for petrin (AAW[illegible]),
CC   a protein involved in mediating neurite growth inhibition. DI
CC   was isolated from an adult rat brain cDNA library by screening with
CC   a monoclonal antibody capable of neutralising the inhibition of
CC   neurite growth by several neuronal types on CNS myelin substrates.
CC   The gene is expressed in neurons in brain tissue, partic. in
CC   cerebellum Purkinje cells. It can be used to produce petrin
CC   protein and to prepare probes. Antisense sequences (see also
CC   AA[illegible]) can be used in gene therapy to enhance axonal regeneration.
XX
SQ   Sequence 47[illegible] BP; 140 A; 105 C; 127 G; 107 T; 0 other;

  Query Match             [illegible]%;  Score [illegible];  DB [illegible];  Length 4[illegible];
  Best Local Similarity   6[illegible]%;  Pred. No. [illegible];
  Matches  [illegible];  Conservative    [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy        754 [illegible]
Db         2[illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
```

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Db        267 ATTATTGGAGTGACAA[illegible]AATATC [illegible]

Qy       1054 [illegible]
Db        327 [illegible]

Qy       1114 [illegible]
Db        387 [illegible]

Qy       1174 AAGGAGCAGGTGGC 1187
Db        447 [illegible]


RESULT 12
AAA02411
ID   AAA02411 standard; cDNA; 729 BP.
XX
AC   AAA02411;
XX
DT   19-MAY-2000  (first entry)
XX
DE   Human colon cancer cell line polynucleotide sequence SEQ ID No:2[illegible]2.
XX
KW   Human; colon cancer; tumour; diagnosis; gene expression product;
KW   probe, detection, cancerous state, metastasis, identification;
KW   breast cancer; oestrogen receptor-positive breast cancer; therapy;
KW   oestrogen receptor negative breast cancer, lung cancer, ss.
XX
OS   Homo sapiens.
XX
PN   WO9958675 A2.
XX
PD   18-NOV-1999.
XX
PF   13-MAY-1999;   99WO-US10602.
XX
PR   14-MAY-1998;   98US-0085[illegible].
PR   15-MAY-1998;   98US-0085537.
PR   15-MAY-1998;   98US-0085696.
PR   21-OCT-1998;   98US-0105234.
PR   27-OCT-1998;   98US-0105877.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE ) HYSEQ INC.
XX
PI   Williams LT,  Escobedo J,  Innis MA,  Garcia PD,  Sudduth-Klinger J;
PI   Reinhard C,  Giese K,  Randazzo F,  Kennedy GC,  Pot D,  Kassam A;
PI   Lamson G,  Drmanac R,  Crkvenjakov R,  Dickson M,  Drmanac S,  Labat I;
PI   Leshkowitz D,  Kita D,  Garcia V,  Jones LW,  Stache-Crain B;
XX
DR   WPI; 2000-126369/11.
XX
PT   Polynucleotide library used to determine cancerous states of mammalian
PT   cells -
XX
PS   Claim 1; Page 909; 1097pp; English.
XX
CC   AAA00016 to AAA02716 represent polynucleotides isolated from cDNA
CC   libraries constructed from human colon cancer cell lines. The present
CC   invention also describes a method of detecting differentially expressed
CC   genes correlated with a cancerous state of a mammalian cell, comprising
CC   detecting at least one differentially expressed gene product in a test
CC   sample derived from a cell suspected of being cancerous, where detection
CC   of the differentially expressed gene product is correlated with a
CC   cancerous state of the cell from which the test sample was derived.
CC   The polynucleotides sequences can be used in a method for detecting
CC   differentially expressed genes correlated with a cancerous state of a
CC   mammalian cell. The polynucleotides can also be used as probes for
CC   detecting and mapping related genes. They can be used in diagnosis and
CC   prognosis of diseases and disorders (e.g. identification of
CC   pre-metastatic or metastatic cancerous states, stages of cancer, or
CC   responsiveness of cancer to therapy). This is particularly for breast
CC   cancer, oestrogen receptor-positive breast cancer, oestrogen receptor
CC   negative breast cancer, lung cancer, and colon cancer.
XX
SQ   Sequence 729 BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; 5 other;

  Query Match             [illegible];  Score [illegible];  DB 21;  Length 729;
  Best Local Similarity   55.0%;  Pred. No. 8.2e-16;
  Matches  2[illegible];  Conservative    [illegible];  Mismatches  20[illegible];  Indels   [illegible];  Gaps   [illegible];

Qy        891 [illegible]
Db         2[illegible] [illegible]

Qy        951 [illegible]
Db         8[illegible] [illegible]

Qy       1011 [illegible]
Db        14[illegible] [illegible]

Qy       1071 [illegible]
Db        207 [illegible]

Qy       1131 [illegible]
Db        265 [illegible]

Qy       1191 [illegible]
Db        325 [illegible]

Qy       12[illegible] [illegible]
Db        385 [illegible]

Qy       1[illegible] [illegible]
Db        445 [illegible]

Qy       1356 GGGC 1359
Db        505 AGGC 508


RESULT 13
AAZ12841
ID   AAZ12841 standard; cDNA; [illegible] BP.
XX
AC   AAZ12841;
XX
DT   12-OCT-1999  (first entry)
XX
DE   Human gene expression product cDNA sequence SEQ ID NO:[illegible].
XX
KW   Human; gene; gene expression product; diagnosis; therapy; probe;
KW   detection; mapping; tissue typing; profiling; forensic; cancer;
KW   genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   WO9938972 A2.
XX
PD   05-AUG-1999.
XX
PF   28-JAN-1999;   99WO-US01[illegible].
XX
PR   03-APR-1998;   98US-00[illegible].
PR   28-JAN-1998;   98US-00[illegible].
PR   24-FEB-1998;   98US-0075951.
PR   [illegible] MAR 1999; [illegible]
PR   [illegible] APR 1999; [illegible]
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE ) HYSEQ INC.
XX
PI   Crkvenjakov R,  Dickson M,  Drmanac R,  Drmanac S;
PI   Escobedo J,  Garcia PD,  Garcia V,  Giese K,  Innis MA;
PI   Jones LW,  Kassam A,  Kennedy GC,  Kita D,  Labat I;
PI   Lamson G,  Leshkowitz D,  Pot D,  Randazzo F,  Reinhard C;
PI   Stache-Crain B,  Sudduth Klinger J,  Williams LT;
XX
DR   WPI; 2000-404[illegible]/41.
XX
PT   Novel human genes and their expression products which are
PT   differentially expressed in different cell types
XX
PS   Claim 1; Page [illegible]; [illegible]pp; English.
XX
CC   The present invention describes a library of human polynucleotides
CC   comprising the sequences given in AAZ1[illegible] to AAZ1[illegible]. Also described is
CC   a method of detecting differentially expressed genes correlated with the
CC   cancerous state of a mammalian cell, comprising detecting at least one
CC   differentially expressed gene product in a test sample from a cell
CC   suspected of being cancerous, where the gene product is encoded by one
CC   of the [illegible] polynucleotide sequences given in AAZ12[illegible] to AAZ1[illegible]. The
CC   polynucleotides can be used as a source of primers and probes, which can
CC   be used for a variety of purposes, e.g. detection of expression levels,
CC   mapping, tissue typing or profiling, forensics, genetic analysis and
CC   detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC   can be used for raising antibodies for experimental, diagnostic and
CC   therapeutic purposes. The polynucleotides may also be used to construct
CC   arrays for diagnostics (which may be used to determine function of an
CC   encoded protein) and to detect differences in expression levels between
CC   two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC   identify a genetic predisposition or susceptibility to a disease such as
CC   cancer). The polynucleotides of the invention are especially used in the
CC   diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC   and lung cancer. The polynucleotides can also be used to screen for
CC   peptide agonists and antagonists.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; [illegible] other;

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. 1.8e-14;
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible]

RESULT 4
AAX98[illegible]
ID   AAX98[illegible] standard; cDNA; [illegible] BP.
XX
AC   AAX98[illegible];
XX
DT   24 SEP 1999 (first entry)
XX
DE   Human validated cancer cell derived cDNA #276.
XX
KW   Cancer; human; colon; breast; lung; transmembrane receptor; ATPase;
KW   integral membrane protein; aspartyl protease; GATA family; wnt family;
KW   transcription factor; G protein alpha subunit; protein phosphatase;
KW   phorbolester binding protein; diacylglycerol binding protein; trypsin;
KW   protein kinase; tyrosine phosphatase; developmental signalling protein;
KW   WW/rsp5/WWP domain; therapy; forensic; genetic mapping; diagnostic;
KW   detection; treatment; cervical; melanoma; colorectal adenocarcinoma;
KW   Wilm's tumour; retinoblastoma; sarcoma; myosarcoma; lung carcinoma;
KW   leukemia; lymphoma; dysplasia; hyperplasia; endometrium; adrenal;
KW   prostate; ss.
XX
OS   Homo sapiens.
XX
PN   W0[illegible]-A2.
XX
PD   [illegible] 1999.
XX
PF   22 DEC 1998; 98W-US[illegible].
XX
PR   21 DEC 1998; 98US-[illegible].
PR   23 DEC 1997; 97US-[illegible].
PR   03-APR 1998; 98US-[illegible].
PR   21 OCT 1998; 98US-[illegible].
PR   27 OCT 1998; 98US-[illegible].
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE ) HYSEQ INC.
XX
PI   Crkvenjakov R,  Dickson M,  Drmanac R,  Drmanac S;
PI   Escobedo J,  Garcia PD,  Garcia V,  Giese K,  Innis MA;
PI   Jones LW,  Kassam A,  Kennedy GC,  Kita D,  Labat I;
PI   Lamson G,  Leshkowitz D,  Pot D,  Randazzo F,  Reinhard C;
PI   Stache-Crain B,  Sudduth Klinger J,  Williams LT;
XX
DR   WPI; 1999-[illegible].
XX
PT   New isolated human polynucleotides
XX
PS   Claim 1; Page [illegible]; [illegible]pp; English.
XX
CC   This invention describes novel isolated human polynucleotides obtained
CC   by screening for differential expression in colon cancer, breast cancer
CC   and lung cancer cell lines. The polynucleotides of the invention are
CC   represented in AAX98[illegible]-X99118 and encode polypeptides of protein
CC   families selected from 4 transmembrane segments integral membrane
CC   proteins, 7 transmembrane receptors, ATPases associated with various
CC   cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of
CC   transcription factors, G protein alpha subunit, phorbolesters or
CC   diacylglycerol binding proteins, protein kinase, protein phosphatase 2C,
CC   protein tyrosine phosphatase, trypsin, wnt family of developmental
CC   signalling proteins and WW/rsp5/WWP domain containing proteins. The
CC   encoded polypeptides also have a functional domain selected from Ank
CC   repeat, basic region plus leucine zipper transcription factors,
CC   bromodomain, EF-hand, SH3 domain, WD domain/G beta repeats, zinc finger
CC   (C2H2 type), zinc finger (C3HC4 class), and zinc binding metallo protease
CC   domain. The polynucleotides encode polypeptides with similarity to known
CC   protein families and are predicted to have similar properties. The novel
CC   polynucleotides can be used to develop products for use as therapeutic
CC   agents and in forensics, genetic analysis, mapping and diagnostic
CC   applications. In particular, the product can be used for the detection
CC   and management of cancers. They can be used for treating e.g. cervical
CC   cancers, melanomas, colorectal adenocarcinomas, Wilm's tumour, sarcomas,
CC   retinoblastoma, myosarcomas, lung carcinomas, leukemias, such as chronic
CC   myelogenous leukemia, promyelocytic leukemia, monocytic leukemia, and
CC   myeloid leukemia, and lymphomas such as histiocytic lymphoma, and, with
CC   hereditary ectodermal dysplasia, congenital alveolar dysplasia,
CC   epithelial dysplasia of the cervix, fibrous dysplasia of bone, and
CC   mammary dysplasia, hyperplasias, e.g. endometrial, adrenal, breast,
CC   prostate or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of
CC   the skin.
XX
SQ   Sequence 750 BP; 170 A; [illegible] C; 182 G; 18[illegible] T; [illegible] other;

  Query Match             7.4%;  Score 102.8;  DB 2[illegible];  Length 750;
  Best Local Similarity   54.4%;  Pred. No. 2.5e-14;
  Matches  257;  Conservative    0;  Mismatches  19[illegible];  Indels   1[illegible];  Gaps    2;

Qy      904 [illegible]
Db       58 AGGACCGGCTGGCCTACAAAAAGATCGAGCTGGAGGATCTCAGGTTTCCTCTGGTCTGT 117

Qy      964 GGACAG[illegible] 1023
Db      118 GGGGAGGGAAAAA[illegible]

Qy     1024 [illegible]
Db      178 [illegible]

Qy     1084 [illegible]
Db      238 [illegible]

Qy     1144 [illegible]
Db      298 [illegible]

Qy     1204 [illegible]
Db      [illegible]

Qy     1264 [illegible]
Db      41[illegible]

Qy     [illegible]
Db      478 [illegible]


RESULT 15
ABL25541
ID   ABL25541 standard; DNA; 2087 BP.
XX
AC   ABL25541;
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DT   28-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID NO 28120.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions
XX
PS   Claim 1; SEQ ID NO 28120; [illegible]pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2087 BP; 71[illegible] A; 582 C; 394 G; 401 T; 0 other;

  Query Match             7.3%;  Score 101.2;  DB 23;  Length 2087;
  Best Local Similarity   50.9%;  Pred. No. 7.9e-14;
  Matches  287;  Conservative    0;  Mismatches  253;  Indels   24;  Gaps   [illegible];

Qy      741 [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible] 1231

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible] 1040
Db     1352 [illegible] 1411

Qy     1041 GGACACAAA[illegible]
Db     1412 [illegible]

Qy     1101 [illegible]
Db     [illegible] 1531

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     1257 [illegible] 1280
Db     [illegible] 1675


Search completed: February 2[illegible], 2003, [illegible]
Job time : 344 secs
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           Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 22, 2003, 21:46:51 ; Search time 66 Seconds
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Perfect score:   1380
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                 Gapop 10.0 , Gapext 1.0

Searched:        441[illegible]2 seqs, 15[illegible]838[illegible] residues

Total number of hits satisfying chosen parameters:       88[illegible]724

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Issued_Patents_NA:*
                 1:  [illegible]*
                 2:  [illegible]*
                 3:  [illegible]*
                 4:  [illegible]*
                 5:  [illegible]*
                 6:  [illegible]*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                  SUMMARIES
                        %
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   No.    Score   Match Length DB  ID                              Description
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c    1     49.8    3.6   6714  4  US-09-299-141-6                 Sequence 6, Appli
c    2     49.8    3.6   6924  4  US-09-299-141-9                 Sequence 9, Appli
c    3     49.8    3.6   6924  4  US-09-299-141-10                Sequence 10, Appl
c    4     49.8    3.6   6924  4  US-09-299-141-11                Sequence 11, Appl
c    5     48.2    3.5   1441  4  US-09-082-352-[illegible]       Sequence [illegible], Appli
c    6     48.2    3.5   1817  4  US-09-288-292A-45               Sequence 45, Appl
     7       47    3.4    349  4  US-09-198-119C-94               Sequence 94, Appl
c    8     46.4    3.4    774  3  US-08-415-655-11                Sequence 11, Appl
c    9     45.2    3.3    645  4  US-09-535-038-[illegible]       Sequence [illegible], Appl
    10     43.6    3.2 152331  3  US-09-128-155-16                Sequence 16, Appl
c   11     43.4    3.1   1488  4  US-09-096-776B-3                Sequence 3, Appli
c   12     43.4    3.1   2534  4  US-09-096-776B-1                Sequence 1, Appli
c   13     43.2    3.1   3946  3  US-09-083-351-1                 Sequence 1, Appli
c   14     43.2    3.1   3946  4  US-09-083-352-1                 Sequence 1, Appli
c   15       43    3.1   1028  4  US-08-118-200-1                 Sequence 1, Appli
c   16       43    3.1   1028  4  US-08-458-745-1                 Sequence 1, Appli
    17     42.8    3.1   8460  1  US-08-469-005A-9                Sequence 9, Appli
    18     42.8    3.1   8519  4  US-09-261-567-1                 Sequence 1, Appli
c   19     42.4    3.1    320  4  US-09-165-264-7                 Sequence 7, Appli
c   20     42.4    3.1    320  4  US-09-165-264-13                Sequence 13, Appl
c   21     41.4    3.0    319  4  US-09-165-264-8                 Sequence 8, Appli
    22     41.4    3.0   4252  2  US-08-475-844-4                 Sequence 4, Appli
    23     41.4    3.0   4252  5  PCT-US95-08429-4                Sequence 4, Appli
    24     41.2    3.0   1413  4  US-08-984-709A-52               Sequence 52, Appl
    25     41.2    3.0   6453  1  US-08-306-691B-14               Sequence 14, Appl
    26     41.2    3.0   6453  3  US-09-209-668-14                Sequence 14, Appl
    27     41.2    3.0   6453  3  US-09-356-552-8                 Sequence 8, Appli
    28     41.2    3.0  12001  1  US-08-458-576A-11               Sequence [illegible], Appl
c   29     40.8    3.0   3978  1  US-08-726-214-1                 Sequence 1, Appli
c   30     40.8    3.0   4523  4  US-09-473-716-1                 Sequence [illegible], Appli
c   31     40.4    2.9   1332  4  US-09-423-890-11                Sequence 11, Appl
c   32     40.2    2.9   8438  1  US-07-945-283-1                 Sequence 1, Appli
c   33       40    2.9   1413  4  US-08-984-709A-52               Sequence 52, Appl
c   34     39.8    2.9    320  4  US-09-165-264-11                Sequence 11, Appl
c   35     39.6    2.9   7218  1  US-08-212-463-14                Sequence 14, Appl
c   36     39.4    2.9   7[illegible]  4  US-09-236-997-7         Sequence 7, Appli
c   37     39.4    2.9   2502  1  US-08-073-384C-7                Sequence 7, Appli
c   38     39.4    2.9   2502  1  US-08-254-359A-7                Sequence 7, Appli
c   39     39.4    2.9   2502  1  US-08-463-043-7                 Sequence 7, Appli
c   40     39.4    2.9   2502  1  US-08-481-238-7                 Sequence 7, Appli
c   41     39.4    2.9   2502  2  US-08-471-066B-7                Sequence 7, Appli
c   42     39.4    2.9   2502  2  US-08-484-956-7                 Sequence 7, Appli
c   43     39.4    2.9   2502  2  US-08-757-653-7                 Sequence 7, Appli
c   44     39.4    2.9   2502  2  US-08-599-491-7                 Sequence 7, Appli
c   45     39.4    2.9   2502  2  US-08-756-386-7                 Sequence 7, Appli

                                  ALIGNMENTS

RESULT 1
US-09-299-141-6/c
; Sequence 6, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: [illegible], MICHAEL
;  TITLE OF INVENTION: [illegible]
;  FILE REFERENCE: 4[illegible]
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: 1999-04-2[illegible]
;  EARLIER APPLICATION NUMBER: 60/08[illegible],[illegible]25
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 6714
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p43[illegible]AT
US-09-299-141-6

  Query Match             3.6%;  Score 49.8;  DB 4;  Length 6714;
  Best Local Similarity   54.7%;  Pred. No. [illegible];
  Matches   99;  Conservative    0;  Mismatches   82;  Indels    0;  Gaps    0;

Qy         19 CGG[illegible] 78
Db       1652 [illegible] 15[illegible]

Qy         79 AGC[illegible] 1[illegible]
Db       1592 GAG[illegible] 1[illegible]

Qy        139 [illegible] 1[illegible]
Db       1532 [illegible] 14[illegible]

Qy        199 C 199
              |
Db       1472 C 1472


RESULT 2
US-09-299-141-9/c
; Sequence 9, Application US/09299141
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible], TERENCE R.
;  APPLICANT: [illegible]
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]-04-24
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: [illegible]
[illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]


RESULT [illegible]
[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible], TERENCE R.
;  APPLICANT: [illegible]
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: [illegible]
US-09-299-141-10

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];
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Db [illegible]

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]

Qy [illegible]

Db 1682 [illegible] 1682


RESULT 4
US-09-299-141-11/c
; Sequence 11, Application US/09299141
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: 4700.011900
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: 1999-04-26
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p43mmsENCB AI
US-09-299-141-11

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity 54.7%; Pred. No. [illegible];
  Matches [illegible]; Conservative 0; Mismatches 82; Indels [illegible]; Gaps [illegible];

Qy [illegible]

Db 1862 [illegible]

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]

Qy [illegible]

Db [illegible]


RESULT 5
US-09-[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;     APPLICANT: Nakai, Atsuhiro
;     APPLICANT: [illegible], Anita
;     APPLICANT: Reuchel, Rainer
;    APPLICANT:  Itoh, Susumu
;    APPLICANT:  Afrakhte, Morvarid
;    APPLICANT:  Souchelnytskyi, Serhiy
;    APPLICANT:  Brodin, Greger
;    APPLICANT:  Lundstrom, Marene
;    APPLICANT:  Heldin, Nils Erik
;    APPLICANT:  Heldin, Carl Henrik
;    APPLICANT:  ten Dijke, Peter
;    TITLE OF INVENTION:  SMAD7 AND USES THEREOF
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  [illegible]
;      FILING DATE:  20 MAY 1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/047,221
;      FILING DATE:  20-MAY-1997
;      APPLICATION NUMBER:  60/060,465
;      FILING DATE:  30-SEP-1997
;      APPLICATION NUMBER:  60/075,910
;      FILING DATE:  25-FEB-1998
;      APPLICATION NUMBER:  60/077,0[illegible]
;      FILING DATE:  06-MAR-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  10401/7022
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617 720 2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  14[illegible] base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-082-[illegible]-5

  Query Match             3.5%;  Score 48.2;  DB 4;  Length 1491;
  Best Local Similarity   54.1%;  Pred. No. 0.015;
  Matches   98;  Conservative    0;  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

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Db        302 [illegible] 241

Qy         65 [illegible]TACCGAGG[illegible]CAGCT 124
Db        242 [illegible]CACTG[illegible] 18[illegible]

Qy        125 [illegible] 184
Db        182 [illegible] 12[illegible]

Qy        185 C 185
Db        122 [illegible] 122
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RESULT 6
US-09-288-252A-45/c
; Sequence 45, Application US/09288252A
; Patent No. 635[illegible]
; GENERAL INFORMATION:
;  APPLICANT: Dean A. Falb
;  APPLICANT:  Katherine Galvin
;  APPLICANT:  Michael Donovan
;  APPLICANT:  Dennis Fiscus
;  APPLICANT:  Michael A. Gimbrone, Jr.
;  TITLE OF INVENTION: Compositions and Methods for the Treatment and [illegible]
;  TITLE OF INVENTION:  Cardiovascular Disease
;  FILE REFERENCE: 785[illegible]
;  CURRENT APPLICATION NUMBER: US/09/288,252A
;  CURRENT FILING DATE:  1999-04-08
;  PRIOR APPLICATION NUMBER: 08/87[illegible],4[illegible]4
;  PRIOR FILING DATE: 1997-06-06
;  PRIOR APPLICATION NUMBER: 08/7[illegible]
;  PRIOR FILING DATE: 1997-02-13
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: 08/485,[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible],844
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
;   LENGTH: 1817
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-288-252A-45

  Query Match             3.5%;  Score 48.2;  DB 4;  Length 181[illegible];
  Best Local Similarity   54.1%;  Pred. No. 0.016;
  Matches   [illegible];  Conservative    [illegible];  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy          5 [illegible]GGGAGCC[illegible] 64
Db        4[illegible] [illegible]

Qy         65 [illegible] 124
Db        3[illegible] [illegible]

Qy        125 [illegible] 184
Db        336 [illegible] 277

Qy        185 C 185
Db        276 C 276


RESULT 7
US-09-198-1190-94
; Sequence 94, Application US/09198[illegible]
; Patent No. 6417428
; GENERAL INFORMATION:
;  APPLICANT:  Thomashow, Michael
;  APPLICANT:  Stockinger, Eric
;  APPLICANT:  Jaglo-Ottosen, Kirsten
;  APPLICANT:  Gilmour, Sarah
;  APPLICANT:  Zarka, Daniel
;  APPLICANT:  Jiang, Cai-Zhong
;  TITLE OF INVENTION:  Plant Having Altered Environmental Stress Tolerance
;  FILE REFERENCE:  [illegible] Seq List
;  CURRENT APPLICATION NUMBER:  US/09/198,1190
;  CURRENT FILING DATE:  1998-11-23
;  PRIOR APPLICATION NUMBER:  US 09/[illegible]
;  PRIOR FILING DATE:  1998-09-04
;  PRIOR APPLICATION NUMBER:  US [illegible]
;  PRIOR FILING DATE:  1998-02-0[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
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;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
; NUMBER OF SEQ ID NOS: [illegible]
; SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: [illegible]
;   FEATURE:
;   OTHER INFORMATION: [illegible]
US-[illegible]

  Query Match             [illegible];  Score 47;  DB 1;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy  [illegible]

Db  [illegible]

Qy  [illegible]

Db  [illegible]

Qy  [illegible]

Db  [illegible]


RESULT [illegible]
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; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;       APPLICANT: [illegible]
;       APPLICANT: [illegible]
;       TITLE OF INVENTION: [illegible]
;       TITLE OF INVENTION: [illegible] KINASE INHIBITOR AND [illegible]
;       TITLE OF INVENTION: SAME
;       NUMBER OF SEQUENCES: [illegible]
;       CORRESPONDENCE ADDRESS:
;         ADDRESSEE: [illegible]
;         STREET: [illegible] Avenue of the Americas
;         CITY: New York
;         STATE: New York
;         COUNTRY: United States of America
;         ZIP: [illegible]
;       COMPUTER READABLE FORM:
;         MEDIUM TYPE: Floppy disk
;         COMPUTER: IBM PC compatible
;         OPERATING SYSTEM: [illegible]
;         SOFTWARE: PatentIn Release [illegible] Version [illegible]
;       CURRENT APPLICATION DATA:
;         APPLICATION NUMBER: [illegible]
;         FILING DATE:
;         CLASSIFICATION: [illegible]
;       ATTORNEY/AGENT INFORMATION:
;         NAME: [illegible]
;         REGISTRATION NUMBER: [illegible]
;         REFERENCE/DOCKET NUMBER: [illegible]
;       TELECOMMUNICATION INFORMATION:
;         TELEPHONE: (212) [illegible]
;         TELEFAX: (212) [illegible]
;  INFORMATION FOR SEQ ID NO: [illegible]
;       SEQUENCE CHARACTERISTICS:
;         LENGTH: [illegible] base pairs
;         TYPE: nucleic acid
;         STRANDEDNESS: single
;         TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       HYPOTHETICAL: NO
;       ANTI-SENSE: NO
US-[illegible]

  Query Match             [illegible];  Score 46.4;  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy  [illegible]

Db  772 [illegible]

Qy  [illegible]

Db  712 [illegible]

Qy  15[illegible] [illegible] 195

Db  6[illegible] [illegible]


RESULT [illegible]
US-09-[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible], Alexander [illegible]
;  APPLICANT: [illegible], Sean V.
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: [illegible] IS A TUMOR SUPPRESSOR THAT IS MUTATED IN [illegible]
;  TITLE OF INVENTION: AND OTHER CANCER TYPES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: 64[illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-[illegible]

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  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches 88;  Indels [illegible];  Gaps [illegible];

Qy  [illegible]

Db  47[illegible] [illegible]

Qy  66 [illegible]

Db  41[illegible] [illegible]

Qy  12[illegible] [illegible]

Db  [illegible]

Qy  186 [illegible] 191

Db  [illegible]


RESULT 1[illegible]
US-[illegible]
; Sequence 1[illegible], Application US/[illegible]
; Patent No. 6117654
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;  TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/128,155
;  CURRENT FILING DATE: 1998-08-03
;  EARLIER APPLICATION NUMBER: US 60/091,650
;  EARLIER FILING DATE: 1998-07-02
;  EARLIER APPLICATION NUMBER: US 60/054,646
;  EARLIER FILING DATE: 1997-08-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 152331
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(152331)
;   OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

  Query Match             [illegible];  Score 43.6;  DB [illegible];  Length 152331;
  Best Local Similarity   51.[illegible]%;  Pred. No. [illegible];
  Matches  10[illegible];  Conservative    0;  Mismatches   99;  Indels    0;  Gaps    0;

Qy          3 [illegible] 62
Db      21997 [illegible] 22056

Qy         63 [illegible] 122
Db      22057 [illegible] 22116

Qy        123 [illegible] 182
Db      22117 [illegible] 22176

Qy        183 [illegible] 204
Db      22177 [illegible] 22198


RESULT 11
US-09-096-776B-3/c
; Sequence 3, Application US/09096776B
; Patent No. 6270994
; GENERAL INFORMATION:
;  APPLICANT:  Miyazono, Kohei
;  APPLICANT:  Kawabata, Masahiro
;  TITLE OF INVENTION:   SMAD6 AND USES THEREOF
;  FILE REFERENCE:   L0461/7038
;  CURRENT APPLICATION NUMBER: US/09/096,776B
;  CURRENT FILING DATE:  1998-06-12
;  PRIOR APPLICATION NUMBER:   US 60/049,990
;  PRIOR FILING DATE:   1997-06-13
;  PRIOR APPLICATION NUMBER:   US 60/053,[illegible]
;  PRIOR FILING DATE:   1997-07-18
;  PRIOR APPLICATION NUMBER:   US 60/066,173
;  PRIOR FILING DATE:   1997-11-18
;  NUMBER OF SEQ ID NOS:   10
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 3
;   LENGTH: 1488
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-096-776B-3

  Query Match             [illegible];  Score 43.4;  DB 4;  Length 1488;
  Best Local Similarity   52.[illegible]%;  Pred. No. [illegible];
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Qy          [illegible] 64
Db        [illegible]

Qy         65 [illegible] 124
Db        [illegible]

Qy        125 [illegible] 184
Db        [illegible]

Qy        185 C 185
Db        [illegible]


RESULT 12
US-09-096-776B-1/c
; Sequence 1, Application US/09096776B
; Patent No. 6270994
; GENERAL INFORMATION:
;  APPLICANT:  Miyazono, Kohei
;  APPLICANT:  Kawabata, Masahiro
;  TITLE OF INVENTION:   SMAD6 AND USES THEREOF
;  FILE REFERENCE:   L0461/7038
;  CURRENT APPLICATION NUMBER: US/09/096,776B
;  CURRENT FILING DATE:  1998-06-12
;  PRIOR APPLICATION NUMBER:   US 60/049,990
;  PRIOR FILING DATE:   1997-06-13
;  PRIOR APPLICATION NUMBER:   US 60/053,440
;  PRIOR FILING DATE:   1997-07-18
;  PRIOR APPLICATION NUMBER:   US 60/066,173
;  PRIOR FILING DATE:   1997-11-18
;  NUMBER OF SEQ ID NOS:   10
;  SOFTWARE:   PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 2534
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (751)..(2235)
US-09-096-776B-1

  Query Match             [illegible];  Score 1[illegible];  DB 4;  Length 2534;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches   95;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy          [illegible] 64
Db       1049 [illegible]

Qy         65 [illegible] 124
Db        [illegible]

Qy        125 [illegible] 184
Db        [illegible]

Qy        185 C 185
Db        869 C 869


RESULT 13
US-09-083-351-1/c
; Sequence 1, Application US/[illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;     APPLICANT:  Sheffield, Val C.
;    APPLICANT:  Alward, Wallace L.M.
;    APPLICANT:  Stone, Edwin M.
;    APPLICANT:  Nishimura, Darryl
;    APPLICANT:  Patil, Shiva
;    TITLE OF INVENTION:  THERAPEUTICS AND DIAGNOSTICS FOR
;    TITLE OF INVENTION:  CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
;    TITLE OF INVENTION:  TRANSCRIPTION FACTOR
;    NUMBER OF SEQUENCES:  2[illegible]
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/[illegible]
;      FILING DATE:  22-MAY-1998
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold, Beth E.
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  UIA-[illegible]
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617 832 1000
;      TELEFAX:  617 832 7000
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  [illegible] base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  47..[illegible]
US-09-[illegible]-1

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy         88 [illegible]
Db        [illegible]

Qy        148 [illegible]
Db        [illegible]

Qy        208 [illegible]
Db        [illegible]


RESULT 14
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; Sequence [illegible], Application US/0[illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;    APPLICANT:  Sheffield, Val C.
;    APPLICANT:  Alward, Wallace L.M.
;    APPLICANT:  Stone, Edwin M.
;    APPLICANT:  Nishimura, Darryl
;    APPLICANT:  Patil, Shiva
;    TITLE OF INVENTION:  GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
;    TITLE OF INVENTION:  BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
;    NUMBER OF SEQUENCES:  2[illegible]
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;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/[illegible]
;      FILING DATE:  22-MAY-1998
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold, Beth E.
;      REGISTRATION NUMBER:  35,430
;      REFERENCE/DOCKET NUMBER:  UIA-[illegible]
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617 832 1000
;      TELEFAX:  617 832 7000
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  [illegible] base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  47..[illegible]
US-09-083-352-1

  Query Match             [illegible];  Score [illegible];  DB 4;  Length [illegible];
  Best Local Similarity   57.4%;  Pred. No. [illegible];
  Matches   78;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy         88 [illegible]
Db        [illegible]

Qy        148 [illegible]
Db        [illegible]

Qy        208 AA[illegible]
Db        [illegible]


RESULT 15
US-[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;    APPLICANT:  SUTHERLAND, Grant R
;    APPLICANT:  RICHARDS, Robert I
;    APPLICANT:  SCHLESSINGER, David
;    APPLICANT:  NAGARAJA, Ramaiah
;    APPLICANT:  KREMER, Eric J
;    APPLICANT:  YU, Sui
;    APPLICANT:  BAKER, Elizabeth
;    APPLICANT:  MULLEY, John C
;    APPLICANT:  MANDEL, Jean Louis
;    APPLICANT:  [illegible], Melanie April
;    APPLICANT:  LYNCH, Michael
;    TITLE OF INVENTION:  DNA SEQUENCES RELATED TO ISOLATED
;    TITLE OF INVENTION:  FRAGILE X SYNDROME
;    NUMBER OF SEQUENCES:  1[illegible]
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BURNS, DOANE, SWECKER & MATHIS
;       STREET:  P.O. Box 1404
;       CITY:  Alexandria
;       STATE:  Virginia
;       COUNTRY:  United States
;       ZIP:  22313-1404
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/118,200
;       FILING DATE:  09-SEP-1993
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/802,650
;       FILING DATE:  05-DEC-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/672,232
;       FILING DATE:  20-MAR-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/638,518
;       FILING DATE:  4-JAN-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/996,517
;       FILING DATE:  23-DEC-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Crane-Feury, Sharon E
;       REGISTRATION NUMBER:  36,113
;       REFERENCE/DOCKET NUMBER:  020160-164
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703) 836-6620
;       TELEFAX:  (703) 836-2021
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1028 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-118-200-1

  Query Match             3.1%;  Score 43;  DB 4;  Length 1028;
  Best Local Similarity   57.4%;  Pred. No. [illegible];
  Matches   97;  Conservative    0;  Mismatches   7[illegible];  Indels    2;  Gaps    1;

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Qy         95 [illegible] 154
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                    GenCore version 5.1.3
             Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 22, 2003, 22:46:59 ; Search time [illegible] Seconds
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                                               8517.169 Million cell updates/sec

Title:           US-09-866-987-3
Perfect score:   1380
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        442118 seqs, 290819700 residues

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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                 2:  /cgn2_6/[illegible]_NEW_PUB.seq:*
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                 14: /cgn2_6/[illegible]MB.seq:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                               SUMMARIES
                     %
Result              Query
  No.    Score      Match Length DB  ID                          Description
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    1     1380      100.0   1380 10  US-09-866-987-3              Sequence 3, Appl
    2      536       38.8    547 10  US-09-867-701-2969           Sequence 2969, Ap
    3    244.4       17.7   5791 10  US-09-920-30[illegible]A-1714     Sequence 1714, Ap
    4    244.4       17.7   5791 12  US-10-033-528-1714           Sequence 1714, Ap
    5       98        7.1    551 10  US-09-867-701-5460           Sequence 5460, Ap
    6     48.2        3.5   1817 10  US-09-924-417-64             Sequence 64, Appl
    7       47        3.4    349  9  US-09-996-140-94             Sequence 94, Appl
c   8     46.8        3.4  43058 10  US-09-954-456-292            Sequence 292, App
c   9     46.8        3.4  43058 10  US-09-954-456-529            Sequence 529, App
c  10     46.8        3.4  43058 10  US-09-880-107-355            Sequence 355, Ap
   11     46.4        3.4   3209 10  US-09-925-301-474            Sequence 474, App
   12     44.4        3.2   2561  9  US-09-976-740-48             Sequence 48, Appl
   13     44.4        3.2   2561 12  US-10-023-529-48             Sequence 48, Appl
   14     44.4        3.2   2561 12  US-10-023-523-48             Sequence 48, Appl
c  15     44.2        3.2   4286 10  US-09-899-634A-1             Sequence 1, Appl
c  16     44.2        3.2   5100  9  US-09-954-483A-14            Sequence 14, Appl
c  17     44.2        3.2   6148  9  US-09-954-483A-13            Sequence 13, Appl
   18     43.6        3.2 152331  9  US-10-095-407-16             Sequence 16, Appl
c  19     43.4        3.1   1488 10  US-09-923-922-3              Sequence 3, Appl
c  20     43.4        3.1   2[illegible]41 10  US-09-923-922-1              Sequence 1, Appl
   21     43.2        3.1   [illegible]  9  US-09-899-510A-87            Sequence 87, Appl
   22       43        3.1   1614  9  US-09-976-740-45             Sequence 45, Appl
   23       43        3.1   1614 12  US-10-023-529-45             Sequence 45, Appl
   24       43        3.1   1614 12  US-10-023-523-45             Sequence 45, Appl
   25       43        3.1  12425  9  US-09-976-740-50             Sequence 50, Appl
   26       43        3.1  12425 12  US-10-023-529-50             Sequence 50, Appl
   27       43        3.1  12425 12  US-10-023-523-50             Sequence 50, Appl
   28     42.2        3.1  42999  9  US-09-799-462A-17            Sequence 17, Appl
   29     42.2        3.1  42999  9  US-10-125-767-17             Sequence 17, Appl
   30     42.2        3.1  42999  9  US-09-8[illegible]-911A-17            Sequence 17, Appl
c  31     41.4        3.0  12733  9  US-10-032-393-47             Sequence 47, Appl
c  32     41.4        3.0  12739  9  US-10-032-393-8              Sequence 8, Appl
c  33     41.2        3.0    485  9  US-10-004-717-59             Sequence 59, Appl
c  34       41        3.0 155024  9  US-10-026-188-6              Sequence 6, Appl
c  35     40.8        3.0   4523  9  US-10-175-158-1              Sequence 1, Appl
c  36     40.4        2.9    477 10  US-09-864-761-14662          Sequence 14662, A
   37     40.4        2.9   1038 10  US-09-917-800A-1479          Sequence 1479, Ap
   38     40.4        2.9   1155 10  US-09-814-777A-21            Sequence 21, Appl
   39     40.4        2.9   17[illegible] 10  US-09-814-777A-19            Sequence 19, Appl
   40     40.4        2.9   [illegible] 10  US-09-814-777A-17            Sequence 17, Appl
c  41     40.4        2.9   3332 12  US-10-090-864-11             Sequence 11, Appl
c  42     40.2        2.9   1157 10  US-09-778-844-166            Sequence 166, App
c  43     40.2        2.9   1183 10  US-09-778-844-167            Sequence 167, App
   44       40        2.9   1496 10  US-09-969-708-132            Sequence 132, App
   45     39.8        2.9   [illegible]  [illegible]  US-09-764-[illegible]-[illegible]4           Sequence [illegible]4, Ap

                               ALIGNMENTS

RESULT 1
US-09-866-987-3
; Sequence 3, Application US/09866987
; Patent No. US2002[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY D.
;  APPLICANT: MARTINEZ, RICARDO
;  APPLICANT: WHYTE, DAVID
;  APPLICANT: MANNING, GERARD
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]ENBERG, SEAN
;  APPLICANT: HILL, [illegible]N
;  APPLICANT: FLANAGAN, PETER
;  TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
;  FILE REFERENCE: 038602/1180
;  CURRENT APPLICATION NUMBER: US/09/866,987
;  CURRENT FILING DATE: 2001-[illegible]
;  PRIOR APPLICATION NUMBER: 60/208,291
;  PRIOR FILING DATE: 2000-05-30
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1380
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: phosphatase nucleotide
US-09-866-987-3

  Query Match            100.0%;  Score 1380;  DB 10;  Length 1380;
  Best Local Similarity  100.0%;  Pred. No. [illegible];
  Matches 1380;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AT[illegible] 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AT[illegible] 60

Qy         61 C[illegible] 120
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Db         61 C[illegible] 120
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[illegible]

Db   1201 [illegible]

Qy   1261 [illegible]

Db   1261 [illegible] 1320

Qy   1321 [illegible]

Db   1321 GACGTCTCTGGTTTCTGATTCCTTGCACAGTCAGGGCAAGAGAGCAGTGACTACTGA 1380


RESULT 2
US-09-867-701-2068
; Sequence 2068, Application US/09867701
; Patent No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Algate, Paul A.
;  APPLICANT: Jones, Robert
;  APPLICANT: Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/867,701
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2068
;   LENGTH: 547
;   TYPE: DNA
;   ORGANISM: Homo sapien
US-09-867-701-2068

  Query Match             38.8%;  Score 536;  DB 10;  Length 547;
  Best Local Similarity   99.8%;  Pred. No. 1.5e-124;
  Matches  547;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy    792 GCTGGCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCGACTGGAGTTCCCTCG 851

Db      1 [illegible]

Qy    852 [illegible]

Db     61 [illegible]

Qy    912 [illegible]

Db    121 [illegible]

Qy    972 [illegible]

Db    181 [illegible]

Qy   1032 [illegible]

Db    241 [illegible]

Qy   1092 [illegible]

Db    301 [illegible]

Qy   1152 [illegible]

Db    361 [illegible]

Qy   1212 [illegible]

Db    421 [illegible]

Qy   1272 [illegible]

Db    480 [illegible]
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Qy       1192 [illegible] 1199
Db        540 [illegible] 547

RESULT 3
US-09-920-300A-1714
; Sequence 1714, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547
;  CURRENT APPLICATION NUMBER: US/09/920,300A
;  CURRENT FILING DATE: 2001-07-31
;  NUMBER OF SEQ ID NOS: 1789
;  SOFTWARE: FastSEQ for Windows Version [illegible]
; SEQ ID NO 1714
;   LENGTH: 5791
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-920-300A-1714

  Query Match             17.6%;  Score [illegible];  DB [illegible];  Length 5791;
  Best Local Similarity   57.9%;  Pred. No. 5.9e-51;
  Matches  452;  Conservative    0;  Mismatches  326;  Indels    [illegible];  Gaps    1;

Qy        500 [illegible] 559
Db        401 [illegible] 460

Qy        560 [illegible] 619
Db        461 [illegible] 520

Qy        620 TGGAGGCCTCAGCCCAGATCGCCGCCTGCACAGCCCTGCTGCCTCTCTCCCTGCAGGCAA 679
Db        521 [illegible] 580

Qy        680 [illegible] 739
Db        581 [illegible] 640

Qy        740 [illegible] 799
Db        641 [illegible] 700

Qy        800 [illegible] 859
Db        701 [illegible] 760

Qy        860 [illegible] 919
Db        761 [illegible] 820

Qy        920 [illegible] 979
Db        821 [illegible] 880

Qy        980 [illegible] 1039
Db        881 [illegible] 940

Qy       1040 [illegible]
Db        941 [illegible]

Qy       1100 [illegible]

Db       1001 [illegible]

Qy       1156 [illegible]
Db       1061 [illegible]

Qy       1217 [illegible] 1276
Db       1121 [illegible] 1180

Qy       1277 G 1277
Db       1181 G 1181


RESULT 4
US-10-033-528-1714
; Sequence 1714, Application US/10033528
; Patent No. US2002[illegible]971A1
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jiangchun
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547C1
;  CURRENT APPLICATION NUMBER: US/10/033,528
;  CURRENT FILING DATE: 2001-12-26
;  NUMBER OF SEQ ID NOS: 1896
;  SOFTWARE: FastSEQ for Windows Version 4.[illegible]
; SEQ ID NO 1714
;   LENGTH: 5791
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-033-528-1714

  Query Match             17.6%;  Score 2474.4;  DB 12;  Length 5791;
  Best Local Similarity   57.9%;  Pred. No. 5.9e-51;
  Matches  452;  Conservative    0;  Mismatches  326;  Indels    [illegible];  Gaps    1;

Qy        500 [illegible] 559
Db        401 [illegible] 460

Qy        560 [illegible] 619
Db        461 [illegible] 520

Qy        620 [illegible] 679
Db        521 [illegible] 580

Qy        680 [illegible] 739
Db        581 [illegible] 640

Qy        740 [illegible] 799
Db        641 [illegible] 700

Qy        800 [illegible] 859
Db        701 [illegible] 760

Qy        860 [illegible] 919
Db        761 [illegible] 820

Qy        920 [illegible] 979
Db        821 [illegible] 880
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[illegible]

[illegible]
; Sequence [illegible], Application US/09866[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: A[illegible] A.
;  APPLICANT: Jones, Robert
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/867,[illegible]
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: [illegible]
;   OTHER INFORMATION: [illegible]
[illegible]

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible]

RESULT 6
US-09-924-417-64/c
; Sequence 64, Application US/09924417
; Patent No. US20020[illegible]A1
; GENERAL INFORMATION:
;         APPLICANT: Falb, Dean
;         TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;                             THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR
;                             DISEASE
;         NUMBER OF SEQUENCES: 67
;         CORRESPONDENCE ADDRESS:
;              ADDRESSEE: PENNIE & EDMONDS LLP
;              STREET: 1155 Avenue of the Americas
;              CITY: New York
;              STATE: NY
;              COUNTRY: USA
;              ZIP: 10036-2711
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Diskette
;              COMPUTER: IBM Compatible
;              OPERATING SYSTEM: DOS
;              SOFTWARE: FastSEQ Version 2.0
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/924,417
;              FILING DATE: [illegible]
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: US/09/034,[illegible]
;              FILING DATE: 04-MAR-1998
;              APPLICATION NUMBER: 08/[illegible]
;              FILING DATE: 06-JUN-1997
;              APPLICATION NUMBER: 08/[illegible]
;              FILING DATE: [illegible]-FEB-1997
;              APPLICATION NUMBER: 60/011,[illegible]
;              FILING DATE: 16-FEB-1996
;              APPLICATION NUMBER: 08/[illegible],654
;              FILING DATE: 09-FEB-1996
;              APPLICATION NUMBER: 08/[illegible]
;              FILING DATE: [illegible]
;              APPLICATION NUMBER: 08/386,844
;              FILING DATE: [illegible]-FEB-1995
;         ATTORNEY/AGENT INFORMATION:
;              NAME: [illegible], Laura A
;              REGISTRATION NUMBER: [illegible]
;              REFERENCE/DOCKET NUMBER: 785[illegible]
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: (212)790-9090
;              TELEFAX: (212)[illegible]
;              TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 64:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: [illegible] base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: both
;              TOPOLOGY: unknown
;         MOLECULE TYPE: cDNA
;         SEQUENCE DESCRIPTION: SEQ ID NO: 64:
US-09-924-417-64

  Query Match [illegible]; Score [illegible]; DB [illegible]; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

[illegible]
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Qy        125 [illegible] 184
Db        336 [illegible] 277

Qy        185 T 185

Db        276 T 276


RESULT 7
US-09-996-140-94
; Sequence 94, Application US/09996140
; Patent No. US20020157136A1
; GENERAL INFORMATION:
;  APPLICANT: Thomashow, Michael
;  APPLICANT:  Stockinger, Eric
;  APPLICANT:  Jaglo-Ottosen, Kirsten
;  APPLICANT:  Gilmour, Sarah
;  APPLICANT:  Zarka, Daniel
;  APPLICANT:  Jiang, Cai-Zhong
;  TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL
;  TITLE OF INVENTION:  STRESS TOLERANCE
;  FILE REFERENCE: MBI-0040US
;  CURRENT APPLICATION NUMBER: US/09/996,140
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: 09/706,270
;  PRIOR FILING DATE: 1996-09-04
;  PRIOR APPLICATION NUMBER: 09/018,233
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/017,816
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,245
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/017,575
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,227
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,234
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/198,119
;  PRIOR FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: PCT/US99/01895
;  PRIOR FILING DATE: 1999-01-29
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94
;    LENGTH: 349
;    TYPE: DNA
;    ORGANISM: Zea mais
US-09-996-140-94

  Query Match              3.4%;  Score 47;  DB 9;  Length 349;
  Best Local Similarity   55.1%;  Pred. No. 0.014;
  Matches   92;  Conservative    0;  Mismatches   75;  Indels    [illegible];  Gaps    [illegible];

Qy         19 [illegible] 78
Db        102 [illegible] 161

Qy         79 AGCCGCCG[illegible]GAGGGCCGGC[illegible]AGCCCAGCCCCGGGCGC 138
Db        162 GTCCGG[illegible]AAGAAG[illegible] 221

Qy        139 GCCGACGCCTCGGGCGGCCAGACTCCGGCCGTGGGCAGCCCCGC 185
Db        222 GCCGCGGCGGCGTACGACGTGGCCGCGCTGGCCCTGCGGGGCGCGC 268


RESULT 8
US-09-954-456-292/c
; Sequence 292, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,726
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,84[illegible]
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,8[illegible]
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2278
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 292
;    LENGTH: 43658
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-954-456-292

  Query Match              3.4%;  Score 46.8;  DB 10;  Length 43658;
  Best Local Similarity   54.7%;  Pred. No. 0.091;
  Matches   93;  Conservative    0;  Mismatches   77;  Indels    0;  Gaps    0;

Qy         18 [illegible] 77
Db      [illegible] [illegible] [illegible]

Qy         78 [illegible] 137
Db      [illegible] [illegible] [illegible]

Qy        138 [illegible] 187
Db      [illegible] [illegible] [illegible]


RESULT 9
US-09-954-456-529/c
; Sequence 529, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn version 3.[illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
[illegible]

  Query Match [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy  [illegible]
Db  [illegible]

Qy  [illegible]
Db  [illegible]

Qy  [illegible]
Db  [illegible]


RESULT [illegible]
[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: [illegible] Expression [illegible] Cancer
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: GenBank Accession No. [illegible]
[illegible]

  Query Match [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy  [illegible]
Db  [illegible]

Qy  [illegible]
Db  [illegible]

Qy  [illegible] 187
Db  2561 [illegible]


RESULT 11
US-09-925-[illegible]-474
; Sequence 474, Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA[illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US00/05882
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.[illegible]
; SEQ ID NO 474
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (427)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-[illegible]-474

  Query Match [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity [illegible];  Pred. No. 0.044;
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy  [illegible]
Db  1268 [illegible]

Qy  [illegible]
Db  1328 [illegible]

Qy  1096 [illegible] 1155
Db  1388 [illegible] 1447

Qy  1156 [illegible]
Db  1448 [illegible]

Qy  1216 [illegible]
Db  [illegible]


RESULT 12
US-09-976-[illegible]
; Sequence 48, Application US/[illegible]
; Publication No. US[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible], Ann M.
;  APPLICANT: Lees, Robert S.
;  APPLICANT: [illegible], Simon W.
;  APPLICANT: [illegible], Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION: ATHEROSCLEROSIS
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-09-976-740-48

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Qy         71 [illegible] 129
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Qy        190 CGACGC 195
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Db        800 [illegible] 805


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US-10-02[illegible]-529-48
; Sequence 48, Application US/10[illegible]529
; Patent No. US2002[illegible]29388A1
; GENERAL INFORMATION:
;  APPLICANT: Loos, Ann M.
;  APPLICANT:  Loos, Robert S.
;  APPLICANT:  Law, Simon W.
;  APPLICANT:  Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION:  ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004-01
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: 09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
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US-10-02[illegible]-529-48

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Qy        190 CGACGC 195
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Db        800 GCCCGC 805


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; Sequence 48, Application US/10[illegible]523
; Patent No. US2002[illegible]
; GENERAL INFORMATION:
;  APPLICANT: Loos, Ann M.
;  APPLICANT:  Loos, Robert S.
;  APPLICANT:  Law, Simon W.
;  APPLICANT:  Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION:  ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004-01
;  CURRENT APPLICATION NUMBER: US/10/[illegible],523
;  CURRENT FILING DATE: 2001-12-17
;  PRIOR APPLICATION NUMBER: US/09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
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;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
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US-10-02[illegible]-523-48

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; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible] Andreas [illegible]
;  TITLE OF INVENTION: [illegible] and its uses
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
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Search completed: February 24, 2003, [illegible]
Job time : [illegible] secs
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Run on:         February 23, 2003, 00:27:59 ; Search time 3587 Seconds
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Perfect score:  [illegible]
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Scoring table:  IDENTITY_NUC
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Searched:       [illegible]

Total number of hits satisfying chosen parameters:     [illegible]

Minimum DB seq length: 0
Maximum DB seq length: 20[illegible]

Post-processing: Minimum Match [illegible]
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                 Listing first 45 summaries

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 Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

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    11   [illegible]     2121  [illegible]-2213                           Sequence 2218, Ap
    12   12[illegible].4  9[illegible]  2124  18  US-09-471-275-7040    Sequence 7040, Ap
    13   12[illegible].4  99.8  2124  76  US-60-324-631-2198            Sequence 2198, Ap
    14   [illegible]                                              Sequence 21[illegible], Ap
    15   [illegible]          [illegible]-135-213-1400            Sequence 1400, Ap
    16   [illegible]                                              Sequence [illegible]
    17   [illegible]                                              Sequence [illegible], Ap
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;  APPLICANT: [illegible]OWMAN, [illegible]
;  APPLICANT: MAR[illegible]NE[illegible], [illegible]
;  APPLICANT: WHYTE, [illegible]
;  APPLICANT: MANNING, [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]ENEPEEL, SEAN
;  APPLICANT: [illegible]
;  APPLICANT: FLANAGAN, PETER
;  TITLE OF INVENTION: [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
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;  PRIOR FILING DATE: [illegible]
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;  SOFTWARE: PatentIn Ver. 2.1
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; Sequence 376, Application PCT/US0230474
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: Zhang, Jie
;  APPLICANT: [illegible]
;  APPLICANT: Xue, Aidong J.
;  APPLICANT: Zhao, Qing A.
;  APPLICANT: Wang, Jian Rui
;  APPLICANT: Wehrman, Tom
;  APPLICANT: Zhou, Ping
;  APPLICANT: [illegible]
;  APPLICANT: Wang, Dunrui
;  APPLICANT: Ma, Yunqing
;  APPLICANT: Asundi, Vinod
;  APPLICANT: Wang, Zhiwei
;  APPLICANT: Wong, Gordon
;  APPLICANT: [illegible]
;  APPLICANT: Drmanac, Radoje T
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION: Polypeptides
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: PCT/US02/30474
;  CURRENT FILING DATE: 2002-09-24
;  PRIOR APPLICATION NUMBER: US [illegible]/324,631
;  PRIOR FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: US [illegible]/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US [illegible]/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: PCT/US00/35017
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US [illegible]/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US [illegible]/496,914
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]/5[illegible],825
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: US [illegible]/5[illegible],126
;  PRIOR FILING DATE: 2000-02-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 376
;   LENGTH: 2054
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (156)..(1535)
PCT-US02-30474-376

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;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
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;  APPLICANT: Wang, Jian Rui
;  APPLICANT: Wehrman, Tom
;  APPLICANT: Zhou, Ping
;  APPLICANT: Ghosh, Malabika
;  APPLICANT: Wang, Dunrui
;  APPLICANT: Ma, Yunqing
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;  APPLICANT: [illegible]
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;  APPLICANT: Drmanac, Radoje T.
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION: Polypeptides
;  FILE REFERENCE: [illegible]
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;  CURRENT FILING DATE: 2001-[illegible]
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;  PRIOR FILING DATE: [illegible]
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;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-[illegible]
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;  PRIOR FILING DATE: [illegible]
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;  PRIOR FILING DATE: [illegible]
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;  SOFTWARE: pt FL genes Version [illegible]
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;   NAME/KEY: [illegible]
;   LOCATION: ([illegible])..([illegible])
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; Sequence 13, Application US/10181590
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  BANDMAN, Olga
;  APPLICANT:  MATHUR, Preete
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  AZIMZAI, Yalda
;  APPLICANT:  YUE, Henry
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  HILLMAN, Jennifer L.
;  APPLICANT:  [illegible]
;  APPLICANT:  WANG, Eureka
;  APPLICANT:  [illegible]
;  APPLICANT:  POLICKY, Jennifer L.
;  TITLE OF INVENTION: PHOSPHATASES
;  FILE REFERENCE: PI-0018 PCT
;  CURRENT APPLICATION NUMBER: US/10/181,590
;  CURRENT FILING DATE:  2002-07-1[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-01-21; 2000-01-28; 2000-02-25; 2000-03-17
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PERL Program
; SEQ ID NO 13
;    LENGTH: 1837
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: misc_feature
;    OTHER INFORMATION: Incyte ID No: 1723447CB1
US-10-181-590-13

  Query Match             [illegible];  Score [illegible];  DB 41;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. 6.5e-271;
  Matches 1380;  Conservative    0;  Mismatches    0;  Indels    [illegible];  Gaps    [illegible];

Qy      1 [illegible]

Db      1 ATGTCCGCGGCTGGTTCGGGCGCGTTCCTGCCTGGGAGCCGC[illegible] 60

Qy     61 [illegible]

Db     61 [illegible] 120

Qy    121 [illegible]

Db    121 [illegible]

Qy    181 [illegible]

Db    181 [illegible] 240

Qy    241 [illegible]

Db    241 [illegible]

Qy    301 [illegible]

Db    301 [illegible]

Qy    361 [illegible]

Db    361 [illegible] 420

Qy    421 [illegible] 480

Db    421 [illegible]

Qy    481 [illegible]

Db    481 [illegible]

Qy    541 [illegible]

Db    541 [illegible]

Qy    601 [illegible]

Db    601 [illegible]

Qy    661 [illegible]

Db    661 [illegible]

Qy    721 [illegible]

Db    721 [illegible]

Qy    781 [illegible]

Db    781 [illegible]

Qy    841 [illegible]

Db    841 [illegible]

Qy    901 [illegible]
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; Sequence [illegible], Application US/[illegible]
;  GENERAL INFORMATION:
;   APPLICANT: [illegible]
;   APPLICANT: [illegible], Y. [illegible]
;   APPLICANT: [illegible], Miriam E.
;   TITLE OF INVENTION: [illegible]
;   FILE REFERENCE: [illegible]
;   CURRENT APPLICATION NUMBER: [illegible]
;   CURRENT FILING DATE: [illegible]
;   NUMBER OF SEQ ID NOS: [illegible]
;   SOFTWARE: [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: [illegible]

  Query Match [illegible]  Score [illegible]  Length [illegible]
  Best Local Similarity [illegible]  Pred. No. [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]
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Qy       1260 [illegible]
Db       1261 [illegible]

Qy       1320 [illegible]
Db       1321 [illegible]

Qy       1380 A 1380

Db       1381 A 1381


RESULT 6
US-09-526-996-1047/c
; Sequence 1047, Application US/09526996
; GENERAL INFORMATION:
;  APPLICANT: Shyjan, Andrew W.
;  TITLE OF INVENTION: [illegible]
;  TITLE OF INVENTION: HUMAN PROSTATE AND BREAST LIBRARIES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/526,996
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: 60/125,469
;  EARLIER FILING DATE: 1999-03-22
;  EARLIER APPLICATION NUMBER: 60/125,56[illegible]
;  EARLIER FILING DATE: 1999-03-22
;  NUMBER OF SEQ ID NOS: 1296
;  SOFTWARE: FastSEQ for Windows Version [illegible]
; SEQ ID NO 1047
;   LENGTH: 2110
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-526-996-1047

  Query Match             93.1%;  Score 1285;  DB 19;  Length 2110;
  Best Local Similarity   99.9%;  Pred. No. 1.2e-25[illegible];
  Matches 1296;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         85 GTGCCCTACCGACGGCCCCGCTTCCTTCGCGGCTCCAGCTCCAGCCCCGGGGCGGCCGAC 144
Db       2110 [illegible] 2051

Qy        145 [illegible] 204
Db       2050 [illegible] 1991

Qy        205 [illegible]
Db       1990 [illegible]

Qy        264 [illegible]
Db       1930 [illegible] 1871

Qy        324 [illegible] 383
Db       1870 [illegible]

Qy        384 [illegible] 443
Db       1810 [illegible]

Qy        444 [illegible]
Db       1750 [illegible]

Qy        504 [illegible]
Db       1690 [illegible]

Qy        564 [illegible] 623
Db       [illegible]

Qy        624 [illegible]
Db       1570 [illegible]

Qy        684 [illegible] 743
Db       [illegible]

Qy        744 [illegible]
Db       1450 [illegible]

Qy        804 [illegible] 863
Db       [illegible]

Qy        864 [illegible] 923
Db       1330 [illegible]

Qy        924 [illegible]
Db       1270 [illegible]

Qy        984 [illegible]
Db       1210 [illegible]

Qy       1044 [illegible]
Db       1150 [illegible]

Qy       1104 [illegible]
Db       1090 [illegible]

Qy       1164 TGTACTGTCCAAGGAGCAGGTGGCATGGTGGTGCGGAGCTTCCTCCCTGGGAACTAAGA 1223
Db       1030 [illegible]

Qy       1224 [illegible]
Db        970 [illegible]

Qy       1284 [illegible]
Db        910 [illegible]

Qy       1344 [illegible] 1380
Db        851 [illegible] 814


RESULT 7
US-09-540-216-1175/c
; Sequence 1175, Application US/09540216
; GENERAL INFORMATION:
;  APPLICANT: Gearing, David P.
;  APPLICANT: Kingsbury, Gillian A.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM
;  TITLE OF INVENTION: HUMAN BONE MARROW AND T CELL LIBRARIES
;  FILE REFERENCE: 1600.1106-001
;  CURRENT APPLICATION NUMBER: US/09/540,216
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 1284
;  SOFTWARE: FastSEQ for Windows Version [illegible]
; SEQ ID NO 1175
;   LENGTH: 2110
;   TYPE: DNA
; ORGANISM: Homo sapiens
[illegible]

Query Match [illegible]
Best Local Similarity [illegible]; Pred. No. [illegible];
Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy [illegible]
Db 2110 [illegible] 2051

[illegible]

Db 1150 [illegible]

Qy 1104 [illegible]

Db 1090 [illegible]

Qy 1164 [illegible]

Db 1030 [illegible]

Qy 1224 [illegible]

Db 970 [illegible]

Qy 1284 AGACAGG[illegible] 1343

Db 910 [illegible]

Qy 1344 [illegible] 1360

Db 850 [illegible] 834


RESULT 8
US-09-617-603-1179/c
; Sequence 1179, Application US/09617603
; GENERAL INFORMATION:
;  APPLICANT: Gearing, David P.
;  APPLICANT: Kingsbury, Gillian A.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM
;  TITLE OF INVENTION: HUMAN BONE MARROW AND T CELL LIBRARIES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/617,603
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]/125,[illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 1264
;  SOFTWARE: FastSEQ for Windows Version [illegible]
; SEQ ID NO 1179
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-617-603-1179

  Query Match [illegible]; Score [illegible]; DB 23; Length [illegible];
  Best Local Similarity [illegible]; Pred. No. [illegible];
  Matches 1296; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 85 [illegible] 144

Db 2110 GTGC[illegible]TACGGACG[illegible]CAGCTCCAG[illegible] 2051

Qy 145 [illegible] 204

Db 20[illegible] [illegible]

Qy 205 [illegible]

Db [illegible]

Qy 264 [illegible] 323

Db [illegible]

Qy 324 [illegible]

Db [illegible]

Qy 384 [illegible]

Db [illegible]

Qy 444 [illegible]
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Db       1750 [illegible] 1691

Qy        504 CATCTGCCCCATTGACCCTCAGTTTGTGGAGGAAAAGGGCATCAGGGCAGAAGACTTGGT 563

Db       1690 CATCTGCCCCA[illegible] 1631

Qy        564 [illegible] 623

Db       1630 [illegible] 1571

Qy        624 GGCCTCA[illegible] 683

Db       1570 [illegible] 1511

Qy        684 [illegible] 743

Db       1510 [illegible] 1451

Qy        744 [illegible] 803

Db       1450 [illegible] 1391

Qy        804 CTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTT[illegible]GGCTGAAGGG 863

Db       1390 CTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCCCTGGGCGGCTGAAGGG 1331

Qy        864 [illegible] 923

Db       1330 [illegible] 1271

Qy        924 [illegible] 983

Db       1270 [illegible] 1211

Qy        984 [illegible] 1043

Db       1210 [illegible] 1151

Qy       1044 [illegible] 1103

Db       1150 [illegible] 1091

Qy       1104 [illegible] 1163

Db       1090 GGACCAGCTGGAGCTACAGGAGGATGATGTCC[illegible]GCAACTGATGGACTCTGGGA 1031

Qy       1164 [illegible] 1223

Db       1030 [illegible] 971

Qy       1224 [illegible] 1283

Db        970 [illegible] 911

Qy       1284 [illegible] 1343

Db        910 [illegible] 851

Qy       1344 [illegible] 1380

Db        850 [illegible] 814


RESULT [illegible]
US-09-760-475-724
; Sequence 724, Application US/09760475
; GENERAL INFORMATION:
;  APPLICANT: [illegible] et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/760,475
;  CURRENT FILING DATE: [illegible]
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 4122
;  SOFTWARE: PatentIn Ver. 2.[illegible]
; SEQ ID NO 724
;   LENGTH: 2156
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (65)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (73)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: ([illegible])
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (2088)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-760-475-724

  Query Match             92.[illegible]%;  Score 127[illegible];  DB [illegible];  Length 2156;
  Best Local Similarity   [illegible]%;  Pred. No. 2e-252;
  Matches 1301;  Conservative    0;  Mismatches    3;  Indels    2;  Gaps    2;

Qy         75 [illegible] 134

Db          1 [illegible]

Qy        135 [illegible] 194

Db         61 [illegible] 120

Qy        195 [illegible] 254

Db        121 [illegible]

Qy        255 [illegible] 314

Db        181 [illegible]

Qy        315 [illegible] 374

Db        240 [illegible]

Qy        375 [illegible] 434

Db        300 [illegible]

Qy        435 [illegible] 494

Db        360 [illegible]

Qy        495 [illegible] 554

Db        420 [illegible]

Qy        555 [illegible] 614

Db        480 [illegible]

Qy        615 [illegible]

Db        540 [illegible]

Qy        675 [illegible] 734

Db        600 [illegible]

Qy        735 [illegible]

Db        660 [illegible]
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Qy     [illegible]
Db     [illegible] 778

Qy     [illegible]
Db     [illegible]

Qy     [illegible] TATTATAAAT[illegible]TAGAAAT[illegible]AA[illegible] [illegible]
Db     [illegible] TATTATAAA[illegible]AAAT[illegible]AA[illegible] [illegible]

Qy     [illegible] TAGG[illegible]TACTAGGAA[illegible] [illegible]
          ||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db     [illegible] TAGG[illegible]TACTAGGAA[illegible] [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible] 1154
Db     [illegible]

Qy     [illegible] 1211
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     12[illegible] [illegible]GAAA[illegible]GAA[illegible] 1334
Db     11[illegible] [illegible]GAAA[illegible]GAA[illegible] 1266

Qy     13[illegible] [illegible] 1355
Db     12[illegible] [illegible]

RESULT [illegible]
[illegible]
; Sequence [illegible], Application [illegible]
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: Zhang, Jie
;  APPLICANT: Ren, Feiyan
;  APPLICANT: Xue, Aidong J.
;  APPLICANT: Zhao, Qing A.
;  APPLICANT: Wang, Jian-Rui
;  APPLICANT: Wehrman, Tom
;  APPLICANT: Zhou, Ping
;  APPLICANT: Ghosh, Malabika
;  APPLICANT: Wang, Dunrui
;  APPLICANT: Ma, Yunqing
;  APPLICANT: Asundi, Vinod
;  APPLICANT: Wang, Zhiwei
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION: Polypeptides
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US00/[illegible]
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: PCT/US01/02623
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 09/515,126
;  PRIOR FILING DATE: 2000-02-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: pt FL_genes Version [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
[illegible]

  Query Match             [illegible];  Score [illegible];  DB 1;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible]e-244;
  Matches [illegible];  Conservative    0;  Mismatches    6;  Indels   [illegible];  Gaps    [illegible];

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible] 120

Qy     194 [illegible]GCAGGCTACGCCGAG[illegible]ATTATCAATGCAGAGAAATCTGAATTC 252
           ||||||||||||||||||||||||||||     | ||||||||||||||||||||||||||||
Db     121 [illegible]ATTATCAATGCAGAGAAATCTGAATTC 18[illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     241 [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible] 480

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
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Db        661 [illegible] 720

Qy        793 [illegible] 852

Db        721 [illegible] 780

Qy        853 [illegible] 912

Db        781 [illegible] 840

Qy        913 [illegible] 972

Db        841 [illegible] 900

Qy        973 [illegible] 1032

Db        901 [illegible] 960

Qy       1033 [illegible] 1092

Db        961 [illegible] 1020

Qy       1093 [illegible] 1152

Db       1021 [illegible] 1080

Qy       1153 [illegible] 1212

Db       1081 [illegible] 1140

Qy       1213 [illegible] ----------------  [illegible] 1247

Db       1141 [illegible] 12[illegible]

Qy       1249 [illegible]

Db       1291 [illegible]

Qy       1308 [illegible]

Db       1261 [illegible]

Qy       1368 [illegible]

Db       1321 [illegible]


RESULT 17
PCT-US02-30474-2218
; Sequence 2218, Application PC/TUS0230474
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Jian Rui
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Chen, Ping
;  APPLICANT:  Ghosh, Malabika
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Wang, [illegible]
;  APPLICANT:  Haley Vicente, Dana
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 816CIP PCT
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE:  2002-09-24
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: US 09/408,725
;  PRIOR FILING DATE: 2000-[illegible]
;  PRIOR APPLICATION NUMBER: US 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: PCT/US00/35017
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US 09/4[illegible],914
;  PRIOR FILING DATE: 200[illegible]
;  PRIOR APPLICATION NUMBER: US 09/5[illegible]
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: PCT/US[illegible]
;  PRIOR FILING DATE: 2001-02-0[illegible]
;  PRIOR APPLICATION NUMBER: US 09/515,126
;  PRIOR FILING DATE: 2000-02-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 34[illegible]
;  SOFTWARE: pt_FL_genes Version [illegible]
; SEQ ID NO 2218
;   LENGTH: 2124
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US02-30474-2218

  Query Match             89.8%;  Score 1249.4;  DB 1;  Length 2124;
  Best Local Similarity   97.3%;  Pred. No. 2.7e-244;
  Matches 1300;  Conservative    0;  Mismatches    5;  Indels   [illegible];  Gaps    [illegible];

Qy         71 [illegible] 134

Db          [illegible]

Qy        135 [illegible] 194

Db         [illegible] 12[illegible]

Qy        195 [illegible] 254

Db        121 [illegible]

Qy        255 [illegible]

Db        181 [illegible] 240

Qy        31[illegible] [illegible]

Db        241 [illegible]

Qy        373 [illegible] 432

Db        301 [illegible]

Qy        433 [illegible] 492

Db        36[illegible] [illegible]

Qy        493 [illegible]

Db        421 [illegible] 480

Qy        553 [illegible] 612

Db        481 [illegible] 540

Qy        613 [illegible] 672

Db        541 [illegible]

Qy        673 [illegible] 732
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Db        [illegible]

Qy        [illegible]
          [illegible]
Db        [illegible]

Qy        [illegible]
          [illegible]
Db        [illegible]

Qy        [illegible]
          [illegible]
Db        [illegible]

Qy        [illegible]
          [illegible]
Db        [illegible]

Qy        [illegible]
          [illegible]
Db        [illegible]

Qy        [illegible]
          [illegible]
Db        [illegible]

Qy        [illegible]
          [illegible]
Db        [illegible]

Qy        [illegible]
          [illegible]
Db        [illegible]

Qy        [illegible]
          [illegible]
Db        [illegible]

Qy        [illegible]
          [illegible]
Db        [illegible]

Qy        [illegible]
          [illegible]
Db        [illegible]

Qy        [illegible] TATTGATTATTTA [illegible]
          [illegible]
Db        [illegible] TATTGATTATTTA [illegible]


RESULT [illegible]
US-09-471-275-7049
; Sequence 7049, Application US/09471275
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
;  TITLE OF INVENTION: From Various Libraries
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/09/471,275
;  CURRENT FILING DATE: 1999-12-23
;  EARLIER APPLICATION NUMBER: US [illegible]
;  EARLIER FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: US 09/2[illegible]
;  EARLIER FILING DATE: 1999-02-22
;  EARLIER APPLICATION NUMBER: US 09/24[illegible]
;  EARLIER FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: US [illegible]
;  EARLIER FILING DATE: 1999-[illegible]
;  EARLIER APPLICATION NUMBER: US [illegible]
;  EARLIER FILING DATE: 1999-[illegible]
;  EARLIER APPLICATION NUMBER: US [illegible]
;  EARLIER FILING DATE: 1999-04-15
;  EARLIER APPLICATION NUMBER: US 09/274,861
;  EARLIER FILING DATE: 1999-03-23
;  EARLIER APPLICATION NUMBER: US 60/125,453
;  EARLIER FILING DATE: 1999-03-19
;  EARLIER APPLICATION NUMBER: US 60/126,605
;  EARLIER FILING DATE: 1999-03-26
;  EARLIER APPLICATION NUMBER: US 09/[illegible]
;  EARLIER FILING DATE: 1999-[illegible]
;  EARLIER APPLICATION NUMBER: US 09/[illegible]
;  EARLIER FILING DATE: 1999-[illegible]-21
;  EARLIER APPLICATION NUMBER: US 09/404,284
;  EARLIER FILING DATE: 1999-09-21
;  EARLIER APPLICATION NUMBER:
;  EARLIER FILING DATE: 1999-12-16
;  NUMBER OF SEQ ID NOS: 10451
;  SOFTWARE: pt_FL genes Version 1.0
; SEQ ID NO 7049
;   LENGTH: 2121
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: ([illegible])..([illegible])
;   OTHER INFORMATION: similar to [illegible] in the genpept database [illegible]
;   OTHER INFORMATION: [illegible] with FASTY [illegible], default parameters
US-09-471-275-7049

  Query Match             89.8%;  Score 1239.4;  DB 18;  Length 2121;
  Best Local Similarity   97.5%;  Pred. No. 2.7e-244;
  Matches 1[illegible];  Conservative    0;  Mismatches    6;  Indels   2[illegible];  Gaps    [illegible];

Qy         7[illegible] [illegible] 134
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Qy        135 [illegible]
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Db         61 [illegible] 120

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Qy        25[illegible] [illegible]
              [illegible]
Db        181 [illegible]

Qy        31[illegible] [illegible]
              [illegible]
Db        241 [illegible]

Qy        37[illegible] [illegible]
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Db        301 [illegible] 360

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Qy        493 [illegible]
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Db        421 [illegible] 480

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              [illegible]
Db        481 [illegible] 540

Qy        613 [illegible]
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Db        541 [illegible]

Qy        673 [illegible]
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Db        601 CAGG[illegible] 660

Qy        733 [illegible] 792

Db        661 [illegible] 72[illegible]

Qy        793 CTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGACTTCACCCACTCCACTTCCCTCGG 852

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Qy        853 [illegible] 912

Db        781 CGGCTGAA[illegible] 840

Qy        913 [illegible] 972

Db        841 [illegible]

Qy        973 AGGCAGCCTCGGTTACTAGGAACAT[illegible] 1032

Db        9[illegible]1 AGGCAG[illegible]

Qy       1033 AGAGT[illegible] 1092

Db        961 AGAGT[illegible] 1020

Qy       1093 [illegible] 1152

Db       1021 [illegible]

Qy       1153 [illegible] 1212

Db       1081 [illegible] 114[illegible]

Qy       1213 GGGAACCAAGAGGACCCA-------------------------C[illegible]AGCTTCTCAAAGCT 1247
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Db       1141 [illegible] 12[illegible]

Qy       1248 [illegible] 1307

Db       1201 [illegible] 12[illegible]

Qy       1308 [illegible] 1367

Db       1261 [illegible] 1320

Qy       1368 CAGTGACCACTGA 1380
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Db       1321 CAGTGACCACTGA 1333


RESULT 13
US-60-324-631-2198
; Sequence 2198, Application US/60324631
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Chawla, Malabika
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Wen, Zhiwei
;  APPLICANT:  Wang, Gezhi
;  APPLICANT:  [illegible]
;  APPLICANT:  Drmanac, Radoje T
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 810
;  CURRENT APPLICATION NUMBER: US/60/324,631
;  CURRENT FILING DATE:  200[illegible]
;  PRIOR APPLICATION NUMBER: US 09/488,72[illegible]
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: PCT/US00/35017
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: PCT/US01/02623
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US 09/496,914
;  PRIOR FILING DATE: 2000-02-[illegible]
;  PRIOR APPLICATION NUMBER: US 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: PCT/US01/03800
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: US 09/515,126
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: US 09/577,409
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: PCT/US01/04927
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: US 09/519,705
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 09/574,454
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: PCT/US01/04941
;  PRIOR FILING DATE: 2001-03-05
;  PRIOR APPLICATION NUMBER: US 09/540,217
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: US 09/649,167
;  PRIOR FILING DATE: 2000-08-23
;  PRIOR APPLICATION NUMBER: PCT/US01/08631
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: US 09/552,[illegible]
;  PRIOR FILING DATE: 2000-04-18
;  PRIOR APPLICATION NUMBER: US 09/770,160
;  PRIOR FILING DATE: 2001-01-26
;  PRIOR APPLICATION NUMBER: PCT/US01/08656
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: US 09/577,408
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: PCT/US01/14827
;  PRIOR FILING DATE: 2001-05-16
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 2198
;   LENGTH: 2124
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-324-631-2198

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  Best Local Similarity   [illegible];  Pred. No. 2.7e-244;
  Matches 1[illegible];  Conservative    0;  Mismatches    6;  Indels   [illegible];  Gaps    [illegible];

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Qy        1[illegible] [illegible] 2[illegible]

Db          [illegible] 1[illegible]

Qy        2[illegible] [illegible]
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[illegible]

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[illegible]

Qy   [illegible]
Db   1321 CAGIGACCACIGA 1333

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; Sequence [illegible] Application US/[illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible] Y. [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: Ren, [illegible]
;  APPLICANT: Xue, Aidong J.
;  APPLICANT: [illegible]
;  APPLICANT: Wang, [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: Wang, [illegible]
;  APPLICANT: Ma, Yunqing
;  APPLICANT: Asundi, Vinod
;  APPLICANT: Wang, Zhiwei
;  APPLICANT: Wang, [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION: Polypeptides
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: 2001-[illegible]
;  PRIOR APPLICATION NUMBER: US 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
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;  PRIOR FILING DATE: [illegible]
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;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US 09/496,914
;  PRIOR FILING DATE: [illegible]
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;  PRIOR FILING DATE: [illegible]
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;  PRIOR FILING DATE: [illegible]
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;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-05-18
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;  PRIOR FILING DATE: [illegible]
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;  PRIOR FILING DATE: 2001-[illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: PCT/US01/14827
;  PRIOR FILING DATE: 2001-05-18
;  NUMBER OF SEQ ID NOS: 4334
;  SOFTWARE: pt_FL_genes Version 1.
; SEQ ID NO 2199
;   LENGTH: 2124
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-824-961-2199

  Query Match             89.8%;  Score 1239.4;  DB 76;  Length 2124;
  Best Local Similarity   97.5%;  Pred. No. 2.7e-211;
  Matches 1300;  Conservative    0;  Mismatches    6;  Indels   27;  Gaps    3;

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Db         61 [illegible] 120

Qy        194 [illegible] 252
Db        121 [illegible] 180

Qy        253 [illegible] 312
Db        181 [illegible] 240

Qy        313 [illegible] 372
Db        241 [illegible] 300

Qy        373 [illegible] 432
Db        301 [illegible] 360

Qy        433 [illegible] 492
Db        361 [illegible] 420

Qy        493 [illegible] 552
Db        421 [illegible]

Qy        553 [illegible] 612
Db        481 [illegible]

Qy        613 [illegible] 672
Db        541 [illegible]

Qy        673 [illegible] 732
Db        601 [illegible]

Qy        733 [illegible] 792
Db        661 [illegible] 720

Qy        793 [illegible] 852
Db        721 [illegible] 780

Qy        853 [illegible] 912
Db        781 [illegible] 840

Qy        913 [illegible] 972
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Qy        973 [illegible]
Db        901 [illegible]

Qy       1033 [illegible]
Db        961 [illegible]

Qy       1093 [illegible]
Db       1021 [illegible]

Qy       1153 [illegible]
Db       1081 [illegible] 1140

Qy       1213 [illegible]
Db       1141 [illegible]

Qy       1248 [illegible] 1307
Db       1201 [illegible]

Qy       1308 [illegible] 1367
Db       1261 [illegible]

Qy       1368 CATTGACCACTGA 1380
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Db       1321 CAGTGACCACTGA 1333


RESULT 13
US-60-185-213-1400
; Sequence 1400, Application US/60185213
; GENERAL INFORMATION:
;  APPLICANT: Hodgson, David M.                       Jones, Alissa I.
;  APPLICANT: Lincoln, Stephen E.             Yu, Jimmy Y.
;  APPLICANT: Russo, Frank D.                         Greenawalt, Lila B.
;  APPLICANT: Spiro, Peter A.                         Panzer, Scott R.
;  APPLICANT: Banville, Steve C.              Roseberry, Ann M.
;  APPLICANT: Bratcher, Shawn R.              Wright, Rachel J.
;  APPLICANT: [illegible]                             [illegible]
;  APPLICANT: Cohen, Howard J.                        [illegible]
;  APPLICANT: Rosen, Bruce                    Yap, Pierre E.
;  APPLICANT: Shah, Purvi                             Stockdreher, Theresa K.
;  APPLICANT: Chalup, Michael S.              Amshey, Stefan
;  APPLICANT: Hillman, Jennifer L.                    [illegible]
;  TITLE OF INVENTION: [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/60/185,213
;  CURRENT FILING DATE: 2000-02-24
;  NUMBER OF SEQ ID NOS: 1642
;  SOFTWARE: PERL Program
; SEQ ID NO 1400
;   LENGTH: 2084
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: [illegible]
US-60-185-213-1400

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Qy        225 [illegible] 284
Db        115 [illegible]
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[illegible]

Search completed: [illegible]
Job time : [illegible] secs

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                         GenCore version 5.1.3
                Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 22, 2003, 22:55:29 ; Search time 290 Seconds
                                             (without alignments)
                                             7401.72? Million cell updates/sec

Title:           US-09-866-987-3
Perfect score:   1380
Sequence:        1 atgtccgacgqctagttccg..........aadagatadtgaccactga 1380

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2850587 seqs, 777717511 residues

Total number of hits satisfying chosen parameters:      [illegible]

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       Pending_Patents_NA_New:*
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               2: [illegible]_NEW_[illegible]:*
               3: [illegible]_NEW_[illegible]:*
               4: [illegible]_NEW_[illegible]:*
               5: [illegible]_NEW_[illegible]:*
               6: [illegible]_NEW_[illegible]:*
               7: [illegible]_NEW_[illegible]:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
                   %
Result           Query
  No.    Score   Match Length DB  ID                            Description
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     1    1346    97.5   2185  6  US-10-072-012-197             Sequence 197, App
     2   843.6    61.1   1285  6  US-10-144-771-11494           Sequence 11494, A
     3     826    59.9   1930  6  US-10-072-012-199             Sequence 199, App
     4   367.2    26.6    476  6  US-10-349-781-54107           Sequence 54107, A
     5   264.8    19.2   [illegible] 6  US-10-242-[illegible]-412  Sequence 412, App
     6   263.2    19.1   1480  1  PCT-US02-39126-65             Sequence 65, Appl
     7   262.?    19.0   1991  6  US-10-144-771-12171           Sequence 12171, A
     8     259    18.8    271  6  US-10-349-781-22954           Sequence 22954, A
     9   252.?    18.3   2462  6  US-10-144-771-6858            Sequence 6858, Ap
    10     248    18.0   1461  1  PCT-US02-39126-63             Sequence 63, Appl
    11   243.4    17.6   1887  5  US-09-620-312D-42             Sequence 42, Appl
    12   233.6    16.9    241  6  US-10-349-781-2[illegible]   Sequence 2[illegible], A
    13   192.6    14.0   1421  1  PCT-US02-39126-62             Sequence 62, Appl
    14   168.8    12.2   1472  1  PCT-US02-39126-64             Sequence 64, Appl
c   15    62.8     4.6    183  6  US-10-349-781-46051           Sequence 46051, A
    16    52.6     3.8    475  5  US-09-606-357A-167            Sequence 167, App
    17      51     3.7   2511  7  US-60-423-552-19              Sequence 19, Appl
    18      51     3.7   2511  7  US-60-427-579-19              Sequence 19, Appl
c   19    49.8     3.6   6714  6  US-10-267-117-6               Sequence 6, Appli
c   20    49.8     3.6   6714  6  US-10-340-112-6               Sequence 6, Appli
c   21    49.8     3.6   6924  6  US-10-267-117-9               Sequence 9, Appli
c   22    49.8     3.6   6924  6  US-10-267-117-10              Sequence 10, Appl
c   23    49.8     3.6   6924  6  US-10-267-117-11              Sequence 11, Appl
c   24    49.8     3.6   6924  6  US-10-340-112-9               Sequence 9, Appli
c   25    49.8     3.6   6924  6  US-10-340-112-10              Sequence 10, Appl
c   26    49.8     3.6   6924  6  US-10-340-112-11              Sequence 11, Appl
c   27    49.4     3.6   1477  5  US-09-724-676-19511           Sequence 19511, A
c   28    49.4     3.6   1477  5  US-09-724-676A-19511          Sequence 19511, A
c   29    49.4     3.6   1483  5  US-09-724-676-19546           Sequence 19546, A
c   30    49.4     3.6   1483  5  US-09-724-676A-19546          Sequence 19546, A
c   31    49.4     3.6   1505  5  US-09-724-676-19539           Sequence 19539, A
c   32    49.4     3.6   1505  5  US-09-724-676A-19539          Sequence 19539, A
c   33    49.4     3.6   1511  5  US-09-724-676-19543           Sequence 19543, A
c   34    49.4     3.6   1511  5  US-09-724-676A-19543          Sequence 19543, A
c   35    49.4     3.6   1512  5  US-09-724-676-19521           Sequence 19521, A
c   36    49.4     3.6   1512  5  US-09-724-676A-19521          Sequence 19521, A
c   37    49.4     3.6   1518  5  US-09-724-676-19525           Sequence 19525, A
c   38    49.4     3.6   1518  5  US-09-724-676A-19525          Sequence 19525, A
c   39    49.4     3.6   1525  5  US-09-724-676-19531           Sequence 19531, A
c   40    49.4     3.6   1525  5  US-09-724-676A-19531          Sequence 19531, A
c   41    49.4     3.6   1531  5  US-09-724-676-19535           Sequence 19535, A
c   42    49.4     3.6   1531  5  US-09-724-676A-19535          Sequence 19535, A
c   43    49.4     3.6   1656  5  US-09-724-676-19538           Sequence 19538, A
c   44    49.4     3.6   1656  5  US-09-724-676A-19538          Sequence 19538, A
c   45    49.4     3.6   1678  5  US-09-724-676-19542           Sequence 19542, A
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                              ALIGNMENTS

RESULT 1
US-10-072-012-197
; Sequence 197, Application US/10072012
; GENERAL INFORMATION:
;  APPLICANT: Tchernev, Velizar
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Li, Li
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Taupier Jr, Raymond J.
;  APPLICANT:  Gusev, Vladimir Y.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Wolenc, Adam R.
;  APPLICANT:  Pena, Carol E. A
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Grosse, William M.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-258
;  CURRENT APPLICATION NUMBER: US/10/072,012
;  CURRENT FILING DATE: 2002-02-[illegible]
;  PRIOR APPLICATION NUMBER: 60/265,[illegible]
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/265,514
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,517
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,412
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,[illegible]
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/26[illegible],40[illegible]
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 60/266,767
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: 60/267,0[illegible]
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/266,[illegible]
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO [illegible]
;   LENGTH: 2185
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-[illegible]-197

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  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches [illegible];  Conservative    0;  Mismatches [illegible];  Indels   24;  Gaps [illegible];

[illegible]

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[illegible]

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Qy       1357 GGCCAAGAGAGCAGTGACCACTGA 1380
Db       1381 GGCCAAGAGAGCAGTGACCACTGA 1404


RESULT 2
US-10-144-771-11494
; Sequence 11494, Application US/10144771
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/10/144,771
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
; SEQ ID NO 11494
;   LENGTH: 1285
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-144-771-11494

  Query Match             61.1%;  Score 843.6;  DB 6;  Length 1285;
  Best Local Similarity   85.9%;  Pred. No. 5.6e-182;
  Matches  962;  Conservative    0;  Mismatches  149;  Indels    9;  Gaps [illegible];

[illegible]
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Db        293 [illegible] 352

Qy        459 [illegible] 518
Db        353 [illegible] 412

Qy        519 [illegible] 578
Db        413 [illegible] 472

Qy        579 [illegible] 638
Db        473 [illegible] 532

Qy        639 [illegible] 698
Db        533 [illegible] 592

Qy        699 [illegible] 758
Db        593 [illegible] 652

Qy        759 [illegible] 818
Db        653 [illegible] 712

Qy        819 [illegible] 878
Db        713 [illegible] 772

Qy        879 [illegible] 938
Db        773 [illegible] 832

Qy        939 [illegible] 998
Db        833 [illegible] 892

Qy        999 [illegible] 1058
Db        893 [illegible] 952

Qy       1059 [illegible] 1118
Db        953 GAAGCCCTTCCTACTCTCCATGCCACAGGTGACTGTGCTGGATGTCCACCAGCTGGCAGT 1012

Qy       1119 [illegible] 1178
Db       1013 [illegible] 1072

Qy       1179 [illegible] 1238
Db       1073 [illegible] 1132

Qy       1239 [illegible] 1298
Db       1133 [illegible] 1192

Qy       1299 [illegible]
Db       1193 [illegible]


RESULT 3
US-10-072-012-199
; Sequence 199, Application US/10072012
; GENERAL INFORMATION:
;  APPLICANT: Tchernev, Velizar
;  APPLICANT: Spytek, Kimberly
;  APPLICANT: Zerhusen, Bryan
;  APPLICANT: Patturajan, Meera
;  APPLICANT: Shimkets, Richard
;  APPLICANT: Li, Li
;  APPLICANT: Gangolli, Esha
;  APPLICANT: Padigaru, Muralidhara
;  APPLICANT: Anderson, David W.
;  APPLICANT: Rastelli, Luca
;  APPLICANT: Miller, Charles E.
;  APPLICANT: Gerlach, Valerie
;  APPLICANT: Taupier Jr, Raymond J.
;  APPLICANT: Gusev, Vladimir Y.
;  APPLICANT: Colman, Steven D.
;  APPLICANT: Wolenc, Adam R.
;  APPLICANT: Pena, Carol E. A
;  APPLICANT: Furtak, Katarzyna
;  APPLICANT: Grosse, William M.
;  APPLICANT: Alsobrook II, John P.
;  APPLICANT: Lepley, Denise M.
;  APPLICANT: Rieger, Daniel K.
;  APPLICANT: Burgess, Catherine E.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-258
;  CURRENT APPLICATION NUMBER: US/10/072,012
;  CURRENT FILING DATE: 2002-[illegible]
;  PRIOR APPLICATION NUMBER: 60/265,102
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/265,514
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,[illegible]
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,412
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,[illegible]
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/266,406
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 60/266,767
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: 60/267,057
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/266,975
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/267,459
;  PRIOR FILING DATE: 2001-02-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1391
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 199
;   LENGTH: 1930
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-072-012-199

  Query Match             [illegible];  Score [illegible];  DB 6;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches 1125;  Conservative  0;  Mismatches  [illegible];  Indels  [illegible];  Gaps  2;

Qy          1 [illegible]
Db          1 [illegible]

Qy         61 [illegible]
Db         61 [illegible]

Qy        121 [illegible]
Db        121 [illegible]

Qy        181 [illegible]
Db        181 [illegible]

Qy        241 [illegible]
Db        241 [illegible]
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[illegible]

RESULT 4
US [illegible]
; Sequence [illegible], Application US/[illegible]
; GENERAL INFORMATION:
;  APPLICANT: [illegible], Jeffrey [illegible]; [illegible], Angelo M.
;  APPLICANT:  Stuart, Susan G.; [illegible], Laura L.
;  APPLICANT:  Mullahy, Sara [illegible]; Naughton, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIV
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: 60/[illegible]
;  PRIOR FILING DATE: 1996-12-1[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible] 12-14
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-12-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 61458
;  SOFTWARE: PERL Program
; SEQ ID NO [illegible]
;   LENGTH: 47[illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: [illegible]
US [illegible]

  Query Match [illegible]
  Best Local Similarity [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

[illegible]
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Db     4?? [illegible] 484

Qy     585 CTTTCAGGAATG 596
           ||||||||||||
Db     465 CTTTCAGGAATG 476


RESULT 5
US-10-342-887-412
; Sequence 412, Application US/10342887
; GENERAL INFORMATION:
;  APPLICANT: [illegible]
;  APPLICANT:  He, Yudong
;  APPLICANT:  Linsley, Peter S.
;  APPLICANT:  Mao, Mao
;  APPLICANT:  Roberts, Christopher J.
;  APPLICANT:  Van 't Veer, Laura Johanna
;  APPLICANT:  Van de Vijver, Marc J.
;  APPLICANT:  Bernards, Rene
;  TITLE OF INVENTION: [illegible]
;  FILE REFERENCE: 9301-188-999
;  CURRENT APPLICATION NUMBER: US/10/342,887
;  CURRENT FILING DATE:  2003-01-15
;  PRIOR APPLICATION NUMBER: 60/298,918
;  PRIOR FILING DATE: 2001-06-18
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2002-05-14
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2002-06-14
;  NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 412
;   LENGTH: 2518
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-342-887-412

  Query Match              16.2%;  Score 241.8;  DB 6;  Length 2518;
  Best Local Similarity   57.7%;  Pred. No. 1.5e-58;
  Matches  537;  Conservative    0;  Mismatches  377;  Indels   17;  Gaps    8;

Qy     445 [illegible] 504
Db    1369 [illegible] 1428

Qy     505 [illegible] 564
Db    1429 [illegible] 1487

Qy     565 [illegible] 624
Db    1488 [illegible] 1547

Qy     625 [illegible] 684
Db    1548 [illegible] 1607

Qy     685 [illegible] 744
Db    1608 [illegible] 1667

Qy     745 [illegible] 804
Db    1668 [illegible] 1727

Qy     805 [illegible] 864
Db    1728 [illegible] 1787

Qy     865 [illegible] 924
Db    1788 [illegible] 1847

Qy     925 [illegible] 984
Db    1848 [illegible] 1907

Qy     985 [illegible] 1044
Db    1908 [illegible] 1967

Qy    1045 [illegible] 1104
Db    1968 [illegible] 2027

Qy    1105 [illegible] 1164
Db    2028 [illegible] 2087

Qy    1165 [illegible] 1224
Db    2088 [illegible] 2147

Qy    1225 [illegible] 1274
Db    2148 [illegible] 2207

Qy    1285 [illegible] 1344
Db    2208 [illegible] 2267

Qy    1345 [illegible] 1359
Db    2268 [illegible] 2297


RESULT 6
PCT-US02-39126-65
; Sequence 65, Application PC/TUS0239126
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  KABLE, Amy E.
;  APPLICANT:  CHIEN, David
;  APPLICANT:  WILSON, Amy D.
;  APPLICANT:  SWARNAKAR, Anita
;  APPLICANT:  CORVAL, Ann E.
;  APPLICANT:  HAFALIA, April J.A.
;  APPLICANT:  EMERLING, Brooke M.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  JIN, Pei
;  APPLICANT:  GRIFFIN, Jennifer A.
;  APPLICANT:  MARQUIS, Joseph P.
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  CHAWLA, Narinder K.
;  APPLICANT:  LEHR MASON, Patricia M.
;  APPLICANT:  KHARE, Reena
;  APPLICANT:  LEE, Sally
;  APPLICANT:  HAWKINS, Phillip R.
;  APPLICANT:  BECHA, Shanya D.
;  APPLICANT:  LEE, Soo Yeun
;  APPLICANT:  [illegible], William W.
;  APPLICANT:  ZEBARJADIAN, Yeganeh
;  TITLE OF INVENTION: KINASES AND PHOSPHATASES
;  FILE REFERENCE: PF-1315 PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/39126
;  CURRENT FILING DATE:  2002-12-[illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: US 60/343,546
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2002-02-14
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2002-[illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PERL Program
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: [illegible]
;  FEATURE:
;   NAME/KEY: [illegible]
;  OTHER INFORMATION: [illegible]
[illegible]

  Query Match              [illegible]
  Best Local Similarity    [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

[illegible]

RESULT [illegible]
[illegible]
; [illegible] Application [illegible]
; GENERAL INFORMATION:
;  APPLICANT: VENTER, [illegible]
;  TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
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;  NUMBER OF SEQ ID NOS: [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: HUMAN
US [illegible]

  Query Match              [illegible]  Score [illegible]  DB [illegible]  Length [illegible]
  Best Local Similarity    [illegible]  Pred. No. [illegible]
  Matches  713;  Conservative    0;  Mismatches  517;  Indels  [illegible]  Gaps  [illegible]

[illegible]
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Db       1121 TAATGGCTACCATTGGGGTGACACGGGGCTTGGGAGACCACAACCTTAAGGTCTGCAGCT 1180

Qy       1046 [illegible] 1105

Db       1181 CTACTCTGTCCATCAAGCCTTTCCTCTCCTGCTTTCCTGAAGTACGAGTGTATGATCTGA 1240

Qy       1106 ACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGG[illegible]AACTGATGGACTCTGGGATG 1165

Db       1241 [illegible]

Qy       1166 T-    A[illegible]GGGAA[illegible]AA 1221

Db       1301 [illegible]

Qy       1222 [illegible]

Db       1361 [illegible] 1419

Qy       1280 [illegible]

Db       1420 [illegible]GGCTGGCGTCT[illegible]CAAACAACAAGCT[illegible]GATGACATCTCG 1479

Qy       1330 [illegible]

Db       1480 [illegible] 1509


RESULT 8
US-10-349-781-22954
; Sequence 22954, Application US/10349781
; GENERAL INFORMATION:
;  APPLICANT: [illegible], Jeffrey J.; Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.; Stuve, Laura L.
;  APPLICANT: [illegible], [illegible]; [illegible], Rebecca [illegible]
;  TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIVE S
;  FILE REFERENCE: PP-1029-2 CON
;  CURRENT APPLICATION NUMBER: US/10/349,781
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 09/549,764
;  PRIOR FILING DATE: 2000-03-[illegible]
;  PRIOR APPLICATION NUMBER: 08/992,868
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-12-13
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-10-18
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1995-10-24
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-10-18
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-12-11
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1995-12-14
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-12-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 61458
;  SOFTWARE: PERL Program
; SEQ ID NO 22954
;   LENGTH: 271
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 1n00078869
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: [illegible]
;   OTHER INFORMATION: a, t, c, g, or other
US-10-349-781-22954

  Query Match             18.8%;  Score 259;  DB 6;  Length 271;
  Best Local Similarity   99.6%;  Pred. No. 1.6e-49;
  Matches  270;  Conservative    0;  Mismatches    1;  Indels    [illegible];  Gaps    [illegible];

Qy       1051 ATCCAGCTCAAGCCCTTCTTGCTCTCTGTGCCACAGGTGACTGTGCTGGATGTGGACCAG 1110

Db          1 ATCCAGCTCAAG[illegible]

Qy       1111 CTGGAGCTACAG[illegible]

Db         61 CT[illegible]

Qy       1171 TCCAA[illegible]

Db        121 TCCAA[illegible]GGAA[illegible]AAGAGGA[illegible]CA 179

Qy       1231 CACAG[illegible]

Db        181 [illegible]

Qy       1291 CTCA[illegible] 1322

Db        241 CTCACAG[illegible]GAA[illegible]TACGATGA 271


RESULT 9
US-10-144-771-6858
; Sequence 6858, Application US/10144771
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig
;  TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
;  FILE REFERENCE: CL001321
;  CURRENT APPLICATION NUMBER: US/10/144,771
;  CURRENT FILING DATE:  2002-05-15
;  NUMBER OF SEQ ID NOS: 47235
; SEQ ID NO 6858
;   LENGTH: 2462
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-144-771-6858

  Query Match             18.[illegible]%;  Score 252.6;  DB 6;  Length 2462;
  Best Local Similarity   [illegible]%;  Pred. No. 8.6e-48;
  Matches  439;  Conservative    [illegible];  Mismatches  [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy        [illegible] GAAAA[illegible]AA 594

Db        446 [illegible]

Qy        [illegible] [illegible]

Db        [illegible] [illegible]

Qy        [illegible] [illegible] 714

Db        [illegible] [illegible]

Qy        [illegible] [illegible] 774

Db        [illegible] [illegible]

Qy        775 CGGCAGCGGAT[illegible] 834

Db        686 CGGCAGAGACT[illegible]

Qy        [illegible] [illegible] 894

Db        746 CATT[illegible]

Qy        [illegible] [illegible]

Db        806 GA[illegible]TTAAATAT[illegible]AATA[illegible]AAAA[illegible]ATTGA[illegible]GAT[illegible]AAGT[illegible]
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Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

RESULT [illegible]
[illegible]
; Sequence [illegible] Application [illegible]
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT: KABLE, Amy E.
;  APPLICANT: CHIEN, David
;  APPLICANT: WILSON, Amy D.
;  APPLICANT: SWARNAKAR, Anita
;  APPLICANT: [illegible], Ann E.
;  APPLICANT: BAHALIA, April [illegible]
;  APPLICANT: EMERLING, Brooke M.
;  APPLICANT: [illegible]
;  APPLICANT: TIN, [illegible]
;  APPLICANT: [illegible], Jennifer A.
;  APPLICANT: MARQUIS, Joseph P.
;  APPLICANT: BAUGHN, Mariah R.
;  APPLICANT: CHAWLA, Narinder K.
;  APPLICANT: [illegible] M.
;  APPLICANT: KHARE, Reena
;  APPLICANT: LEE, [illegible]
;  APPLICANT: HAWKINS, Phillip E.
;  APPLICANT: BECHA, [illegible]
;  APPLICANT: LEE, [illegible] Youn
;  APPLICANT: [illegible], William W.
;  APPLICANT: [illegible]BAHIAN, Yeganeh
;  TITLE OF INVENTION: KINASES AND PHOSPHATASES
;  FILE REFERENCE: PF [illegible] PCT
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2002-02-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: [illegible]
; SEQ ID NO [illegible]
;  LENGTH: [illegible]
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  OTHER INFORMATION: Incyte ID No: [illegible]
PCT-US02-[illegible]

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  628;  Conservative    0;  Mismatches  485;  Indels   [illegible];  Gaps   [illegible];

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
Db       [illegible]

Qy       [illegible]
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Db       1109 [illegible] 1168

Qy       1240 [illegible]-----A[illegible] 1287

Db       1169 ACAGGCTCTGGCCCAAGCTCTGGTCCTGGGGGCCGGGGTACCCCCCGAGACCGTGGCTGG 1228

Qy       1288 AGTCTCACAGATGAAGGGCAGGTTTCCTACGATGACGTCTCTGTTTCTGATTCCCTTG 1347

Db       1229 CGTCTCCCCAACAATAAGCTTGGTTCCGGGGATGACATCTCTGTCTTCGTCATCCCCCTC 1288

Qy       1348 CACAGTCAGCCC 1359

Db       1289 [illegible] 1300


RESULT 11
US-[illegible]-42
; Sequence 42, Application [illegible]
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Liu, Chenghua
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  [illegible]
;  APPLICANT:  Chen, Rui hong
;  APPLICANT:  [illegible]
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  [illegible]
;  APPLICANT:  Yang, Yonghong
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  [illegible]
;  APPLICANT:  John Tillinghast
;  APPLICANT:  [illegible]
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 784CIP2B
;  CURRENT APPLICATION NUMBER: US/09/620,312B
;  CURRENT FILING DATE:  2000-07-19
;  PRIOR APPLICATION NUMBER: 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 42
;   LENGTH: 1887
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (55)..(1563)
US-09-620-312B-42

  Query Match             17.[illegible];  Score 243.4;  [illegible];  Length 1887;
  Best Local Similarity   57.9%;  Pred. No. [illegible];
  Matches  452;  Conservative    0;  Mismatches  326;  Indels    3;  Gaps    1;

Qy        500 [illegible]

Db        [illegible]

Qy        560 [illegible] 619

Db        [illegible]

Qy        620 TGGAGGCCTCAGGCCAGATGGGGGGCTGCACAGCCCTGGTGGCTGTGTCCCTGCAGGGAA 679

Db        797 [illegible]

Qy        680 AGCTGTACATGGCCAATGCTGGGGATAGCAGGGCTACCTTGGTGCCGAGAGATGACATAC 739

Db        857 [illegible]

Qy        740 GGCCACTGAGCTTCGAGTCCACCCCAGAGACTGAGCGGCAGCGGATCCAGCAGCTGCCCT 799

Db        917 [illegible]

Qy        800 [illegible]

Db        977 [illegible]

Qy        860 [illegible]

Db       1037 [illegible]

Qy        920 [illegible]

Db       1097 [illegible]

Qy        980 [illegible]

Db       1157 [illegible]

Qy       1040 [illegible] 1099

Db       1217 [illegible]

Qy       1100 [illegible]

Db       1277 ATCTTTCAAAATATGATCATGGATCAGATGATGTGCTGATCTTGGCCACTGATGGACTCT 1336

Qy       1160 [illegible]

Db       1337 [illegible] 1396

Qy       1217 [illegible] 1276

Db       1397 [illegible]

Qy       1277 G 1277

Db       1457 G [illegible]


RESULT 12
US-10-349-781-23865
; Sequence 23865, Application US/[illegible]781
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.; Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.; Sturve, Laura L.
;  APPLICANT:  [illegible] Sara J.; Naughton, Rebecca F.
;  TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIV
;  FILE REFERENCE: PD 1028 [illegible]
;  CURRENT APPLICATION NUMBER: US/10/349,781
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 09/54[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: 60/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1996-10-18
;  PRIOR APPLICATION NUMBER: 60/006,111
;  PRIOR FILING DATE: 1995-11-21
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible],364
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PERL Program
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: [illegible]
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: [illegible]
;   OTHER INFORMATION: [illegible] or other
[illegible]

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  [illegible];  Conservative    [illegible];  Mismatches    [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]

Db        [illegible]


RESULT [illegible]
[illegible]
; [illegible] Applicant [illegible]
;  GENERAL INFORMATION:
;   APPLICANT: INCYTE GENOMICS, INC.
;   APPLICANT: KABLE, Amy E.
;   APPLICANT: CHIEN, David
;   APPLICANT: WILSON, Amy D.
;   APPLICANT: SWARNAKAR, Anita
;   APPLICANT: GORVAD, Ann E.
;   APPLICANT: HAFALIA, April J.A.
;   APPLICANT: EMERLING, Brooke M.
;   APPLICANT: RAMKUMAR, Jayalaxmi
;   APPLICANT: DING, Li
;   APPLICANT: GRIFFIN, Jennifer A.
;   APPLICANT: MARQUIS, Joseph P.
;   APPLICANT: [illegible]
;   APPLICANT: CHAWLA, Narinder K.
;   APPLICANT: TRIBOULEY, Catherine M.
;   APPLICANT: KHARE, Reena
;   APPLICANT: LEE, [illegible]
;   APPLICANT: HAWKINS, [illegible]
;   APPLICANT: BECHA, Shanya D.
;   APPLICANT: LEE, Soo Yeun
;   APPLICANT: SPRAGUE, William W.
;   APPLICANT: ZEBARJADIAN, Yeganeh
;  TITLE OF INVENTION: [illegible] KINASES AND PHOSPHATASES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: PCT/US02/39126
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 60/343,007
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: US 60/343,546
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: US [illegible]
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: US 60/357,675
;  PRIOR FILING DATE: 2002-02-15
;  NUMBER OF SEQ ID NOS: 84
;  SOFTWARE: PERL Program
; SEQ ID NO 62
;   LENGTH: 1421
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: [illegible]
PCT-US02-39126-62

  Query Match             [illegible];  Score [illegible];  DB 1;  Length 1421;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  386;  Conservative    0;  Mismatches  264;  Indels   15;  Gaps    [illegible];

Qy        710 [illegible] 769
Db        [illegible]

Qy        770 [illegible]
Db        637 CTGAGGGCAGGGTGCTTCAGGCAGCTTGGCTTCCTGAAACCAGAGCTGCTAGGCAGTGAAT 696

Qy        830 [illegible]
Db        [illegible]

Qy        890 [illegible]
Db        [illegible]

Qy        [illegible]
Db        817 [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]

Db        1237 [illegible] 1241
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RESULT 14
PCT-US02-39126-64
; Sequence 64, Application PCT/US0239126
; GENERAL INFORMATION:
;  APPLICANT:  INCYTE GENOMICS, INC.
;  APPLICANT:  KABLE, Amy E.
;  APPLICANT:  CHIEN, David
;  APPLICANT:  WILSON, Amy D.
;  APPLICANT:  SWARNAKAR, Anita
;  APPLICANT:  GORVAD, Ann E.
;  APPLICANT:  HAFALIA, April J.A.
;  APPLICANT:  EMERLING, Brooke M.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  JIN, Pei
;  APPLICANT:  GRIFFIN, Jennifer A.
;  APPLICANT:  MARQUIS, Joseph P.
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  CHAWLA, Narinder K.
;  APPLICANT:  LEHR-MASON, Patricia M.
;  APPLICANT:  KHARE, Reena
;  APPLICANT:  LEE, Sally
;  APPLICANT:  HAWKINS, Phillip R.
;  APPLICANT:  BECHA, Shanya D.
;  APPLICANT:  LEE, Soo Yeun
;  APPLICANT:  SPRAGUE, William W.
;  APPLICANT:  ZEBARJADIAN, Yeganeh
;  TITLE OF INVENTION:  KINASES AND PHOSPHATASES
;  FILE REFERENCE: PF-1315 PCT
;  CURRENT APPLICATION NUMBER:  PCT/US02/39126
;  CURRENT FILING DATE:  2002-12-06
;  PRIOR APPLICATION NUMBER: US 60/340,225
;  PRIOR FILING DATE: 2001-12-07
;  PRIOR APPLICATION NUMBER: US 60/343,097
;  PRIOR FILING DATE: 2001-12-19
;  PRIOR APPLICATION NUMBER: US 60/343,546
;  PRIOR FILING DATE: 2001-12-21
;  PRIOR APPLICATION NUMBER: US 60/354,289
;  PRIOR FILING DATE: 2002-02-04
;  PRIOR APPLICATION NUMBER: US 60/357,675
;  PRIOR FILING DATE: 2002-02-15
;  NUMBER OF SEQ ID NOS: 94
;  SOFTWARE: PERL Program
; SEQ ID NO 64
;   LENGTH: 1472
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 7507107CB1
PCT-US02-39126-64

  Query Match             12.2%;  Score 169.9;  DB 1;  Length 1472;
  Best Local Similarity   65.3%;  Pred. No. 7.7e-29;
  Matches  248;  Conservative    0;  Mismatches  132;  Indels    0;  Gaps    0;

Qy        536 AAAAGGGCATCAGGCCAGAAGACTTGGTCATCGGGGCATTGGAGAGTCCCTTTCACCAAT 595
              | ||||    | ||     ||    | ||||  | |||||  | |||| |||||| |||
Db        516 AGAAGGAATTGAGCCACGAGAGCCTGGTAGTGGCCCCATTCACAATGCCTTCCAGCTCA 575

Qy        596 GTGATGAGGTGATCGGGCGGGACTTGGAGGCCTCAGGCCAGATGGGAGCCTGCACAGCCC 655
                 ||||| ||| | ||||||| |   | |             | ||| ||||||   || |
Db        576 TGGATGAGCAGATGGCCGGGGAGCGGGTGGCCACCAAGTGGAGGGGGCTGCTGTGCAC 635

Qy        656 TGGTGGTTGTGTGCCTGCAGGGAAAGTTGTACATGGGCAATGGTGGGATAGCAGGGGCA 715
              |||| |     | | |||||  || ||| |||| ||||||||| || ||||||||||||
Db        636 TGGTTGTGATGTACCTGCTAGGCAAGGTGTACGTGGGCAATGGAGGGATAGGCAGGGGCA 695

Qy        716 TCTTGGTGCCTGCCATGAAAATACTCCCACTCAGCTTCCAGTTTACCCCAGAGACTGAGC 775
              || | || | |  | ||| ||    ||| ||  |   ||||| ||||| |||||||||
Db        696 TCATTGTCGGGAATGGTGAAATCATTCCAATGTCCGGGGAGTTTACCCGGAGACTGAGC 755
```

```
Qy        776 GGCAGCGGATCCAGCAGCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCAGCC 835
              | |||||  | |||| ||| | |||  |  | || ||||| || |    | || ||||||
Db        756 GCCAGCGTCTTCAGCTGCTTGGCTTCCTGAAACCAGAGCTGGCTAGGCAGTGAATTCACCC 815

Qy        836 [illegible] 895
                 || |||||||| ||  |  |   |    | ||  |||| |||| | | | |   | ||
Db        816 [illegible] 875

Qy        896 ATCAGCACATGAGTGGCTGG 915
              | ||  ||||||  ||||||
Db        876 AACAGAAGATGACGGGCTGG 895


RESULT 15
US-10-349-781-46051/c
; Sequence 46051, Application US/10349781
; GENERAL INFORMATION:
;  APPLICANT: Seilhamer, Jeffrey J.; Delegeane, Angelo M.
;  APPLICANT:  Stuart, Susan G.; Stuve, Laura L.
;  APPLICANT:  Mullahy, Sara J.; Naughton, Rebecca E.
;  TITLE OF INVENTION: POLYNUCLEOTIDES OF CELLS AND TISSUES OF THE FEMALE REPRODUCTIV
;  FILE REFERENCE: PD-1628-2 CON
;  CURRENT APPLICATION NUMBER: US/10/349,781
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: 09/540,764
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 08/992,868
;  PRIOR FILING DATE: 1997-12-11
;  PRIOR APPLICATION NUMBER: 60/032,838
;  PRIOR FILING DATE: 1996-12-13
;  PRIOR APPLICATION NUMBER: 08/734,050
;  PRIOR FILING DATE: 1996-10-18
;  PRIOR APPLICATION NUMBER: 60/006,111
;  PRIOR FILING DATE: 1995-10-24
;  PRIOR APPLICATION NUMBER: 08/733,814
;  PRIOR FILING DATE: 1996-10-18
;  PRIOR APPLICATION NUMBER: 60/005,864
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: 08/764,920
;  PRIOR FILING DATE: 1996-12-11
;  PRIOR APPLICATION NUMBER: 60/008,794
;  PRIOR FILING DATE: 1995-12-14
;  PRIOR APPLICATION NUMBER: 08/772,783
;  PRIOR FILING DATE: 1996-12-23
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 61458
;  SOFTWARE: PERL Program
; SEQ ID NO 46051
;   LENGTH: 183
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 6801029588
US-10-349-781-46051

  Query Match             4.6%;  Score 62.8;  DB 6;  Length 183;
  Best Local Similarity   74.5%;  Pred. No. 4.7e-05;
  Matches   79;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy        736 [illegible] 795
              |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db        182 [illegible] 124

Qy        796 GCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCGGACTGG 841
              |     || | |        |    ||||    || ||  |   ||||
Db        123 GTAGGTGCCCTTGGCAGCATGGAGGCTGTGAAGCTCCACGTCCTGG 78


Search completed, February 22, 2003, 08:41:33
Job time : 306 secs
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                        GenCore version 5.1.x
               Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 23, 2003, 00:37:35 ; Search time 2236 Seconds
                                        (without alignments)
                                        9995.426 Million cell updates/sec

Title:           US-09-866-987-3
Perfect score:   1380
Sequence:        1 atgtccgccggctggttccg..........aagaagcagtgaccactga 1380

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        16154766 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters:       32368132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        EST:*
                 1:   em_estba:*
                 2:   em_esthum:*
                 3:   em_estin:*
                 4:   em_estmu:*
                 5:   em_estov:*
                 6:   em_estpl:*
                 7:   em_estro:*
                 8:   em_htc:*
                 9:   gb_est1:*
                 10:  gb_est2:*
                 11:  gb_htc:*
                 12:  gb_est3:*
                 13:  gb_est4:*
                 14:  gb_est5:*
                 15:  em_estfun:*
                 16:  em_estom:*
                 17:  gb_gss:*
                 18:  em_gss_hum:*
                 19:  em_gss_inv:*
                 20:  em_gss_pln:*
                 21:  em_gss_vrt:*
                 22:  em_gss_fun:*
                 23:  em_gss_mam:*
                 24:  em_gss_mus:*
                 25:  em_gss_other:*
                 26:  em_gss_pro:*
                 27:  em_gss_rod:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                                  SUMMARIES
                     %
Result             Query
  No.     Score   Match Length DB   ID                     Description
-------------------------------------------------------------------------------
    1      1027    74.4   1737  11  AK013149               AK013149 Mus musculu
    2     793.2    57.5    908  13  BI911260               BI911260 603062811
    3       732    53.0    756  10  AW960759               AW960759 EST372830
    4     591.6    42.9   1182  11  AK017245               AK017245 Mus musculu
    5     556.2    40.3    760  13  BI909341               BI909341 603065418
c   6       547    39.6    547  14  BM719494               BM719494 UI-E-EJ1
    7       536    38.8    547   9  AA2922[illegible]      AA2922[illegible]
    8     520.6    37.7    [illegible]  12  B[illegible]079142      B[illegible]079142 [illegible]
    9       498    36.1    [illegible]  13  BM56[illegible]        BM56[illegible] AGENCOURT
   10       498    36.1   1038  13  BM56[illegible]742     BM56[illegible]742 AGENCOURT
   11     496.6    36.0    [illegible]  10  AW742[illegible]       AW742[illegible] [illegible]
   12       493    35.7    494  12  BF059521               BF059521 7k61h07.x
   13     488.6    35.4    [illegible]  13  BI344[illegible]       BI344[illegible] MA
   14     483.4    35.0    550  13  BI847199               BI847199 [illegible]4149 MA
   15     478.2    34.7    589  12  BF415112               BF415112 UI-R-BJ2-
   16     476.1    34.5    512  10  AW654617               AW654617 [illegible] MA
   17       473    34.3    473   9  AI924511               AI924511 wn61a07.x
   18       473    34.3    474  12  BF515449               BF515449 UI-H-BW1-
   19       468    33.9    680  16  BB[illegible]16        BB[illegible]16 BB[illegible]
   20     451.4    32.7    675  16  BB645[illegible]12     BB645[illegible]12 BB645[illegible]
   21       447    32.4    447   9  AI924[illegible]       AI924[illegible] wn5[illegible].x
   22     446.2    32.3    707  15  BF6[illegible]822      BF6[illegible]822 [illegible]
   23       433    31.4    551  12  BF419[illegible]       BF419[illegible] UI-R-BJ2
   24       431    31.2   1058  12  BE[illegible]         BE[illegible] [illegible]
   25     426.4    30.9    708  12  BG754589               BG754589 [illegible]
c  26     425.2    30.8    472  12  BE[illegible]         BE[illegible] [illegible]
   27     413.4    30.0    504  10  AW434[illegible]       AW434[illegible] UI-R-BJ1
   28     409.2    29.7    446   9  AA6[illegible]        AA6[illegible] [illegible]
   29     407.2    29.5    501  10  AW434[illegible]       AW434[illegible] UI-R-BJ1
c  30     405.8    29.4    409  13  BM15[illegible]        BM15[illegible] DBAPLE1
   31     397.6    28.8    492   9  AI430626               AI430626 [illegible]
   32     393.4    28.5    657  12  BF56[illegible]        BF56[illegible] UI-H-BI4
   33     387.2    28.1    519   9  AA116660               AA116660 mn28b05.r
   34       379    27.5    416  12  BF750[illegible]       BF750[illegible] BN04
   35       373    27.0    [illegible]  10  AW630065               AW630065 hh74g05.y
   36     372.2    27.0    687   9  AI236519               AI236519 EST234481
   37     369.2    26.8    456  12  BF411984               BF411984 UI-R-BJ2
   38       367    26.6    496  14  W50667                 W50667 me92h05.r1
   39       367    26.6    649  13  BG923[illegible]       BG923[illegible] [illegible]
   40     363.4    26.3    625  16  BB[illegible]          BB[illegible] BB[illegible]
   41     360.8    26.1    364  12  BF195640               BF195640 [illegible]
   42     356.8    25.9    478   9  AI590672               AI590672 [illegible]
c  43       356    25.8    626   9  AI011509               AI011509 EST[illegible]
   44       355    25.7    516  10  AW[illegible]          AW[illegible] [illegible] MA
   45     351.2    25.4    [illegible]  13  BI486[illegible]       BI486[illegible] [illegible] MA

                                  ALIGNMENTS

RESULT 1
AK013149
LOCUS       AK013149                1737 bp    mRNA    linear   HTC 19-JAN-2002
DEFINITION  Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
            enriched library, clone:2810423O19:Protein phosphatase 2C
            containing protein, full insert sequence.
ACCESSION   AK013149
VERSION     AK013149.1  GI:12850381
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) 10, 11 days embryo cDNA to mRNA.
            clone_lib:RIKEN full-length enriched mouse cDNA library
            clone:2810423O19.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
```

```
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
            Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,
            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
            Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,
            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,
            Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5  (bases 1 to 1737)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
            Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T.,
            Kato,H., Kawai,J., Kojima,Y., Konno,H., Koya,M., Koya,S.,
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H.,
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.go.jp/) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5'-GAGAGAGAGAGAGAGAGAGAGAGAGATCTCGAGTTTTTTTTTTTTTTTTTTTVN-3'] and was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. cDNA went
            through one round of normalization to Rot = 7.5 and subtraction to
            Rot = 37.5. Second strand cDNA was prepared with the primer adapter
            of sequence [5'-
```

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            GAGAGAGAGAGATCTCGAGCTCAAGCAAGCAAGCACGGGGGG-3'], cDNA was cleaved
            with XhoI and SstI. Cloning sites; 5' end: XhoI; 3' end: SstI.
            Host: SOLR.
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                     /strain="C57BL/6J"
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                     /db_xref="MGD:MGI:1898307"
                     /db_xref="taxon:10090"
                     /clone="2810423O19"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="10, 11 days embryo"
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                     /note="Protein phosphatase 2C containing protein
                     data source:Pfam, source key:PF00481, evidence:ISS
                     putative"
                     /codon_start=1
                     /protein_id="BAB28679.1"
                     /db_xref="GI:12850332"
                     /db_xref="MGD:MGI:1915155"
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                     VCPEEFLTGHYWALFDGHGGPAAAILAANTLHSCLRRQLEAVVEGMIAPQPPMHLSGR
                     CVCPSDPQFVEEKGIQAEDLVIGALENAFQECDEVIGRELEASGQVGGCTALVAVFLQ
                     GKLYVANAGDSRAILVRRHEIRQLSSEFTPETERQRIQQLAFTYPELLAGEFTRLEFP
                     RRLKGDDLGQKVLFRDHHMRGWSYKRVEKFDLKYPLIHGQGRQARLLGTLAVSRGLGD
                     HQLRVLDTDIQLKPFLLSTPQVTVLDVHQLAVGEEDVVVMATDGLWDVLSNEQVALLV
                     RSFLTGNQKDDPHRFSELAKMLIHNTQGKDNGATGDGQVSYDDVSVFVIPLHSQAQEG
                     SGH"
BASE COUNT      379 a    477 c    514 g    367 t
ORIGIN

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  Best Local Similarity   85.7%;  Pred. No. 2.8e-223;
  Matches 1167;  Conservative    0;  Mismatches  185;  Indels    9;  Gaps    2;

Qy         29 TCCTGCCTGGGGAGCCGCTCCCCGCGCCGCGGCCGCCTGGGCCGCATGCCAGCCCCGTGC 88
              |||| || ||||   || || || | |||||||||   | |||||||    |||||| ||||
Db          2 TCCTACCCGGGGGTCCACTTCCAGAGCCGCGGGCAGCCGGGCCGCGCTCCAGCCCGGTGC 61

Qy         89 CCTACCGACGGCCCCGCTTCCTTCGCGGCTCCAGCTCCAGCCCGGGGCGGCGGACGCCT 148
              |||| |  |||||||||||| || |||||||||| |||||||||| || ||  | ||||||
Db         62 CCTATCACCGGCCCCGCTTCCTACGCGGCTCCGGCTCCAGCCCGGGCGCCACTGACGCCT 121

Qy        149 [illegible] AGCCGGAGCAGAGGAGGAGGAGCTAGCCGGGA 208
              ||||||||| ||   |||||| |||||||||| ||||| || ||||| || || |||
Db        122 CCGCCGCCCCCGATCCCCGCCCGGCCCAGCCCAGCACGGGGCCGCACACTGCCCTCGGA 181

Qy        209 ATGCAGGCTAGCCCGAGATCATCAATGAGAGAAATCGAATCAAGGAGGATCAAGCCG 268
              | ||||||||||| ||| |||||||||||||| ||||||||||||||| || || || || |
Db        182 ACGCAGGCTAGCCAGAGATTATCAATGAGAAAAATCGAATCAACGAAGACCAGGCTG 241

Qy        269 [illegible]                 AAGAGTGGC 322
              | || |||||||| |||||||| |||||||||||||    ||||        ||||||||
Db        242 [illegible] AGCAAGAGTGGC 301

Qy        323 TGACCCTGTGGCCAGAGGAGTTCCTGACAGGCCATTACTGGGCACTGTTCGATGGGCACG 382
              ||||   ||||||||||||||||||||| || || ||||||||||||| |||||||| |
Db        302 TGACGGTGTGGCCAGAGGAGTTCCTGACGGGTCACTACTGGGCACTGTTTGATGGGCATG 361

Qy        383 GCGGTCCTGCAGCAGCCATCTTGGCTGCCAACACCCTGCACTCCTGCTTGCGCCGGCAGC 442
              | || ||||| |||| |||||||||||||||||||||||||||| ||| | ||||||||
Db        362 GTGGCCCTGCTGCAGCTATCTTGGCTGCCAACACCCTGCACTCTTGCCTTCGCCGGCAGC 421

Qy        443 TGGAGGCGGTGGTGGAAGGCTTGGTGGCCACTCAGCCCCCCATGCACCTCAATGGCCGCT 502
              ||||||| ||||| |||||| || | ||| |||||||||||||||||||||| |||||||
Db        422 [illegible] AGTGGCCGCT 481

Qy        503 [illegible] AAGACTTGG 562
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Db        482 [illegible] AAGACTTGG 541
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Qy        5[illegible] [illegible] 622
Db        542 [illegible] 601

Qy        62[illegible] [illegible] 682
Db        602 [illegible] 661

Qy        68[illegible] [illegible] 742
Db        662 [illegible] 721

Qy        74[illegible] [illegible] 802
Db        722 [illegible] 781

Qy        80[illegible] [illegible] 862
Db        782 [illegible] 841

Qy        86[illegible] [illegible] 922
Db        842 [illegible] 901

Qy        92[illegible] [illegible] 982
Db        902 [illegible] 961

Qy        98[illegible] [illegible] 1042
Db        962 GGTTACTGGGAACACTGGCTGTCTCTAGAGGGCTGGGCACCATCAGTTAGACTCCTGG 1021

Qy        104[illegible] [illegible] 1102
Db        1022 [illegible] 1081

Qy        110[illegible] [illegible] 1162
Db        1082 [illegible] 1141

Qy        116[illegible] [illegible] 1221
Db        1142 [illegible] 1201

Qy        1222 [illegible] 127[illegible]
Db        1202 [illegible] 12[illegible]

Qy        12[illegible] [illegible] 13[illegible]
Db        1262 [illegible] 1321

Qy        134 [illegible]
Db        1322 [illegible]


RESULT 2
BI911260
LOCUS       BI911260                908 bp    mRNA    linear   EST 16-OCT-2001
DEFINITION  [illegible] NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212011 5',
            mRNA sequence.
ACCESSION   BI911260
VERSION     BI911260.1  GI:16174900
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 908)
  AUTHORS   NIH MGC [illegible]
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11532  row: e  column: 4
            High quality sequence start: [illegible]
            High quality sequence stop: 851.
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                     /clone_lib="NIH_MGC_118"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from [illegible]
                     non activated adult donors. Library is oligo dT primed
                     and directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.7 kb, insert size range
                     1.2-3.3 kb. Library is normalized and enriched for
                     full length clones and was constructed by [illegible]
                     (Invitrogen). Research Genetics tracking code [illegible]. Note:
                     this is a NIH_MGC Library."
BASE COUNT      178 a    252 c    307 g    171 t
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  357;  Conservative    [illegible];  Mismatches   1[illegible];  Indels    [illegible];  Gaps    [illegible];

Qy         8[illegible] [illegible] 142
Db         [illegible] 92

Qy         143 [illegible] 202
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Qy         20[illegible] [illegible] 262
Db         153 [illegible] 212

Qy         263 [illegible] 322
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Qy         [illegible] 382
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Qy         383 [illegible] 442
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Qy         443 [illegible] 502
Db         393 [illegible] 452

Qy         503 [illegible] 562
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Qy         563 [illegible] 622
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Qy         62[illegible] [illegible] 682
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Db     [illegible]
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Db     [illegible]
Qy     [illegible]
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Db     [illegible]
Qy     [illegible]
Db     [illegible]

RESULT 2
AW[illegible]
LOCUS       AW[illegible]          [illegible] bp    mRNA    linear   [illegible]
DEFINITION  [illegible] MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW[illegible]
VERSION     AW[illegible]  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Hegde,P., Qi,R., Abernathy,K., [illegible], Gaspard,R., [illegible], Hoit
            [illegible], Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
  TITLE     [illegible] gene expression patterns [illegible]
            [illegible] DNA [illegible]
  JOURNAL   Unpublished ([illegible])
COMMENT     [illegible] Quackenbush
            The Institute for Genomic Research
            [illegible] Medical Center Dr., Rockville, MD [illegible], USA
            [illegible]
            [illegible]
            [illegible]
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ORIGIN

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  Best Local Similarity   [illegible]  Pred. No. [illegible];
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible];

Qy     [illegible]
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Qy     425 [illegible] 484
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Qy     785 [illegible]
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Qy     845 [illegible] 904
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Qy     905 [illegible]
Db     661 [illegible] 720
Qy     965 [illegible]
Db     721 [illegible]
Qy     1025 [illegible]
Db     781 [illegible]

RESULT 3
AK017245
LOCUS       AK017245          1182 bp    mRNA    linear   HTC [illegible]
DEFINITION  Mus musculus 6 days neonate head cDNA, RIKEN full-length enriched
            library, clone:5430400123:Protein phosphatase 2C containing
            protein, full insert sequence.
ACCESSION   AK017245
VERSION     AK017245.1  GI:[illegible]
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (strain:C57BL/6J) 6 days neonate head cDNA to mRNA,
            clone_lib:RIKEN full-length enriched mouse cDNA library
            clone:5430400123.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   [illegible]
   PUBMED   [illegible]
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 1[illegible] (1[illegible]), 1[illegible]17-1630 (2000)
  MEDLINE   204[illegible]
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., [illegible], Watahiki,M.,
            Yoneda,Y., Ishikawa,T., [illegible], Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   205[illegible]
   PUBMED   11076861
REFERENCE   4
  AUTHORS   Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
            Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,
            Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,
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            Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,
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            Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,
            Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,
            Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,
            Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,
            Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,
            Fletcher,C., Fujita,M., Gariboldi,M., [illegible],
            Hofmann,M., Hume,D.A., Kamiya,M., [illegible],
            Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,
            Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,
            Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,
            Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,
            Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.
            and Hayashizaki,Y.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409 (6821), 685-690 (2001)
  MEDLINE   21085660
   PUBMED   11217851
REFERENCE   5  (bases 1 to 1182)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A.,
            Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C.,
            Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T.,
            Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F.,
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            [illegible]
            Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K.,
            Numazaki,R., Ohno,M., [illegible]
            Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,
            [illegible], Shibata,K., [illegible]
            Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
            Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunaga,T.,
            Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and
            Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa [illegible], Japan. [illegible]
            URL:http://[illegible], Tel:81-45-503-9222,
            Fax:81-[illegible])
  COMMENT   Please visit our web site ([illegible]) for
            further details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5'-GAGAGAGAGAAAAAGCAAGATTTTTTTTTTTTTTTTVN-3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full length by cap-trapper. cDNA went
            through one round of normalization to Rot = [illegible] and subtraction to
            Rot = 100.0. Second strand cDNA was prepared with the primer
            adapter of sequence [5'-
            GA[illegible]-3']. cDNA was cleaved
            with BamHI and XhoI. Vector: a modified pBluescript KS(+), after
            bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'
            end: BamHI. Host: DH10B.
FEATURES             Location/Qualifiers
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                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:54[illegible]J23"
                     /db_xref="MGI:MGI:1894715"
                     /db_xref="taxon:10090"
                     /clone="5430400J23"
                     /tissue_type="head"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="[illegible] days neonate"
     CDS             <1..[illegible]
                     /note="Protein phosphatase 2C containing protein
                     data source:Pfam, source key:PF00481, evidence:ISS
                     putative"
                     /codon_start=2
                     /protein_id="BAB[illegible]49.1"
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                     /db_xref="MGD:MGI:1915[illegible]"
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                     [illegible]
                     [illegible]VVVMA[illegible]VLSNE[illegible]VALLVR[illegible]NQK[illegible]SELAKML[illegible]N
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                     /note="putative"
     polyA_site      1182
                     /note="putative"
BASE COUNT      [illegible] a   [illegible] c   [illegible] g   [illegible] t
ORIGIN

  Query Match             42.9%;  Score 591.6;  DB 11;  Length 1182;
  Best Local Similarity   86.7%;  Pred. No. 3.3e-124;
  Matches  664;  Conservative    0;  Mismatches   99;  Indels    3;  Gaps    1;

Qy        616 GCTGGA[illegible]CAG[illegible]AGATGG[illegible]GCACAG[illegible]TGGTGG[illegible] 677
              [illegible]
Db          1 GCTGGAGGCCTTAGGA[illegible]AGGTGGGTGG[illegible]ACAGCCCTGGTGG[illegible]AAGG 60

Qy        [illegible]
              [illegible]
Db         61 [illegible] 12[illegible]

Qy        7[illegible] 797
              [illegible]
Db        12[illegible] 18[illegible]

Qy        7[illegible] [illegible]
              [illegible]
Db        18[illegible] CTT[illegible]GGAGAGTTAA[illegible]GACTGGA[illegible]ACGG[illegible] 240

Qy        [illegible]
              [illegible]
Db        24[illegible]

Qy        [illegible]
              [illegible]
Db        3[illegible] CTA[illegible]

Qy        [illegible]
              [illegible]
Db        361 GG[illegible]TACTGGGAA[illegible]TAGAG[illegible]TGGG[illegible]ATCAG[illegible]AGAG 420

Qy        [illegible]
              [illegible]
Db        421 [illegible]
```

```
Qy     [illegible] [illegible] [illegible]
                   [illegible]
Db     [illegible] [illegible] [illegible]

Qy     [illegible] [illegible] 1217
                   [illegible]
Db     [illegible] [illegible] [illegible]

Qy     [illegible] [illegible] [illegible]
                   [illegible]
Db     [illegible] [illegible] [illegible]

Qy     [illegible] [illegible] 1334
                   [illegible]
Db     [illegible] [illegible] [illegible]

Qy     [illegible] [illegible] [illegible]
                   [illegible]
Db     [illegible] [illegible] [illegible]


RESULT 5
BI[illegible]
LOCUS       BI[illegible]                 [illegible] bp    mRNA    linear   EST [illegible]
DEFINITION  [illegible] NIH_MGC_11 Homo sapiens cDNA clone IMAGE:[illegible] 5',
            mRNA sequence.
ACCESSION   BI[illegible]
VERSION     BI[illegible].1  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM[illegible] [illegible]
            High quality sequence stop: [illegible].
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="Homo sapiens"
                     /db_xref="taxon:[illegible]"
                     /clone="IMAGE:[illegible]"
                     /clone_lib="NIH_MGC_11"
                     /tissue_type="leukocyte"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV
                     (destroyed); RNA source leukocytes from an anonymous pool of
                     [illegible] adult donors. Library is oligo dT primed
                     and directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size [illegible] kb. Insert size range
                     [illegible] kb. Library is normalized and enriched for
                     full length clones and was constructed by [illegible] Gruber
                     (Invitrogen). Research Genetics tracking code [illegible]. Note:
                     this is a NIH MGC Library."
BASE COUNT  [illegible]
ORIGIN

  Query Match             [illegible]
  Best Local Similarity   [illegible]  Pred. No. [illegible]
  Matches [illegible]  Conservative  [illegible]  Mismatches  [illegible]  Indels  [illegible]  Gaps  [illegible]

Qy     [illegible] [illegible] [illegible]
                   [illegible]
Db     1 [illegible] [illegible]

Qy     848 [illegible] [illegible]
                   [illegible]
Db     61 [illegible] [illegible]

Qy     908 [illegible] [illegible]
                   [illegible]
Db     [illegible] [illegible] [illegible]

Qy     968 [illegible] [illegible]
                   [illegible]
Db     180 [illegible] [illegible]

Qy     1028 [illegible] [illegible]
                   [illegible]
Db     240 [illegible] [illegible]

Qy     1086 [illegible] [illegible]
                   [illegible]
Db     [illegible] [illegible] [illegible]

Qy     1147 [illegible] [illegible]
                   [illegible]
Db     [illegible] [illegible] [illegible]

Qy     1207 [illegible] [illegible]
                   [illegible]
Db     [illegible] [illegible] [illegible]

Qy     [illegible] [illegible] [illegible]
                   [illegible]
Db     [illegible] [illegible] [illegible]

Qy     [illegible] [illegible] 1371
                   [illegible]
Db     [illegible] [illegible] 584


RESULT 6
BM719494/c
LOCUS       BM719494                   547 bp    mRNA    linear   EST  [illegible]
DEFINITION  UI-E-EJ1-[illegible] UI-E-EJ1 Homo sapiens cDNA clone
            UI-E-EJ1-[illegible] 3', mRNA sequence.
ACCESSION   BM719494
VERSION     BM719494.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   [illegible]
COMMENT     Contact: Soares MB
            Program for Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA [illegible], USA
            Tel: [illegible]
            Fax: [illegible]
            Email: mbsoares@blue.weeg.uiowa.edu
            Tissue Procurement: Dr. [illegible]
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
```

```
FEATURES             Location/Qualifiers
     source          1..547
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "UI-E-EJ1-ajt-m-24-0-UI"
                     /clone_lib "UI-E-EJ1"
                     /tissue_type="fetal eyes, lens, eye anterior segment,
                     optic nerve, retina, Retina Foveal and Macular, RPE and
                     Choroid"
                     /dev_stage "fetal and adult"
                     /lab_host "[illegible]"
                     /note "Organ: eye; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-EJ1 is a subtracted cDNA library constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tags for this library are: fetal eyes, ACAATCAACA
                     ; lens, CGATTAGGCA; eye anterior segment, AATCCGCTAT;
                     optic nerve, CCATTAAGTG; retina, TCCT; Retina Foveal and
                     Macular, GTCC; RPE and Choroid, ACTA. This library was
                     created for the program, Gene Discovery in the Visual
                     System, supported by National Eye Institute (NEI)."
BASE COUNT      117 a    179 c    134 g    117 t
ORIGIN

  Query Match             39.6%;  Score 547;  DB 14;  Length 547;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-114;
  Matches  547;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        672 GCAGGGAAAGTTGTACATGGTTAATGCTGGGATAGCAGGGCATCTTCCTCCGAGAGA 731
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GCAGGGAAAGTTGTACATGGTTAATGCTGGGATAGCAGGGCATCTTCCTCCGAGAGA 488

Qy        732 [illegible] 791
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 [illegible] 428

Qy        792 GCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCGGACTGGAGTTCCTTCG 851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 GCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCGGACTGGAGTTCCTTCG 368

Qy        852 GCGGCTGAAGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCACCACATGAGTGG 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        367 [illegible] 308

Qy        912 CTGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGACAGGG 971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 CTGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGACAGGG 248

Qy        972 TAGGCAGGTTGGGTTACTAGGAAGACTGGCTGGTTGGGAGGGGTGGGAGAGTCATCAGCT 1031
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 TAGGCAGGTTGGGTTACTAGGAAGACTGGCTGGTTGGGAGGGGTGGGAGAGTCATCAGCT 188

Qy       1032 CAGAGTCCTGGAGACAAAAGATCCAGTTCAAGCCCTTCTTGCTTTCTGTGGACACAGTGAC 1091
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CAGAGTCCTGGAGACAAAAGATCCAGTTCAAGCCCTTCTTGCTTTCTGTGGACACAGTGAC 128

Qy       1092 TGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGGGTTGTCATGGCAACTGA 1151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 TGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGGGTTGTCATGGCAACTGA 68

Qy       1152 TGGACTCTGGGATGTACTGTGCAACGAGCAGGTGGCATGGCTGGTGGGAGCTTCCTCCC 1211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TGGACTCTGGGATGTACTGTGCAACGAGCAGGTGGCATGGCTGGTGGGAGCTTCCTCCC 8

Qy       1212 TGGGAAC 1218
              |||||||
Db          7 TGGGAAC 1


RESULT 7
AA292266
LOCUS       AA292266                 547 bp    mRNA    linear   EST [illegible]
DEFINITION  zt50f12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone
            IMAGE:725807 5' similar to SW:P2C2_ARATH P49598 PROTEIN PHOSPHATASE
            2C ;, mRNA sequence.
ACCESSION   AA292266
VERSION     AA292266.1  GI:1940[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 547)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
            ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
            ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
            Schellenberg,K., Soares,M.B., Tan,F., Thierry-Mieg,J., Trevaskis,E.,
            Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1457   Std Error: 0.00
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 479.
FEATURES             Location/Qualifiers
     source          1..547
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "IMAGE:725807"
                     /clone_lib "Soares ovary tumor NbHOT"
                     /sex "female"
                     /tissue_type "ovarian tumor"
                     /lab_host "DH10B (ampicillin resistant)"
                     /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     [illegible]GAGCGGCCGCTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. "
BASE COUNT      123 a    135 c    171 g    118 t
ORIGIN

  Query Match             38.8%;  Score 5[illegible];  DB 9;  Length 547;
  Best Local Similarity   99.8%;  Pred. No. 1.1e-111;
  Matches  547;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy        792 GCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCGGACTGGAGTTCC[illegible] 851
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCGGACTGGAGTTCC[illegible] 60

Qy        852 [illegible] 911
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCGGCTGAAGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCACCACATGAGTGG 120

Qy        912 [illegible] 971
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGACAGGG 180
```

```
Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]

Qy    [illegible]
Db    [illegible]


RESULT [illegible]
[illegible]
LOCUS       [illegible]              [illegible] bp    mRNA    linear   [illegible]
DEFINITION  [illegible] NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
            [illegible] mRNA sequence.
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Kargul,G.J., Dudekula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka,
            T.S., Carter,M.G. and Ko,M.S.H.
  TITLE     Verification and initial annotation of NIA mouse 15K cDNA clone set
  JOURNAL   Unpublished (2001)
COMMENT     Other_ESTs: [illegible]
            Contact: George J. Kargul
            Laboratory of Genetics
            National Institute on Aging/National Institutes of Health
            333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
            Email: [illegible]
            This clone set has been freely distributed to the community. Please
            visit http://[illegible]/cDNA/15k.html for details.
            Plate: [illegible] row: [illegible] column: 10
            Seq primer: -21M13 forward
            High quality sequence stop: [illegible]
            POLYA=N.
FEATURES             Location/Qualifiers
     source          [illegible]
                     /organism="Mus musculus"
                     /strain="[illegible]"
                     /db_xref="[illegible]"
                     /db_xref="taxon:10090"
                     /clone="[illegible]"
                     /clone_lib="NIA Mouse 15K cDNA Clone Set"
                     /sex="[illegible] cDNA libraries"
                     /dev_stage="[illegible] cDNA
                     libraries"
                     /lab_host="DH10B"
                     /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
                     clone is among a rearrayed set of [illegible] clones from 15
                     embryo cDNA libraries (including preimplantation stage
                     embryos from unfertilized egg to blastocyst, embryonic
                     part of E7.5 embryos, extraembryonic part of E7.5 embryos
                     , and E12.5 female mesonephros/gonad) and one newborn
                     ovary cDNA library. Average insert size 1.5 kb. All
                     source libraries are cloned unidirectionally with [illegible] (dT
                     ) NotI primers. References include: (1) Genome-wide
                     expression profiling of mid-gestation placenta and embryo
                     using a 15,000 mouse developmental cDNA microarray. 2000,
                     Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2)
                     Large-scale cDNA analysis reveals phased gene expression
                     patterns during preimplantation mouse development. 2000,
                     Development, 127: 1737-1749; (3) Genome-wide mapping of
                     unselected transcripts from extraembryonic tissue of
                     7.5-day mouse embryos reveals enrichment in the t-complex
                     and under-representation on the X chromosome. 1998, Hum.
                     Mol Genet 7: 1967-1978."
BASE COUNT      138 a    154 c    214 g    125 t
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB 12;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative  [illegible];  Mismatches   69;  Indels  [illegible];  Gaps  [illegible];

Qy    436 [illegible] 495
Db      1 [illegible]

Qy    496 [illegible]
Db     61 [illegible]

Qy    556 [illegible] 615
Db    121 [illegible]

Qy    616 [illegible]
Db    181 [illegible]

Qy    676 [illegible]
Db    241 [illegible]

Qy    736 [illegible]
Db    301 [illegible]

Qy    796 GCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCGACTGGAGTTCCCTCGGCGG 855
Db    361 [illegible]

Qy    856 [illegible]
Db    421 [illegible] 480

Qy    916 AGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGACAGGGTAGG 975
Db    481 [illegible]

Qy    976 [illegible]
Db    541 [illegible]

Qy   1036 GTCCTGGATATAAATATCCAGCTCAAGCCCT 1066
Db    [illegible]


RESULT [illegible]
BM[illegible]
LOCUS       BM[illegible]              997 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  [illegible] NIH_MGC_98 Homo sapiens cDNA clone IMAGE:[illegible]
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```
            5', mRNA sequence.
ACCESSION   [illegible]
VERSION     BM5[illegible]7.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 997)
  AUTHORS   NIH MGC http://[illegible]
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1916  row: l  column: 12
            High quality sequence stop: 697.
FEATURES             Location/Qualifiers
     source          1..997
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5441819"
                     /clone_lib="NIH_MGC_98"
                     /tissue_type="astrocytoma grade IV, cell line"
                     /lab_host="DH10B (phage resistant)"
                     /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed  by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      245 a    274 c    271 g    207 t
ORIGIN

  Query Match             [illegible]%;  Score 498;  DB 13;  Length 997;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-103;
  Matches  498;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        [illegible] 942
              [illegible]
Db          1 [illegible]

Qy        [illegible]
              [illegible]
Db         61 [illegible] 120

Qy       1003 GTCTCCGGGGCCTGGGAGACCATCAGCCAGAGTCCGGACACAAACATCCAGCTCAAC 1062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCTCCGGGGCCTGGGAG[illegible]

Qy       [illegible] 1122
              [illegible]
Db        181 [illegible]

Qy       1123 [illegible]
              [illegible]
Db        241 [illegible]

Qy       1183 GTGGCATGGCTGGTGCGGAGCTTCCTCCTGGGAACCAAGAGGA[illegible] 1242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGGCATGGCTGGTGCGGA[illegible]

Qy       1243 AA[illegible]
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGCTGG[illegible] 42[illegible]
```

```
Qy       [illegible]
              [illegible]
Db        421 [illegible] 48[illegible]

Qy       [illegible] 1589
              [illegible]
Db        481 [illegible]


RESULT 10
BM5[illegible]742
LOCUS       BM5[illegible]742          1018 bp    mRNA    linear   EST [illegible]
DEFINITION  AGENCOURT [illegible] NIH_MGC_98 Homo sapiens cDNA clone IMAGE:[illegible]
            5', mRNA sequence.
ACCESSION   BM5[illegible]742
VERSION     BM5[illegible]742.1  GI:[illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1018)
  AUTHORS   NIH MGC http://[illegible]
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1916  row: m  column: 14
            High quality sequence stop: 607.
FEATURES             Location/Qualifiers
     source          1..1018
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5441845"
                     /clone_lib="NIH_MGC_98"
                     /tissue_type="astrocytoma grade IV, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Library constructed by Ling Hong
                     in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
BASE COUNT      2[illegible] a    28[illegible] c    268 g    211 t
ORIGIN

  Query Match             [illegible];  Score 4[illegible];  DB 13;  Length 1018;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-103;
  Matches  4[illegible];  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        [illegible] 942
              [illegible]
Db          1 [illegible] 60

Qy        [illegible]
              [illegible]
Db         61 CTCAAGTACCCAGTGATCCATGGACAGGTAGGCAGGCTCGGTACTAGGAACACTGGCT 120

Qy       [illegible]
              [illegible]
Db        121 [illegible] AAG 180

Qy       [illegible] 1122
```

```
                [illegible]
Db        181 [illegible] 240

Qy       1123 [illegible] 1182
                [illegible]
Db        241 [illegible] 300

Qy       1183 [illegible] 1242
                [illegible]
Db        301 [illegible] 360

Qy       1243 [illegible] 1302
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAGCTGGCCCAGATGCTGATACACAGCACACAGGGAAAGGAAGACAGTCTCACAGAGGAA 420

Qy       1303 GGGCAGGTGTCCTACGATGACGTCTCTGTGTTCGTGATTCCCTTGGACAGTCAGGGCCAA 1362
                [illegible]
Db        421 GGGCAGGTGTCCTACGATGACGTCTCTGTGTTCGTGATTCCCTTGCACAGTCAGGGCCAA 480

Qy       1363 GAGAGCAGTGACCACTGA 1380
                ||||||||||||||||||
Db        481 GAGAGCAGTGACCACTGA 498


RESULT 11
AW742365
LOCUS       AW742365                 639 bp    mRNA    linear   EST [illegible]
DEFINITION  up56b05.y1 Soares mouse NMIE Mus musculus cDNA clone IMAGE:2786049
            5' similar to WP:C42C1.2 CE16566 PROTEIN PHOSPHATASE ;, mRNA
            sequence.
ACCESSION   AW742365
VERSION     AW742365.1  GI:[illegible]4152
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 639)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40RP from Gibco
            High quality sequence stop: 400.
FEATURES             Location/Qualifiers
     source          1..639
                     /organism "Mus musculus"
                     /strain "C3H x 101 F1"
                     /db_xref "taxon:10090"
                     /clone "IMAGE:2786049"
                     /clone_lib "Soares mouse NMIE"
                     /sex "male"
                     /dev_stage "newborn"
                     /lab_host "DH10B"
                     /note "Organ: inner ear, 170 pooled; Vector: pT7T3D-Pac;
                     Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed
                     with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCACTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not
                     I and Eco RI sites of the modified pT7T3 vector. Library
                     is normalized, and was constructed and donated by Bento
                     Soares and M.Fatima Bonaldo (University of Iowa) and E.
                     Hardisty, A. Varela-Carver, E. Mburu and S.D.M. Brown (MRC
                     UK Mouse Genome Centre and Mammalian Genetics Unit,
                     Harwell, UK)."
BASE COUNT      142 a    151 c    205 g    141 t
ORIGIN
```

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  Query Match             [illegible]
  Best Local Similarity   [illegible]
  Matches [illegible]; Conservative [illegible]; Mismatches [illegible]; Indels [illegible]; Gaps [illegible];

Qy        562 [illegible]
                [illegible]
Db          1 [illegible]

Qy        622 [illegible]
                [illegible]
Db         61 [illegible]

Qy        682 [illegible]
                [illegible]
Db        121 [illegible]

Qy        742 [illegible]
                [illegible]
Db        181 [illegible]

Qy        802 [illegible]
                [illegible]
Db        241 [illegible]

Qy        862 [illegible]
                [illegible]
Db        301 [illegible]

Qy        922 [illegible]
                [illegible]
Db        361 [illegible]

Qy        982 [illegible]
                [illegible]
Db        421 [illegible]

Qy       1042 [illegible]
                [illegible]
Db        481 [illegible]

Qy       1102 [illegible]
                [illegible]
Db        541 [illegible]

Qy       1162 [illegible]
                [illegible]
Db        601 [illegible]


RESULT 12
[illegible]
LOCUS       [illegible]
DEFINITION  [illegible]
ACCESSION   [illegible]
VERSION     [illegible]
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., [illegible]
            R. Emmert-Buck, M.D., Ph.D.
            cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
            Bonaldo, Ph.D.
            cDNA Library Arrayed by: Greg Lennon, Ph.D.
            DNA sequencing by: Washington University Genome Sequencing Center
            Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 467.
FEATURES             Location/Qualifiers
     source          1..494
                     /organism "Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3480060"
                     /clone_lib "NCI_CGAP_GC6"
                     /tissue_type "pooled germ cell tumors"
                     /lab_host "DH10B"
                     /note "Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA
                     from the normalized library NCI_CGAP_GC4 was prepared, and
                     ss circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     1257048-1258663, 1469044-1470083, and 1475592-1476743).
                     Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       91 a    164 c    153 g     86 t      1 others
ORIGIN

  Query Match             35.7%;  Score 493;  DB 12;  Length 494;
  Best Local Similarity   99.8%;  Pred. No. 6.7e-102;
  Matches  493;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         75 TGCCAGCCCCGTGCCCTACCGACGGCCCCGCTTCCTTCGGCGGCTCCAGCTCCAGCCCCGG 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCCAGCCCCGTGCCCTACCGACGGCCCCGCTTCCTTCGGCGGCTCCAGCTCCAGCCCCGG 60

Qy        135 GGCGGCCCACGGCCTCGGCGCGGCCCAGACTCCCGGCCCGTGCGCAGCCCCGGCACGAGGACG 194
              [illegible]
Db         61 GGCGGCCCACGGCCTCGGCGCGGCCCAGACTCCCGGCCCGTGCGCAGCCCCGGCACGAGGACG 120

Qy        195 [illegible] 254
              [illegible]
Db        121 CAGGTTACCTTGGAA[illegible]AGATTATCAAT[illegible]GAATTCAA 180

Qy        255 [illegible]GAAGA 314
              [illegible]
Db        181 TGAGGAT AA[illegible]GAAGA 240

Qy        315 AGAGTGG[illegible]TGA[illegible]CCAGAGGAG[illegible]TGACAGG[illegible]CATTACTGG[illegible]ACT[illegible]TCGA 374
              [illegible]
Db        241 AGAGTGG[illegible]TGA[illegible]CCAGAGGAGTT[illegible]TGACAGG[illegible]CATTACTGG[illegible]ACTG[illegible]TCGA 300

Qy        375 [illegible]ACT[illegible]TGCCTTGCG 434
              [illegible]
Db        301 [illegible]AAACACC[illegible]ACT[illegible]TGCCTTGCG 360

Qy        435 CCGGCAGCTGGAGGCCGTGGTGGAAGGCTTGGTGGCCACTCAGCCCCCCATGCACCTCAA 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CCGGCAGCTGGAGGCCGTGGTGGAAGGCTTGGTGGCCACTCAGCCCCCCATGCACCTCAA 420

Qy        495 [illegible]GCATCTGCCCCAGTGA[illegible]TCAG[illegible]AAAA[illegible]AT[illegible]AGGGCAGA 554
              [illegible]
Db        421 [illegible]GCATC[illegible]CAG[illegible]AAAA[illegible]AGA 480

Qy        555 AGATTTGTTGATCG 568
              [illegible]
Db        481 AGATTTGTTGATCG 494


RESULT 13
BI344088
LOCUS       BI344088                 597 bp    mRNA    linear   EST 10-JUL-2001
DEFINITION  472440 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BI344088
VERSION     BI344088.1  GI:15037377
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 597)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and a.t_trimmed with phred
            [illegible] Vector [illegible] by cross_match with [illegible]
            and -minmatch 12 options.
            PCR Primers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 115  row: [illegible]  column: 22
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1..597
                     /organism "Sus scrofa"
                     /db_xref "taxon:9823"
                     /clone_lib "MARC 2PIG"
                     /tissue_type "pooled"
                     /lab_host "DH10B"
                     /note "Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                     Library made from pooled tissue from testis, ovary,
                     endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT      114 a    141 c    211 g    131 t
ORIGIN

  Query Match             35.1%;  Score 488.6;  DB 13;  Length 597;
  Best Local Similarity   [illegible];  Pred. No. 7.2e-101;
  Matches  537;  Conservative    [illegible];  Mismatches   54;  Indels    [illegible];  Gaps    [illegible]

Qy        237 AGACAAAT[illegible]AAT[illegible]AAT[illegible]AAC[illegible]CAACCTCT[illegible]A[illegible] [illegible]
              [illegible]
Db          1 ACACAAA[illegible]CCAACCTATGTAT[illegible]A[illegible]

Qy        297 TGAGTTTGGG[illegible]GAA------AAGAGTGGCTGACCTTGCCCAGAGGAGG[illegible] [illegible]
              [illegible]
Db         61 TGGGTTTGGG[illegible]GAAGAGGA[illegible]AAGAATGGCTGACCTTGTGTCCAGAGGAGG[illegible] 120

Qy        351 AGGCCAT[illegible]GCAGCAG[illegible] [illegible]
              [illegible]
Db        121 AGGTCAT[illegible]GCATGGCGGTCCAGCTGCAGGTAT[illegible] 180

Qy        411 CAACACCCTGCACTCCTGCTTGCGCCGGCAGCTGGAGGCCGTGGTGGAAGGCTTGGTGGC 470
              [illegible]
Db        181 CAACACC[illegible]TACAGGCTGTGGTAGAT[illegible]AT[illegible] [illegible]

Qy        471 CACTCAG[illegible]CCCCAGTCACC[illegible] [illegible]
              [illegible]
Db        241 CACTCAG[illegible]CCCAGTGA[illegible] [illegible]

Qy        531 GGAGGAAAA[illegible] [illegible]
              [illegible]
Db        301 GGAGGAAAAG[illegible]ATTGGGG[illegible]AGA[illegible]A [illegible]

Qy        591 GGAATTGGATGAGGT[illegible]AGGCCAGATGG[illegible] [illegible]
              [illegible]
Db        361 GGAGTGGGATGAGG[illegible]CCTCAGGCCAGGT[illegible] [illegible]

Qy        651 A[illegible]AAAG[illegible]ACATGCCCAATG[illegible] [illegible]
              [illegible]
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```
Db    421 [illegible] 480

Qy    711 [illegible] 770
          [illegible]
Db    481 [illegible] 540

Qy    771 [illegible] 827
          [illegible]
Db    541 [illegible] 597


RESULT 14
BI847199
LOCUS       BI847199                 550 bp    mRNA    linear   EST [illegible]
DEFINITION  484149 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   BI847199
VERSION     BI847199.1  GI:15[illegible]718
KEYWORDS    EST.
SOURCE      pig.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 550)
  AUTHORS   Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
            Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.L., Laegreid,W.W.
            and Keele,J.W.
  TITLE     Design and use of two pooled tissue normalized cDNA libraries for
            EST discovery in swine
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933 0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and qual trimmed with phred
            20.98090[illegible]. Vector identified by cross_match with the minscore 18
            and minmatch 12 options.
            PCR PRimers
            FORWARD: A[illegible]
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 132  row: A  column: 6
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1..550
                     /organism "Sus scrofa"
                     /db_xref "taxon:9823"
                     /clone_lib "MARC 2PIG"
                     /tissue_type "pooled"
                     /lab_host "DH10B"
                     /note "Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;
                     Library made from pooled tissue from testis, ovary,
                     endometrium, hypothalamus, pituitary, and placenta."
BASE COUNT      164 a    133 c    137 g    116 t
ORIGIN

  Query Match             [illegible]%;  Score 485.4;  DB 15;  Length [illegible];
  Best Local Similarity   92.5%;  Pred. No. 1.1e-[illegible];
  Matches  508;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy    468 [illegible] 527
          [illegible]
Db      1 [illegible] 60

Qy    528 [illegible] 587
          [illegible]
Db     61 [illegible] 120

Qy    588 [illegible] 647
          [illegible]
Db    121 [illegible] 180

Qy    648 [illegible] 707
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```
          [illegible]
Db    [illegible] [illegible]

Qy    [illegible] [illegible]
          [illegible]
Db    [illegible] [illegible]

Qy    [illegible] [illegible]
          [illegible]
Db    [illegible] [illegible]

Qy    [illegible] [illegible]
          [illegible]
Db    [illegible] [illegible]

Qy    [illegible] [illegible]
          [illegible]
Db    [illegible] [illegible]

Qy    948 [illegible]
          [illegible]
Db    [illegible] [illegible]

Qy    [illegible]

Db    [illegible]


RESULT [illegible]
BF41[illegible]
LOCUS       BF41[illegible]        [illegible] bp    mRNA    linear   [illegible]
DEFINITION  [illegible] Rattus norvegicus cDNA [illegible]
            [illegible] mRNA sequence.
ACCESSION   BF41[illegible]
VERSION     [illegible]
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible]
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), [illegible] (1996)
  MEDLINE   [illegible]
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            [illegible] Eckstein Medical Research Building Iowa City, IA [illegible]
            Tel: [illegible]
            Fax: [illegible]
            Email: [illegible]
            [illegible]
            [illegible] cDNA Library [illegible]
            [illegible]
            Research [illegible]
            Seq primer: M13 Forward
            POLYA N[illegible].
FEATURES             Location/Qualifiers
     source          [illegible]
                     /organism "Rattus norvegicus"
                     /strain "[illegible]"
                     /db_xref "taxon:[illegible]"
                     /clone "[illegible]"
                     /clone_lib "[illegible]"
                     /lab_host "[illegible]"
                     /note "Vector: [illegible]
                     polylinker; Site 1: NotI; Site 2: EcoRI; [illegible]
                     library is a subtracted library derived from [illegible]
                     [illegible]
                     [illegible]
```

```
                    dpc, AV canal at 15 dpc.  For a detailed description of
                    the library from which this clone was derived, please
                    visit our web site at [illegible]. The
                    subtraction has been previously described in (Bonaldo,
                    Lennon and Soares, Genome Research 6:791-806, 1996)
                    TAG_SEQ None found"
BASE COUNT      141 a    147 c    176 g    125 t
ORIGIN

  Query Match            41.7%;  Score 478.2;  DB 12;  Length 589;
  Best Local Similarity  88.4%;  Pred. No. 1.7e-98;
  Matches  519;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy        496 [illegible] 555
              [illegible]
Db          3 [illegible] 62

Qy        556 GACTTGGTGATCGGGGCATTGGAGAGTGCCTTTTAGGAATGTGATGAGGTGATCGGGCGG 615
              |||||||||| |||||  ||||||  ||||| ||||||||||||||| ||||||||| |
Db         63 GACTTGGTGATTGGGGTCTTGGAGAAGGCCTTGCAGGAATGTGATGATGTGATTGGGACA 122

Qy        616 [illegible] 675
              [illegible]
Db        123 AAGCTGGAGGCTCAGG[illegible]GGCTGTACAGG[illegible]GGTGGTAGTGTTCCTGCAG 182

Qy        676 GGAAA[illegible]GGGATA[illegible]AGATGAG 735
              || ||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GGGAAGCTGTATGTGGCTAATGCTGGGGATAGCAGGGCATCTTGTTGCGGAGAGATGAG 242

Qy        736 ATA[illegible]CAGGAGCTG 795
              [illegible]
Db        243 ATAC[illegible]CAGGAGCTG 302

Qy        796 GCCTTTGTCTATCCTGACCTTCTGGCTGCTGAGTTCACCGACTGGAGTTCCCTCGGCGG 855
              [illegible]
Db        303 [illegible]GGTGAGT[illegible]GACTGGA[illegible]CAGGGCGG 362

Qy        856 CTGAAGGGGGATGACTTGGGATAGAAGGTTTTGTTCAGGGATCACCACATGAGTGGCTGG 915
              [illegible]
Db        363 CTGAA[illegible]GATGAC[illegible]AGAAGGT[illegible]AGGCTGG 422

Qy        916 [illegible]GATAGGTAGG 975
              [illegible]
Db        423 [illegible]GATACAGGTAGA 482

Qy        976 CAGG[illegible]CAGA 1035
              [illegible]
Db        483 CAG[illegible]GTTAC[illegible]CAGA 542

Qy       1036 [illegible]GGACACAAACAT[illegible]AAGCC[illegible]TGTGG[illegible] 1082
              [illegible]
Db        543 GTGCTGGACACGACAT[illegible]AAGCC[illegible]ATGCC 589

Search completed: February 23, 2003, 03:22:41
Job time : 2255 secs
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                         GenCore version 5.1.3
              Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          February 22, 2003, 21:38:54 ; Search time 3784 Seconds
                                              (without alignments)
                                              [illegible] Million cell updates/sec

Title:           US-09-866-987-3
Perfect score:   1380
Sequence:        1 atgtcccacgactgattccg.........aagaagagttgaccactga 1380

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters:       4[illegible]

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        GenEmbl:*
                 1:  gb_ba:*
                 2:  gb_htg:*
                 3:  gb_in:*
                 4:  gb_om:*
                 5:  gb_ov:*
                 6:  gb_pat:*
                 7:  gb_ph:*
                 8:  gb_pl:*
                 9:  gb_pr:*
                 10:  gb_ro:*
                 11:  gb_sts:*
                 12:  gb_sy:*
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                 15:  em_ba:*
                 16:  em_fun:*
                 17:  em_hum:*
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                 20:  em_om:*
                 21:  em_or:*
                 22:  em_ov:*
                 23:  em_pat:*
                 24:  em_ph:*
                 25:  em_pl:*
                 26:  em_ro:*
                 27:  em_sts:*
                 28:  em_un:*
                 29:  em_vi:*
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      Pred. No. is the number of results predicted by chance to have a
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      score greater than or equal to the score of the result being printed,
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c   16   260.2   18.9 240294  2  AC044892                 AC044892 Homo sapi
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c   34    64.8    4.7 [illegible]  2  AC[illegible]       AC[illegible] Rattus no
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LOCUS       AX352514                 1380 bp    DNA     linear   PAT 01-FEB-2002
DEFINITION  Sequence 5 from Patent WO0192491.
ACCESSION   AX352514
VERSION     AX352514.1  GI:18617749
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Plowman,G.D., Whyte,D., Sudarsanam,S., Manning,G., Caenepeel,S.,
            Martinez,R., Hill,R.J. and Flanagan,P.
  TITLE     Mammalian protein phosphatases
  JOURNAL   Patent: WO 0192491-A 3 06-DEC-2001;
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            Saten, Inc. (US)
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ACCESSION   AX[illegible]
VERSION     AX[illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; [illegible]
REFERENCE   [illegible] (bases [illegible])
  AUTHORS   [illegible], Acharya[illegible], Yue[illegible], Bandman,O.,
            Hillman,J.L., Lal,P., Walia,[illegible], Sandhu,A.[illegible], [illegible]
            Mathur,P.
  TITLE     Phosphatases
  JOURNAL   Patent: WO [illegible]
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Qy         [illegible]
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Qy      481 CCCATGCACCTCAATGGGCGCTGCATCTGCCCCAGTGACCCTCAGTTTCTGGAGCAAAAC 540
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Qy      541 GGCATCACGGCAGAAGACTTGGTGATCGGGGCATTGGAGAGTGCCTTTCAGGAATCTCAT 600
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Qy     1141 ATGGCAATTCATGGACTTTGGGATCTACTCTCCAA[illegible] 1200
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Qy     1380 A 1380
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RESULT 5
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DEFINITION  Homo sapiens cDNA FLJ39862 fis, clone PEBLM2005282, weakly similar
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ACCESSION   AK096681
VERSION     AK096681.1  GI:21756226
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens peripheral blood mononuclear cells (HPBMC5939) cDNA to
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Oshima,A., Takahashi-Fujii,A., Tanase,T., Imose,N., Takeuchi,K.,
            Arita,M., Musashino,K., Yuuki,H., Hara,H., Sugiyama,T., Irie,R.,
            Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y.,
            Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H.,
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            Wagatsuma,M., Murakawa,K., Kanehori,K., Sugiyama,A., Kawakami,B.,
            Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and
            Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2121)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04 JUL 2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics.hri.co.jp, Tel.81-438-52-3975, Fax.81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
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ACCESSION   AL832484
VERSION     AL832484.1  GI:[illegible]
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SOURCE      human.
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; [illegible]
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   [illegible] Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) [illegible] Neuherberg, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de
            sequenced by DKFZ (German Cancer Research Center
            Heidelberg/Germany) within the cDNA sequencing [illegible]
            German Genome Project.
            This clone (DKFZp[illegible]) is available at the [illegible]
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            Berlin-Charlottenburg, GERMANY. [illegible]
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Db        248 GGCTGCCAACACCCTGCACTCCTGCTTGCCGCGGCAGCTGGAGGCCGTGGTGGAAGGCTT 307

Qy        465 GGTGGCCACTCAGCCCCCCATGCACCTCAATGGCGGCTGCATCTGCCCCAGTGACCCTCA 524
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Qy        585 CTTTCAGCAATGTGATGAGGT-GATCGGGCGGGAGCTGGAGGCCTCAGGCCAGATGGGCGG 644
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Db        428 CTTTCAGCAATGTGATGAGGTGATCGGGCGGGAGCTGGAGGCCTCAGGCCAGATGGGCGG 487

Qy        645 CTGCACAGCCCTGGTGGCTGTGTCCCTGCAGGGAAAGCTGTACATGGCCAATGCTGGGCA 704
              ||||||||||||||| |||||||||||||||||||||||||||||||||||| ||||||||
Db        488 CTGCACAGCCCTGGTGGCTGTGTCCCTGCAGGGAAAGCTGTACATGGCCAATGCTGGGCA 547

Qy        705 TAGCAGGGCCATCTTGGTGCGGAGAGATGACATACGGCCACTCAGCTTGGACTTCACCCC 764
              ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Db        548 TAGCAGGCCCATCTTGGTGCGGAGAGATGAGATACGGCCACTCAGCTTGGACTTCACCCC 607

Qy        765 AGAGACTCAGGGGCAGGGGATCCAGCAGCT------------------------------ 794
              ||||||||||||| |||||||||||||||
Db        608 AGAGACTCAGGGGCAGGGGATCCAGCAGCTGGTAGGTGGCCCTGGAAGGATGGAGGCTGT 667

Qy        795 ------------------------------------------------------------ 794

Db        668 GAAGCTCCAACTCCTGGGTCCAGGGCATAAGAAGGAGTATGACCTCAGTCCAGCCTCCC 727

Qy        795 -------CGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCC 847
                     ||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        728 CACCCAGGCCTTTGTCTATCCTGAGCTTCTGGCTGCTGAGTTCACCCGACTGGAGTTCC 787

Qy        848 CTCGGCGCCTGAAGGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGCATCACCACATGA 907
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        788 CTCGGCGGCTGAAGGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCACCACATGA 847

Qy        908 GTGGCTGGAGCTACAAA[illegible] 967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        848 GTGGCTGCAGCTACAAAGTGTGCACAAATCCCATCTCAACTACCTCATCATCCATCCAC 907

Qy        968 [illegible] 1027
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        908 AGGTTAGCCAGCCTCCGTTACTACAAGACTTGGTGTTTTCTCAGGCTTAGGACAGCATC 967

Qy       1028 AGCTCAGAGTCCTGGACACAAACATCCAGCTCAAGCCCTTCTTCCTCTCTGTCCCACAGG 1087
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        968 AGCTCAGAGTCCTGGACACAAACATCCAGCTCAAGCCCTTCTTCCTCTCTGTCCCACAGG 1027

Qy       1088 TGACTGTCCTGGATGTGGATTACTTGGAGCTACAGCAGCATGATGTCCTTGTCATCGGAA 1147
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1028 TGACTGTCCTGGATGTGGATTACTTGGAGCTACAGCAGCATGATGTCCTTGTCATCGGAA 1087

Qy       1148 [illegible] 1207
              |||||||||||||| |||||||||||||||||||||||||||||||||||| ||||||||
Db       1088 CTGATGGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTCC 1147

Qy       1208 TCCCTGGCAACCAAGAGGACCCACACAGGTTCTCAAAGCTGGCCCAGATGCTGATACACA 1267
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1148 TCCCTGGGAACCAAGAGGACCCACACAGGTTCTCAAAGCTGGCCCAGATGCTGATACACA 1207

Qy       1268 GCACACAGCCAAAGCAAGACAGTCTCACACAGGAAGCCCAGCTCTCCTACGATCACCTCT 1327
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1208 GCACACAGCCAAAGCAAGACAGTCTCACACAGGAAGCCCAGCTCTCCTACGATCACCTCT 1267

Qy       1328 CTGTGTTCGTGATTCCCTTCCACAGTCAGGGCAAGAGAGCAGTGACCACTGA 1379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1268 CTGTGTTCGTGATTCCCTTCCACAGTCAGGGCAAGAGAGCAGTGACCACTGA 1319


RESULT 5
AK056894
LOCUS       AK056894                2429 bp    mRNA    linear   PRI 01-AUG-2002
DEFINITION  Homo sapiens cDNA FLJ32332 fis, clone PROST2005121, weakly similar
            to PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16).
ACCESSION   AK056894
VERSION     AK056894.1  GI:16552415
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens prostate cDNA to mRNA, clone_lib:PROST2
            clone:PROST2005121.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   [illegible], Kanehori,K., Yoshida,H., Watanabe,S., Ishida,S.,
            Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S.,
            Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
            Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
            Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
            Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y.,
            Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A.,
            Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2429)
  AUTHORS   Isogai,T., Otsuki,T. and Sugiyama,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-OCT-2001) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: RAB and
            HRI.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="PROST2005121"
                     /tissue_type="prostate"
                     /clone_lib="PROST2"
                     /note="cloning vector: pME18SFL3"
     CDS             405..1217
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="BAB71302.1"
                     /db_xref="GI:16552416"
                     /translation="MHLNGKTICFSDFQFVEEKGIRAE[illegible]
                     ELEASGQ[illegible]
                     [illegible]
                     GQGRQARLLCTLAVSRGLGDHQLRVLDTNIQLKPFLLSVPQVTVLDVDQLELQEDDVV
                     [illegible]K"
BASE COUNT      527 a    658 c    706 g    538 t
ORIGIN

  Query Match             [illegible];  Score 1014.4;  DB 9;  Length 2429;
  Best Local Similarity   99.9%;  Pred. No. 2.6e-190;
  Matches 1015;  Conservative    0;  Mismatches    1;  Indels    [illegible];  Gaps    [illegible];

Qy        225 GATTATCAATGCAGAGAAATCTGAATTCAATGAGGATCAAGCCGCCTGTGGGAAGCTGTG 284
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 GATTATCAATGCAGAGAAATCTGAATTCAATGAGGATCAAGCCGCCTGTGGGAAGCTGTG 205
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Qy        285 CATCGGAGATGTGAGTTTGGGGCTGAAGAAGAGTGGCTGACCCTGGGCCCAGAGGAGTT 344
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 CATCGGAGATGTGAGTTTGGGGCTGAAGAAGAGTGGCTGACCCTGGGCCCAGAGGAGTT 265

Qy        345 CCTGACAGGCCATTACTGGGACTGTTCGATGGGACGGCGGTCCTGGAGCAGCCATCTT 404
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 CCTGACAGGCCATTACTGGGACTGTTCGATGGGACGGCGGTCCTGGAGCAGCCATCTT 325

Qy        405 GGCTGCCAACACCCTGCACTCCTGCTTGCGCCGGCAGCTGGAGGCCGTGGTGGAAGGCTT 464
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 GGCTGCCAACACCCTGCACTCCTGCTTGCGCCGGCAGCTGGAGGCCGTGGTGGAAGGCTT 385

Qy        465 GGTGGCCACTCAGCCCCCCATGCACCTCAATGGCCGCTGCATCTGCCCCAGTGACCCTCA 524
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Db        386 GGTGGCCACTCAGCCCCCCATGCACCTCAATGGCCGCTGCATCTGCCCCAGTGACCCTCA 445

Qy        525 GTTTGTGGAGGAAAAGGGCATCAGGGCAGAAGACTTGGTGATCGGGGCATTGGAGAGTGC 584
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 GTTTGTGGAGGAAAAGGGCATCAGGGCAGAAGACTTGGTGATCGGGGCATTGGAGAGTGC 505

Qy        585 CTTTCAGGAATGTGATGAGGTGATCGGGCGGGAGCTGGAGGCCTCAGGCCAGATGGGCGG 644
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 CTTTCAGGAATGTGATGAGGTGATCGGGCGGGAGCTGGAGGCCTCAGGCCAGATGGGCGG 565

Qy        645 CTGCACAGCCCTGGTGGCTGTGTCCCTGCAGGGAAAGCTGTACATGGCCAATGCTGGGGA 704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 CTGCACAGCCCTGGTGGCTGTGTCCCTGCAGGGAAAGCTGTACATGGCCAATGCTGGGGA 625

Qy        705 TAGCAGGGCCATCTTGGTGCGGAGAGATGAGATACGGCCACTGAGCTTCGAGTTCACCCC 764
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        626 TAGCAGGGCCATCTTGGTGCGGAGAGATGAGATACGGCCACTGAGCTTCGAGTTCACCCC 685

Qy        765 AGAGACTGAGCGGCAGCGGATCCAGCAGCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGG 824
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 AGAGACTGAGCGGCAGCGGATCCAGCAGCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGG 745

Qy        825 TGAGTTCACCCGACTGGAGTTCCCTCGGCGGCTGAAGGGGGATGACTTGGGACAGAAGGT 884
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        746 TGAGTTCACCCGACTGGAGTTCCCTCGGCGGCTGAAGGGGGATGACTTGGGACAGAAGGT 805

Qy        885 TTTGTTCAGGGATCACCACATGAGTGGCTGGAGCTACAAAGTTGTGGAGAAAGCGGATCC 944
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Db        806 TTTGTTCAGGGATCACCACATGAGTGGCTGGAGCTACAAAGTTGTGGAGAAAGCGGATCC 865

Qy        945 CAAGTACCTCACTGATCCATGGACAGGGTAGGCAGGCTCGGTTACTAGGAACACTGGCTGT 1004
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        866 CAAGTACCTCACTGATCCATGGACAGGGTAGGCAGGCTCGGTTACTAGGAACACTGGCTGT 925

Qy       1005 CTCCCGGGGCCTGGGAGACCATCAGCTCAGAGTCCTGGACACAAACATCCAGCTCAAGCC 1064
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        926 CTCCCGGGGCCTGGGAGACCATCAGCTCAGAGTCCTGGACACAAACATCCAGCTCAAGCC 985

Qy       1065 CTTCTTGCTCTCTGTGCCACAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGA 1124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        986 CTTCTTGCTCTCTGTGCCACAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGA 1045

Qy       1125 GGATGATGTGGTTGTCATGGCAACTGATGGACTCTGGGATGTACTGTCCAATGAGGAGGT 1184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1046 GGATGATGTGGTTGTCATGGCAACTGATGGACTCTGGGATGTACTGTCCAATGAGGAGGT [illegible]

Qy       1185 GGCATGGCTGGTGCGGAGCTTCCTCCCTGGGAACCAAGAGGACCCACAGAGTTCCT 1240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1106 GGCATGGCTGGTGCGGAGCTTCCTCCCTGGGAACCAAGAGGACCCACAGAGTTCCT [illegible]


RESULT 6
BC009644
LOCUS       BC009644                1820 bp    mRNA    linear   PRI 22-OCT-2001
DEFINITION  Homo sapiens, clone MGC:17869 IMAGE:[illegible], mRNA, complete cds.
ACCESSION   BC009644
VERSION     BC009644.1  GI:16307110
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1820)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD [illegible],
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA [illegible]
            Web site: http://www-shgc.stanford.edu
            Contact: (Dickson, Mark) mrd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 14 Row: p Column: 20.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
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                     /tissue_type="Uterus, leiomyosarcoma"
                     /clone_lib="NIH_MGC_71"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
     CDS             264..[illegible]
                     /codon_start=1
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                     /protein_id="AAH09644.1"
                     /db_xref="GI:[illegible]"
                     /translation="[illegible]
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                     [illegible]
                     LQTDVVVMATDGLWDVLSNEQVAWLVRSFLPGNQEDPHRFSKLAQMLIHSTQGKED
                     LTEDGQVSYDDVSVFVIPLHSQGQESSDH"
BASE COUNT      445 a    469 c    515 g    391 t
ORIGIN

  Query Match             56.2%;  Score [illegible];  DB 9;  Length 1820;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-144;
  Matches  733;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        [illegible]
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Db        225 GATGAGGTGAT[illegible] 284

Qy        [illegible]
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Db        [illegible]

Qy        [illegible]
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        [illegible]

Qy        778 [illegible]
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        405 [illegible]

Qy        [illegible]
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Db        465 [illegible]
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Qy        898 CACCACATGAGTGGCTGGAGCTACAAACTCTCCAGAAATGGACTTGAACTACCCACTG 957
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Db        525 CACCACATGAGTGGCTGGAGCTACAAACTCTCCAGAAATGGACTTGAACTACCCACTG 584

Qy        958 ATCCATGGACAGGGTAGGCAGGCTGGGTTACTAGGAACACTGGCTGTCTCCCGGGGCCTG 1017
              |||||| |||||||||  |||||||||||||||||||||||||||||||||||||||||
Db        585 ATCCATGGACAGGGTAGGCAGGCTCGGTTACTAGGAACACTGGCTGTCTCCCGGGGCCTG 644

Qy       1018 GGAGACCATCAGCTCAGAGTCCTGGACACAAACATCCAGCTCAACCCTTTCTTGCTCTCT 1077
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Db        645 GGAGACCATCAGCTCAGAGTCCTGGACACAAACATCCAGCTCAACCCTTTCTTGCTCTCT 704

Qy       1078 GTGCCACAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTT 1137
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Db        705 GTGCCACAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTT 764

Qy       1138 GTCATGGCAACTGATGGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATCCCTCGTG 1197
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Db        765 GTCATGGCAACTGATGGACTCTGGGATGTACTCTCCAACGAGCAGCTGGCATCCCTCGTG 824

Qy       1198 CGGAGCTTCCTCCCTGGGAACCAAGAGGACCTACACAGCTTCTCAAAGCTGGCCCAGATG 1257
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Db        825 CGGAGCTTCCTCCCTGGGAACCAAGAGGACCTACACAGCTTCTCAAAGCTGGCCCAGATG 884

Qy       1258 CTGATACACAGTACAATACCCAAAGAAGACAGTTTCAGACAGCAAGGGGACGTGCCCTAC 1317
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Db        885 CTGATACACAGTACAATACCCAAAGAAGACAGTTTCAGACAGCAAGGGGACGTGCCCTAC 944

Qy       1318 GATGACGTCTCTGTGTTCGTGATTCCCTTCCACAGTCAGGGCAACAGCGCAGTGACCAC 1377
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Db        945 GATGACGTCTCTGTGTTCGTGATTCCCTTGCACAGTCAGGGCAACAGCGCAGTGACCAC 1004

Qy       1378 TGA 1380
              |||
Db       1005 TGA 1007


RESULT 7
AK093270
LOCUS       AK093270                1687 bp    mRNA    linear   PRI 15 JUL 2002
DEFINITION  Homo sapiens cDNA FLJ35951 fis, clone TESTI2012104, weakly similar
            to PROBABLE PROTEIN PHOSPHATASE 2C T23F11.1 (EC 3.1.3.16).
ACCESSION   AK093270
VERSION     AK093270.1  GI:21752092
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens testis cDNA to mRNA, clone_lib:TESTI2
            clone:TESTI2012104.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ishibashi,T., Kanehori,K., Yosida,M., Watanabe,S., Ishida,S.,
            Ono,Y., Hotuta,T., Hiraoka,S., Murakawa,K., Takiguchi,S.,
            Kusano,J., Watanabe,M., Fujimori,K., Tanai,H., Ishida,M.,
            Yamashita,H., Chiba,Y., Sugiyama,T., Irie,R., Otsuki,T., Sato,H.,
            Wakamatsu,A., Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y.,
            Saito,K., Nishikawa,T., Kimura,K., Matsuo,K., Nakamura,Y.,
            Sekine,M., Kikuchi,H., Kanda,K., Wagatsuma,M., Takahashi-Fujii,A.,
            Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1687)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04 JUL 2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="TESTI2012104"
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                     /clone_lib="TESTI2"
                     /note="cloning vector: pME18SFL3"
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ORIGIN

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  Best Local Similarity   54.6%;  Pred. No. 1.3e-45;
  Matches  723;  Conservative    0;  Mismatches  547;  Indels   53;  Gaps    6;

Qy         87 GCCCTACCGACGGACCGGCTCGTTCGGGGCTCCAGCTCCAGCCCCGGGGCGGCGACCGC 146
              || | | |||     | |     ||   |      || |||||    ||| ||||     | ||||
Db        194 GCTCGAGCCGAGCTTCTCCACACCGACCTTCTGCAGCTGAGCCCGGGGGGGCGGACGC 253

Qy        147 [illegible] 204
                ||      | |      | |||             ||   ||| |       || |||     | | |
Db        254 GCCGATGACCACGGGGGCGGGCTGTGCAAAGCCCCCGGACACGGGCCGCCGCCTGCCC 313

Qy        205 [illegible] 264
              ||||     ||||||||||||| | ||||||||| |   ||     |         |||||||||| ||
Db        314 TGGAGAACAGGTAGGCGGAGGCATCAATGTTGGCAACAGTCGGCACAATGATGGACAC 373

Qy        265 [illegible] 324
              ||     |||||        | |||     |           |   |      |    ||     | |  | |     | |       ||   |
Db        374 GCTTGCTGTGAAGTGGTGTATGTGGAAGGTCGGAGGAGTGTTACAGGACTACTTAGGCAG 433

Qy        325 [illegible] 384
                 |       ||| ||      ||       ||            | |  |||||||     ||  ||  ||||||| |
Db        434 CCTA   GCCGAGGCCAGGGACTCTGCTTCTACTACTGGGGCCTATTTGATGGGCATGCA 490

Qy        385 GGTCCTGCAGCAGCCATCTTGGCTGGCAACACCCTGCACTCCTGCTTGCGGCCGCAGCTG 444
              ||       | ||| ||         ||||   |          ||||||      |        |  ||      |||||
Db        491 GGGGGCGGAGTTGCTGAAATGGGCTCACGGCTCCTGCATGGCCATATCCGAGAGCAGCTA 550

Qy        445 GAGGCCGTGGTGGA---------AGGCTTGGTGGCCACTCAGCCCCCCATGCACCTCA 493
                ||| |  |||| ||               |    |||  |      ||||  |    |    ||           |||  |
Db        551 AAGGACCTGGTAGAGATACTTCAGGACCTTCGGCCACCACCCCTCTGCCTCCTAACCCACT 610

Qy        494 ATGGCCGCTGCATCTGCCCCACTGACCCTCAGTTTGTGGAG 534
                 ||     |    ||    |  ||  |  |       |          |||         |
Db        611 CCGGGGACCCTAGATTCCTCCGATCCCTCTCACTTGCTTGGCCCTCAGTCCTGCTGGTCT 670

Qy        535    GAAAAGGGCATCAGGCCAGAAGACTTGGTGATCGGGGCATGGAGAGTCCCTTTCAG 591
                   |  ||||      |  ||         ||       |  ||||      |  |||||     |  ||||  |   | |  |  |
Db        671 [illegible] CAG 730

Qy        592 [illegible] 651
                          ||||||    | | |    |||||||  |         | |                      |    |||  ||||||
Db        731 [illegible] GGAGGGGGCTGCTGT 790

Qy        652 [illegible] 711
              || ||||||  |       |  |  ||||  ||  ||  ||||  ||||||||||  ||  ||||||||
Db        791 GCACTGGTTGTGATCTACCTGCTAGGCAAGGTTACGTGGCCAATGCAGGCGATAGCAGC 850

Qy        712 [illegible] 771
              |||||  |  ||  ||||      |  ||  ||           |||  ||     |        |||||  ||||     |||||
Db        851 GCCATCATTGTCGGGAATGGTGAAATCATTCCAATGTCCGGGAGTTTACCCCGGAGACT 910

Qy        772 GAGCGGCAGCGGATCCAGCAGCTGGCCTTGTCTATCCTGAGCTTCTGGCTGGTGAGCTC 831
              |||||  |||||     |  ||||  ||  |  |||    |    |  ||  |||||  ||  |          |  |  |||
Db        911 GAGCGGCAGCGTCTTCAGCTGCTTGGCTTCCTGAAACCAGAGCTGCTAGGCAGTGAATTC 970

Qy        832 ACCCGACTGGAGTTCCCTGGCGGCTGAAGCCCGATCACTTGGACAGAAGCTTTTGTTC 891
              ||||   ||  |||||||| ||    |    |     |      |  ||    ||||  ||||  |  |  ||||  |
Db        971 ACCCACCTTGAGTTCCCCGGCAGAGTTCTGCCCAAGGAGCTGGGGCAGAGGATGTTGTAC 1030
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Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      1091 CCTCTGGTCTGTGGGGAGGGCAAAAAGGCTGGGGTGATGGCCACCATTGGGGTGACCCGA 1150

Qy      1012 GGCCTGGGAGACCATCAG[illegible]
Db      1151 [illegible]

Qy      1072 [illegible]
Db      1211 [illegible]

Qy      [illegible]
Db      1271 [illegible]

Qy      [illegible]
Db      1331 ACTGTGGACAGGGTGCTGTCGGCTATGAGCCTAATGACCACAGCAGGTATACAGCTCTG 1390

Qy      1249 GCCCAGATGCTGATACACAGCACACAGGGAA            AGGAAGACAGTCTCACA [illegible]
Db      1391 [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]


RESULT 8
BC011803
LOCUS       BC011803                1695 bp    mRNA    linear   PRI [illegible] AUG 2001
DEFINITION  Homo sapiens, Similar to RIKEN cDNA 2310008J22 gene, clone
            MGC:19531 IMAGE:4336762, mRNA, complete cds.
ACCESSION   BC011803
VERSION     BC011803.1  GI:15080039
KEYWORDS    MGC.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1695)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (30 JUL 2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis Staudt
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: [illegible]
            Contact: [illegible]
            Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
            Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,[illegible]
            Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., [illegible]
            Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
            McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
            [illegible]
            Hamrah,H. and [illegible]

            [illegible]
            through the I.M.A.G.E. Consortium/LLNL at: http[illegible]
            Series: IRAL [illegible]
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA [illegible]
FEATURES             Location/Qualifiers
     source          1..1695
                     /organism="Homo sapiens"
                     /[illegible]
                     /clone="MGC:19531 IMAGE:4336762"
                     /tissue_type="[illegible]"
                     /clone_lib="NIH_MGC_[illegible]"
                     /lab_host="[illegible]"
                     /note="Vector: [illegible]"
     CDS             [illegible]
                     /[illegible]
                     /product="[illegible] RIKEN cDNA 2310008J22 [illegible]"
                     /protein_id="AAH11803.1"
                     /db_xref="GI:[illegible]"
                     /translation="MASELLHEHIRKQLKLLVEI[illegible]
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                     GKVYVANAGDSRAIIVRNGEIIPMSKEFTPETERQRLQ[illegible]
                     [illegible]
                     [illegible]
                     [illegible]
                     [illegible]"
BASE COUNT     [illegible]
ORIGIN

  Query Match          [illegible]
  Best Local Similarity   [illegible]
  Matches [illegible]  Conservative [illegible]  Mismatches [illegible]  Indels [illegible]  Gaps [illegible]

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Qy      147 [illegible]
Db      207 [illegible]

Qy      [illegible]
Db      267 [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      444 [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
Db      [illegible]

Qy      [illegible]
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Db        [illegible] 743

Qy        652 [illegible] 711

Db        744 [illegible] 803

Qy        712 [illegible] 771

Db        [illegible]

Qy        772 [illegible] 831

Db        864 [illegible]

Qy        832 [illegible] 891

Db        [illegible]

Qy        892 [illegible]

Db        [illegible]

Qy        [illegible]

Db       1044 [illegible]

Qy       1012 [illegible]

Db       1104 [illegible]

Qy       1072 [illegible]

Db       1164 [illegible]

Qy       1132 GTGGTTGTCATGGCAA[illegible]

Db       1224 [illegible]

Qy       1192 [illegible]

Db       1284 ACTGTGGACAGGGTGCT[illegible]GGGCTATGAGCCTAAT[illegible]

Qy       [illegible] [illegible]

Db       [illegible] [illegible]

Qy       1297 [illegible]

Db       [illegible]

Qy       [illegible]

Db       [illegible]


RESULT [illegible]
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LOCUS       AX419118                2518 bp    DNA     linear   PAT 18-JUN-2002
DEFINITION  Sequence [illegible] from Patent W[illegible].
ACCESSION   AX419118
VERSION     AX419118.1  [illegible]
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human protein phosphatase IIc-like enzyme
  JOURNAL   Patent: W[illegible]-A [illegible]-MAR-2002;
            Bayer AktienGesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1..2518
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                     /db_xref="taxon:9606"
     CDS             [illegible]
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="[illegible]"
                     /db_xref="GI:[illegible]"
                     /translation="MA[illegible]
                     [illegible]
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                     [illegible]
                     [illegible]
                     [illegible]S"
BASE COUNT      507 a    768 c    759 g    484 t
ORIGIN

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length 2518;
  Best Local Similarity   57.7%;  Pred. No. 2.7e-42;
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy        445 [illegible] 504

Db        [illegible]

Qy        505 [illegible] 564

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Qy        565 [illegible] 624

Db        [illegible] 1512

Qy        625 [illegible] 684

Db       1548 [illegible] 1607

Qy        685 [illegible] 744

Db       1608 [illegible]

Qy        745 CTGAG[illegible]GAGACTGAG[illegible]GCAGCGGATCCAGCAGCTGG[illegible] 804

Db        [illegible]

Qy        805 [illegible] 864

Db        [illegible]

Qy        865 [illegible] 924

Db       1788 [illegible] 1847

Qy        925 [illegible] 984

Db       1848 [illegible]

Qy        985 [illegible] 1044

Db       1908 [illegible] 1967

Qy       1045 [illegible] 1104

Db       1968 [illegible] 2027

Qy       1105 [illegible] 1164

Db       2028 ACACAATATGA[illegible] 2087

Qy       1165 [illegible]

Db       2088 [illegible] 2147
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Qy     [illegible]
Db     2148 [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]


RESULT 10
HSM80[illegible]
LOCUS       HSM80[illegible]               [illegible] bp    mRNA    linear   PRI [illegible]
DEFINITION  Homo sapiens mRNA; cDNA DKFZp434P1514 (from clone DKFZp434P1514);
            partial cds.
ACCESSION   AL133644
VERSION     AL133644.1  GI:[illegible]
KEYWORDS    .
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to [illegible])
  AUTHORS   Koehrer,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
  TITLE     Direct Submission
  JOURNAL   Submitted ([illegible]) MIPS, Am Klopferspitz 18a, D-82152
            Martinsried, GERMANY
COMMENT     Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
            Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
            sequenced by BMFZ (Biomedical Research Center at the Charite,
            Berlin/Germany) within the cDNA sequencing consortium of the German
            Genome Project.
            This clone (DKFZp434P1514) is available at the RZPD in Berlin.
            Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
            Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
            information about the clone and the sequencing project is available
            at http://www.[illegible]
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "DKFZp434P1514"
                     /tissue_type "testis"
                     /clone_lib "434 (synonym: htes3); Vector pSport1; host
                     DH10B; sites NotI + SalI"
                     /dev_stage "adult"
     gene            1410..[illegible]
                     /gene "DKFZp434P1514"
     CDS             1410..[illegible]
                     /gene "DKFZp434P1514"
                     /note "similarity to [illegible], unspliced"
                     /codon_start 1
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                     /protein_id "CAB[illegible]"
                     /db_xref "GI:[illegible]"
                     /translation "[illegible]
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                     LGFLKP[illegible]SEF[illegible]PVLPK[illegible]NM[illegible]WAYKK[illegible]
                     EGKKAKVMA[illegible]VIE[illegible]SLKV[illegible]SS[illegible]
                     L[illegible]VAAIV[illegible]AVL[illegible]N[illegible]
                     NKLGSGD[illegible]SVPVIP[illegible]GSYS"
     polyA_signal    2456..2461
     polyA_site      2469
BASE COUNT     [illegible] a    768 c    7[illegible] g    484 t
ORIGIN

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  Best Local Similarity   57.[illegible];  Pred. No. [illegible];
  Matches  537;  Conservative    0;  Mismatches  377;  Indels   1[illegible];  Gaps    [illegible];
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Qy     [illegible]
Db     [illegible]

Qy     [illegible]
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Qy     [illegible]
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Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     2148 [illegible]

Qy     [illegible]
Db     [illegible]

Qy     [illegible]
Db     [illegible]


RESULT 11
AX[illegible]
LOCUS       AX[illegible]
DEFINITION  [illegible]
ACCESSION   AX[illegible]
VERSION     AX[illegible]
KEYWORDS    .
SOURCE      [illegible]
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  ORGANISM  H. sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human protein phosphatase IIc like enzyme
  JOURNAL   Patent: WO 0218565-A 1 07-MAR-2002;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
     source          1..[illegible]
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      186 a    247 c    282 g    185 t
ORIGIN

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  Best Local Similarity   [illegible].8%;  Pred. No. [illegible].8e-42;
  Matches  561;  Conservative    0;  Mismatches  [illegible];  Indels   1[illegible];  Gaps    2;

Qy        52[illegible] [illegible]
Db         37 CAGCTAAAGGACCTGAAGGAAGTGAGCTACGAGAGCCTGGTAG[illegible]GGGCCATTGAGAAT 96

Qy        5[illegible] [illegible]CAGATGCCC 642
Db         97 [illegible] 15[illegible]

Qy        643 [illegible]
Db        157 GGCTGCTGTGCACTGGTTGTGATCTACTTG[illegible]TAGGCAAGGTGGTA[illegible]TGGCCAATG[illegible]AGG[illegible] 216

Qy        70[illegible] GATAGCAGGGC[illegible] 762
Db        217 GATAGCAGGG[illegible] 27[illegible]

Qy        763 CCAGACACTGAG[illegible] 822
Db        277 [illegible]CCGAGACTGAGG[illegible] [illegible]

Qy        823 GGTGAGTTCA[illegible]GGCTGAAGG[illegible] 882
Db        3[illegible] [illegible]

Qy        8[illegible] [illegible] 942
Db        397 ATG[illegible] 45[illegible]

Qy        943 [illegible] 100[illegible]
Db        457 [illegible]

Qy        1[illegible] [illegible]
Db        517 [illegible]

Qy        106[illegible] [illegible] 112[illegible]
Db        577 [illegible]

Qy        112[illegible] [illegible]
Db        6[illegible] [illegible]

Qy        1183 [illegible]
Db        6[illegible]7 [illegible]

Qy        124[illegible] [illegible]
Db        757 [illegible]

Qy        128[illegible] [illegible]
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Db        [illegible] [illegible]

Qy       1348 [illegible] 13[illegible]
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RESULT 12
AX4[illegible]71
LOCUS       AX4[illegible]71            11[illegible] bp    DNA     linear   PAT [illegible]-JUN-2002
DEFINITION  Sequence 242 from Patent WO0218424.
ACCESSION   AX400071
VERSION     AX400071.1  GI:21336493
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   [illegible], [illegible], [illegible], Aue,A.J., Ren,F., Zhang,[illegible],
            Wang,J.R., Zhao,Q.A., Wang,D., Liu,C., Drmanac,R.T. and Wehrman,T.
  TITLE     Nucleic acids and polypeptides
  JOURNAL   Patent: WO 0218424-A 242 07-MAR-2002;
            HYSEQ, INC. (US)
FEATURES             Location/Qualifiers
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                     GKVYVANA[illegible]SEAIIVRNGH[illegible]PMSREFTPETERQRLQLLGFLKPELLGSEFTHLEFP
                     RRVLPKEL[illegible]WAYEKTLLE[illegible]VIRGLGP
                     ns[illegible]KV[illegible]AAIV
                     DRVLSAYEPN[illegible]HSRYTALAQALVLGARGTPPDRGWKLPNNKLGS[illegible]VPVIPLGGP
                     GSYS"
BASE COUNT      243 a    3[illegible] c    373 g    2[illegible]2 t
ORIGIN

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  Best Local Similarity   5[illegible]%;  Pred. No. 8.3e-42;
  Matches  49[illegible];  Conservative    0;  Mismatches  329;  Indels   [illegible];  Gaps    2;

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Qy        5[illegible] [illegible] [illegible]55
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Qy        [illegible] [illegible]
Db        456 [illegible] 5[illegible]7

Qy        [illegible] [illegible]
Db        [illegible]28 [illegible] 5[illegible]7

Qy        [illegible] [illegible]
Db        5[illegible]8 [illegible]

Qy        [illegible] [illegible]
Db        648 [illegible] 707

Qy        [illegible] [illegible]
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Db        708 ACCAGAACATGAC[illegible]AAAAAGAT[illegible] 767

Qy        956 TGATGCATGGACAGGGTAGG[illegible]AGGCTGGGTTACTAGGAACACTGG[illegible] 1015
              [illegible]
Db        768 [illegible] 827

Qy       1016 [illegible]AGACTAT[illegible] 1075
              [illegible]
Db        828 [illegible] 887

Qy       1076 [illegible] 1135
              [illegible]
Db        888 GCTTCCCTGAGGTACGAGTGTATGACCTGACACAATATGAGCAC[illegible]CAGATGATGTGC 947

Qy       1136 TTGTCATGGCAACTGATGGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGC 1195
              [illegible]
Db        948 TAGTCCTGGGAA[illegible] 1007

Qy       1196 TGCGGAGCTT[illegible]GGAACCAAGAGGAC[illegible]ACAGG[illegible]AAAG[illegible] 1252
              [illegible]
Db       1008 TGGACAGGG[illegible]TATGAGC[illegible]AATGA[illegible]AGCAGGTATACAG[illegible] 1067

Qy       1253 AGA[illegible]ATACACAG[illegible]AGGGAA              AGGAAGAC[illegible] 1300
              [illegible]
Db       1068 AAG[illegible]GGGTACC[illegible]GAGA[illegible]AACA 1127

Qy       1301 AAGG[illegible]ACGAGGAC[illegible] 1359
              [illegible]
Db       1128 ACAAG[illegible] 1187


RESULT [illegible]
A[illegible]
LOCUS       AC006252               82098 bp    DNA     linear   PRI [illegible]
DEFINITION  Homo sapiens 9p21.1 contig 9 PAC RPCI5 [illegible] (Roswell Park Cancer
            Institute Human PAC Library) complete sequence.
ACCESSION   AC006252
VERSION     AC006252.4  GI:4309923
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 82098)
  AUTHORS   Muzny,D., Arenson,A.D., Bouck,J., Buhay,C., Chen,[illegible]
            Culpepper,P., Ding,Y., Dugan,S.P., Durbin,K.[illegible]
            Ganesh,K.P., Garcia,C., Garcia,D.K., Gorrell,H., Gorrell,[illegible]
            He,X., Hernandez,J., Jackson,L.E., Kondejewski,N., Leal,B.,
            Lichtarge,O., Liu,W., Logan,O., Lu,J., Martinez,C., Moore,S.,
            Moorish,I., Nguyen,N., Oswal,G., Pampell,L.R., Parish,R.[illegible]
            Perez,L.M., Rashid,N.D., Rives,C.M., Scherer,S.E., Shen,H.,
            Simon,M.L., Vo,Q.K., Wei,Y., Williamson,A.[illegible] Worley,K.[illegible] Zhao,X.,
            Naylor,S.L. and Gibbs,R.A.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 82098)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-DEC-1998) Molecular and Human Genetics, Baylor
            College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 82098)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-FEB-1999) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Mar 1, 1999 this sequence version replaced gi:[illegible].
            INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
            hgc-help@bcm.tmc.edu

            CLONE LENGTH: This sequence does not necessarily represent the
            entire insert of this clone, overlapping regions of clones are only
            sequenced and submitted once, so the sequence for the remainder of
            the insert may be found in the record for the adjacent [illegible]
            overlapping clones are noted at the beginning and end of the
            features listing.

            ANNOTATION [illegible]
              [illegible]
              [illegible]
              [illegible]
              Repeats are identified using RepeatMasker [illegible]
            [illegible]
              [illegible]
            (Nucl. Acids Res. [illegible]) similarity (expect [illegible]
            EST and cDNA sequences. Genes demonstrate at least [illegible]
            flanked by consensus splice sites that maintained sequence
            continuity across the splice junctions. Sequences that are not
            identical matches are annotated as similar.

            SEQUENCING READ COVERAGE: Sequencing is completed [illegible]
            standard of double strand coverage with a minimum [illegible]
            reads with no ambiguities or 2 chemistries with a [illegible]
            [illegible] and 3 reads with no ambiguities. If the sequence [illegible]
            a region does not meet this standard, it will be [illegible]
            annotated as low coverage.

            QUALITY OF INDIVIDUAL BASES: This sequence meets [illegible]
            standards: estimated error rate less than 1 per [illegible]
            Reports of lowest quality individual bases and [illegible]
            quality are [illegible] below. [illegible] of the [illegible]
            at [illegible]: http://[illegible]/quality.[illegible]
            [illegible]

            [illegible]


                          Summary Statistics
            [illegible] Length:                                     [illegible]
            Phrap Values (in estimate):                         [illegible]
            Average error rate (BCM [illegible] estimate):      [illegible]
            [illegible]
            Number [illegible]
            Number of N[illegible]


                          [illegible]
            [illegible]
            [illegible]      [illegible](n)[illegible]      [illegible](n)[illegible]
            [illegible]      [illegible](n)[illegible]      [illegible](n)[illegible]
            [illegible]      [illegible](n)[illegible]      [illegible](n)[illegible]
            40[illegible]    [illegible](n)[illegible]      [illegible](n)[illegible]
            4[illegible]     [illegible](n)[illegible]      [illegible](n)[illegible]
            [illegible]      [illegible](n)[illegible]      [illegible](n)[illegible]


                      [illegible]

                    [illegible]                                               *
                    [illegible]                                               *
                    [illegible]                                               *
            #       [illegible]                                               *
            bases   [illegible]                                          *    *
                    [illegible]                                          *    *
                    4[illegible]                                         *    *
                    [illegible]                                          *    *
                    [illegible]                                     *    *    *
                    [illegible]                       *    *        *    *    *
                          *    *    *    *    *    *    *    *
                      [illegible]
                               Phrap Value [illegible]


            Version: [illegible]
```

```
FEATURES             Location/Qualifiers
     source          1..182098
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="RP11-1157M23"
                     /note="Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
                     Eutheria; Primates; Catarrhini; Hominidae; Homo."
     repeat_region   1..69
                     /rpt_family="Alu"
     repeat_region   78..379
                     /rpt_family="AluSx"
     gene            complement(join(588..1542,1865..2013,2124..2237,
                     2487..2550,2734..2853))
                     /note="UniGene cluster containing AI[illegible], [illegible],
                     AA2275[illegible], [illegible], AA728883, [illegible], and AA292266."
     STS             647..783
                     /standard_name="stSG4882"
                     /db_xref="GDB:4[illegible]6425"
     STS             [illegible]
                     /standard_name="[illegible]"
                     /db_xref="dbSTS:32797"
     misc_feature    5021..5289
                     /note="Region: Similar to H.sapiens genomic DNA, X875[illegible]."
     repeat_region   5178..5235
                     /rpt_family="GC_rich"
     repeat_region   5290..5532
                     /rpt_family="GC_rich"
     misc_feature    553[illegible]..5638
                     /note="Region: Similar to H.sapiens genomic DNA, X87538."
     repeat_region   6319..6602
                     /rpt_family="AluSx"
     repeat_region   complement(7672..7715)
                     /rpt_family="L1M4"
     repeat_region   complement(7717..7929)
                     /rpt_family="AluSp"
     repeat_region   8106..8173
                     /rpt_family="MER4A2"
     repeat_region   complement(8207..8491)
                     /rpt_family="AluSx"
     repeat_region   complement(8512..8591)
                     /rpt_family="AluSp"
     repeat_region   9144..9289
                     /rpt_family="MER4[illegible]"
     repeat_region   complement(9421..958[illegible])
                     /rpt_family="FRAM"
     repeat_region   complement(9586..9631)
                     /rpt_family="(TAGA)n"
     repeat_region   complement(9663..9894)
                     /rpt_family="AluJo"
     repeat_region   9935..10052
                     /rpt_family="MIR"
     repeat_region   complement(10124..10260)
                     /rpt_family="L2"
     repeat_region   11050..11126
                     /rpt_family="L2"
     repeat_region   11143..11426
                     /rpt_family="AluSp"
     repeat_region   11960..12050
                     /rpt_family="GC_rich"
     gene            join(12104..12195,16081..16158,19065..19243,19956..20060,
                     20[illegible]2..20317,21117..21267,21405..21526,21986..22575)
                     /note="UniGene cluster containing [illegible], [illegible],
                     W93722, [illegible], AA[illegible], [illegible], and AA298126."
     repeat_region   complement(14187..14295)
                     /rpt_family="MIR"
     repeat_region   complement(14866..15168)
                     /rpt_family="A[illegible]Sq"
     repeat_region   complement(15624..15725)
                     /rpt_family="(CA)n"
     repeat_region   complement(17254..17540)
                     /rpt_family="AluY"
     repeat_region   complement(18160..18451)
                     /rpt_family="AluSp"
     STS             182[illegible]
                     /standard_name="[illegible]"
                     /db_xref="dbSTS:7[illegible]"
     STS             22820..[illegible]
                     /standard_name="stSG1[illegible]"
                     /db_xref="GDB:4564423"
     repeat_region   complement(22833..23325)
                     /rpt_family="MLT1D"
     repeat_region   complement(24[illegible]..24822)
                     /rpt_family="L2"
     repeat_region   complement(25824..26124)
                     /rpt_family="AluSp"
     repeat_region   complement([illegible]..[illegible]74)
                     /rpt_family="([illegible]A)n"

  Query Match             18.[illegible]%;  Score [illegible];  DB 9;  Length [illegible];
  Best Local Similarity   [illegible]%;  Pred. No. 1.[illegible]e-41;
  Matches  262;  Conservative  [illegible];  Mismatches  [illegible]3;  Indels  [illegible];  Gaps  [illegible];

Qy        [illegible]4 [illegible] [illegible]
                       [illegible]
Db       4222 [illegible] [illegible]

Qy        [illegible]4 [illegible] [illegible]
                       [illegible]
Db       4162 [illegible] [illegible]

Qy        454 [illegible] [illegible]
                       [illegible]
Db       4102 [illegible] [illegible]

Qy        514 AGTGA[illegible]TCAG[illegible]GGCAGAAGACTTGG[illegible] 573
                       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4042 AGTGA[illegible]GGCAGAAGAC[illegible] [illegible]

Qy        574 TTGGAGAGTGCCTTTCAG[illegible]AA[illegible] 598
                       [illegible]
Db       [illegible]982 TTGGAGAGTG[illegible]TTTCAG[illegible]AA[illegible] [illegible]


RESULT 14
A[illegible]92045/c
LOCUS       A[illegible]          17[illegible] bp    DNA     linear   [illegible]
DEFINITION  Homo sapiens chromosome [illegible] clone RP11 168J14, complete sequence.
ACCESSION   A[illegible]
VERSION     A[illegible]45.2  GI:[illegible]
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; [illegible];
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 171348)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C. and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 171348)
  AUTHORS   Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J., [illegible] and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUN-20[illegible]) Genome Center, University of Washington,
            Box 352145, Seattle, WA [illegible], USA
REFERENCE   3  (bases 1 to 171348)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Raymond,C. and
            Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (2[illegible]) Genome Center, University of Washington,
            Box 352145, Seattle, WA [illegible], USA
COMMENT     On Aug 23, 20[illegible] this sequence version replaced gi:[illegible].
            ---------------- Genome Center
                Center: University of Washington Genome Center
                Center Code: UWGC
                Web site: http://www.genome.washington.edu
     Contact: [illegible]@u.washington.edu
     Drafting Center: BCM
   -------          Project Information
     Center project name: chr 3
     Center clone name: RP11-168J18 (bc0380)
   -------        Summary Statistics
     Sequencing vector: M13; L08821; 58% of reads
     Sequencing vector: plasmid; L08752; 42% of reads
     Chemistry: Dye-terminator ET; 38% of reads
     Chemistry: Dye-primer Bodipy; 18% of reads
     Chemistry: Dye-terminator Big Dye; 44% of reads
     Assembly program: Phrap; version [illegible]
     Consensus quality: 171265 bases at least Q40
     Consensus quality: 171335 bases at least Q30
     Consensus quality: 171343 bases at least Q20
     Insert size: 180350; 10.2% error; agarose-fp
     Insert size: 171343; sum-of-contigs
     Quality coverage: 8.2x in Q20 bases; agarose-fp
     Quality coverage: 8.6x in Q20 bases; sum-of-contigs
  -------------
Overlapping Sequences:
     5':  RP5-1157M23 (BWGT:bc0711) AC[illegible]
     3':  RP11-258M15 (BWGT:bc0551) AC[illegible]
  -------
Sequence Quality Assessment:
 This entry has been annotated with sequence quality
 estimates computed by the Phrap assembly program.
 All manually edited bases have been reduced to quality zero.
 Quality levels above 40 are expected to have less than
 1 error in 10,000 bp.
 Base-by-base quality values are not generally visible from the
 GenBank flat file format but are available as part
 of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:
all regions were either double-stranded or sequenced with an
alternate chemistry or covered by high quality data (i.e., Phred
quality >= 30); an attempt was made to resolve all sequencing
problems, such as compressions and repeats; all regions were
covered by at least one plasmid subclone or more than one M13
subclone; and the assembly was confirmed by restriction digest.
  ------
Sequence Validation:
 This sequence has been validated by Multiple Complete Digest
 fingerprinting. Comparison of the experimentally derived digest
 fragments with sequence-predicted fragments is given below.
 The electronically digested sequence consists of both insert and
 vector, in order to accurately represent the entire circular BAC.
 Small fragments below a variable cutoff (approximately 400-800 bp)
 are not resolved in the fingerprint and hence do not appear
 in the table. There are no significant remaining discrepancies
 between the experimental and predicted values. Uniquely ordered
 fragments are separated by dashed lines.
       BglII                   EcoRI                  HindIII
       ---                                            -----
SeqPerMap    FingPrint    SeqPerMap    FingPrint    SeqPerMap    FingPrint
---------


      5494         5465         8696         8744         2164         2154
  ------
      2067         [illegible]     6         [illegible]  6382         [illegible]
                            ------
     10422         [illegible]  5201         [illegible]   512         [illegible]
  --- ---
     11234         [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
                            ------
      [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
  -------                   -------
      [illegible]  [illegible]   753         [illegible]  [illegible]  [illegible]
                            -------
      [illegible]  [illegible]  8245         [illegible]  [illegible]  [illegible]
  ------                    ------
```

```
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]  [illegible]  [illegible]  [illegible]  [illegible]
     [illegible]  [illegible]                            [illegible]  [illegible]
     [illegible]  [illegible]                            [illegible]  [illegible]
     [illegible]  [illegible]                            [illegible]  [illegible]
     [illegible]  [illegible]                            [illegible]  [illegible]
     [illegible]  [illegible]                            [illegible]  [illegible]
     [illegible]  [illegible]                            [illegible]  [illegible]
     [illegible]  [illegible]                            [illegible]  [illegible]
     [illegible]  [illegible]                            [illegible]  [illegible]
     [illegible]  [illegible]
     [illegible]  [illegible]
     [illegible]  [illegible]
     [illegible]  [illegible]
     [illegible]  [illegible]
     [illegible]  [illegible]
     [illegible]  [illegible]
     [illegible]  [illegible]
FEATURES             Location/Qualifiers
```

```
     source          1..171343
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /chromosome "3"
                     /clone "RP11 168J18"
                     /clone_lib "RPCI human BAC library 11"
BASE COUNT     43231 a   40155 c   45178 g   40769 t
ORIGIN

  Query Match             18.3%;  Score 200.2;  DB 9;  Length 171343;
  Best Local Similarity   98.9%;  Pred. No. 1.2e-41;
  Matches  202;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        334 [illegible]
              || | | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     165894 [illegible]AGGCCATTACTGGGTACTGTTCGATGGCAG[illegible]A 165835

Qy        394 GCAGCCATCTTGGCTGCCAACACCTGCACTCCTGCTTGCTGCCGGCAGCTGGAGGCCGTG 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     165834 GCAGCCATCTTGGCTGCCAACACCTGCACTCCTGCTTGCCGCCGGCAGCTGGAGGCCGTG 165775

Qy        454 TTGGAAGG[illegible]ACTCAG[illegible]ATCCATCCAATGGCCGCTGCATCTGCCCC 513
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     165774 TTGGAAGG[illegible]CAGTCAG[illegible]ATCCATCCAATGGCCGCTGCATCTGCCCC 165715

Qy        514 ATTGACCCTCAGTTTCTGGAGGAAAAGCCATCAGCCCAGAAGACTTCCTGATCCCCCCA 573
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     165714 ATTGACCCTCAGTTTCTGGAGGAAAAG[illegible]A[illegible]AGAAGACTTCCTGAT[illegible]A 165655

Qy        574 TTGGAGAGTGCCTTTCAGGAATGTG 598
              |||||||||||||||||||||||||
Db     165654 TTGGAGAGTGCCTTTCAGGAATGTG 165630


RESULT 15
AC094021
LOCUS       AC094021               214160 bp    DNA     linear   PRI 27-MAR-2002
DEFINITION  Homo sapiens chromosome 3 clone RP11 804L18, complete sequence.
ACCESSION   AC094021 AC069253
VERSION     AC094021.2  GI:19745061
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-SEP-2001) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
REFERENCE   3  (bases 1 to 214160)
  AUTHORS   Kaul,R.K., Olson,M.V., Zhou,Y., James,R.A., Rouse,G., Wu,Z.,
            Saenphimmachak,C., Phelps,K.A., Raymond,C. and Haugen,E.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (27-MAR-2002) Genome Center, University of Washington,
            Box 352145, Seattle, WA 98195, USA
COMMENT     On Mar 27, 2002 this sequence version replaced gi:15594339.
            ------------ Genome Center
                Center: University of Washington Genome Center
                Center code: UWGC
                Web site: http://www.genome.washington.edu
                Contact: uwgchtgs@u.washington.edu
                Drafting Center: BCM
            ------------ Project Information
                Center project name: chr 3
                Center clone name: RP11 804L18 (b-565)
            ------------ Summary Statistics
                Sequencing vector: M13; U28821; 49% of reads
                Sequencing vector: plasmid; 51% of reads
                Chemistry: Dye terminator ET; 36% of reads
                Chemistry: Dye primer Bodipy; 11% of reads
                Chemistry: Dye-terminator Big Dye; 53% of reads
                Assembly program: Phrap; version 0.990319
                Consensus quality: 213971 bases at least Q40
                Consensus quality: 214139 bases at least Q30
                Consensus quality: 214157 bases at least Q20
                Insert size: 214160; sum-of-contigs
                Quality coverage: 6.8X in Q20 bases; sum-of-contigs
            ------------
            Overlapping Sequences:
                5': Mapping in progress
                3': RP11 [illegible] (GAG[illegible]) AC068208
            ------------
            Sequence Quality Assessment:
             This entry has been annotated with sequence quality
             estimates computed by the Phrap assembly program.
             All manually edited bases have been reduced to quality zero.
             Quality levels above 40 are expected to have less than
             1 error in 10,000 bp.
             Base-by-base quality values are not generally visible in the
             GenBank flat file format but are available as part
             of this entry's ASN.1 file.

            This sequence was finished as follows unless otherwise noted:
            all regions were either double stranded or sequenced with an
            alternate chemistry or covered by high quality data (i.e., phred
            quality [illegible] 30); an attempt was made to resolve all sequencing
            problems, such as compressions and repeats; all regions were
            covered by at least one plasmid subclone or more than one M13
            subclone; and the assembly was confirmed by restriction digest.
            ------------
            Sequence Validation:
             This sequence has been validated by Multiple Complete Digest
             Fingerprinting. Comparison of the experimentally derived digest
             fragments with sequence-predicted fragments is given below.
             The electronically-digested sequence consists of both insert and
             vector, in order to accurately represent the entire circular BAC.
             Small fragments below a variable cutoff (approximately 4 - 6 kb)
             are not resolved in the fingerprint and hence do not appear
             in the table. There are no significant remaining discrepancies
             between the experimental and predicted values. Uniquely ordered
             fragments are separated by dashed lines.
                    BglII                      EcoRI                   HindIII
            -----------------------------------------------------------------
            SeqBerMap  FragPrint     SeqBerMap  FragPrint     SeqBerMap  FragPrint
            -----------------------------------------------------------------

            ----------              ------
                  3254       [illegible]       8696       8704       [illegible]       [illegible]
            ---                     ----------
                  [illegible]       [illegible]       [illegible]       [illegible]       [illegible]       [illegible]
            --------                ------
                 [illegible]       [illegible]       4872       4941        [illegible]       [illegible]
            --------
                 14[illegible]      14[illegible]       7562       7599        [illegible]       [illegible]
            ---------
                  [illegible]       [illegible]       1627       1647       [illegible]       [illegible]
            -----
                 11235      [illegible]       14[illegible]       1443      [illegible]       [illegible]
            --------                --------
                  1606       15[illegible]       4966       4941        [illegible]       [illegible]
            ------
                  1601       1579       5201       5277       41[illegible]       [illegible]
                                    ----------
                  4216       41[illegible]       [illegible]       6041       [illegible]       [illegible]
            --------                ----------
                  1426       [illegible]       8[illegible]       [illegible]       [illegible]       [illegible]
            ------                  ----------             ----------
                    1[illegible]       [illegible]        7[illegible]       [illegible]       [illegible]       [illegible]
            ---------               --------
                  5[illegible]       5[illegible]       8244       8[illegible]       2[illegible]       [illegible]
```

```
   3538      3570      2219      2197       628      <800
   2713      2738      3014      3012      1010       995
   9242      9087      2374      2384       805       860
   9003      9087      4571      4633     10279     10159
    336      <800      1146      1130        92      <800
   2644      2738     25960     26349      2927      2934
   3542      3570      1677      1647      4985      5017
   1498      1579     14734     14440       710      <800
  19887     19976      1490      1443      3758      3774
   6637      6645      3498      3525     11877     11696
    957       957      5268      5272      6471      6448
   1644      1579       227      <800     17475     17857
     33      <800      3689      3974      5558      5511
   2908      2968     27557     26349      5475      5511
   5002      4976      3966      3974     14272     13913
   2867      2927      8435      8387      7102      7266
   1250      1244     18224     17631      9289      9276
  19519     19976      8602      8704      1878      1877
    259      <800       284      <800      6412      6448
   6540      6645       241      <800      6309      6448
   2193      2230     25108     26349     13796     13913
   5173      5214       449      <800      3283      3316
   1022      1021      2474      2502      3498      3529
   8390      8419                          5169      5017
   1767      1760                          1165      1154
   1669      1579                          8966      8942
   4595      4593                          5129      5017
   5655      5629                         14047     13913
    478      <800
   2518      2549
  16099     15788
   3517      3570
   6529      6645
FEATURES             Location/Qualifiers
     source          1..214160
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /chromosome "3"
                     /clone "RP11-801L18"
                     /clone_lib "RPCI human BAC library 11"
BASE COUNT    60584 a  57394 c  [illegible] g  48[illegible] t
ORIGIN

  Query Match             18.[illegible]%;  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   98.[illegible]%;  Pred. No. 1.1e-41;
  Matches  262;  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy        334 [illegible] 393
              [illegible]
Db      25941 [illegible] 26000

Qy        394 [illegible] 453
              [illegible]
Db      26001 [illegible] 26060

Qy        454 [illegible] 513
              [illegible]
Db      26061 [illegible] 26120

Qy        514 [illegible] 573
              [illegible]
Db      26121 [illegible] 26180

Qy        574 [illegible]
              [illegible]
Db      26181 [illegible]

Search completed: February 2[illegible], 2003, [illegible]
Job time : 4117 secs
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                    GenCore version 5.1.[illegible]
              Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         February 22, 2003, 18:02:04 ; Search time 318 Seconds
                                              (without alignments)
                                              9772.823 Million cell updates/sec

Title:          US-09-866-987-3
Perfect score:  1380
Sequence:       1 atat[illegible]..........[illegible] 1380

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       2185[illegible] seqs, 1125999159 residues

Total number of hits satisfying chosen parameters:      43[illegible]478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       N_Geneseq_101002:*
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                 2:  [illegible]
                 3:  [illegible]
                 4:  [illegible]
                 5:  [illegible]
                 6:  [illegible]
                 7:  [illegible]/geneseqn-embl/NA1986.DAT:*
                 8:  [illegible]/NA1987.DAT:*
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                 12: [illegible]1991.DAT:*
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                 14: [illegible]
                 15: [illegible]
                 16: [illegible]
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                 18: [illegible]/NA1997.DAT:*
                 19: [illegible]
                 20: [illegible]
                 21: [illegible]
                 22: [illegible]
                 23: [illegible]
                 24: [illegible]

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result               Query
  No.      Score     Match Length DB  ID                          Description
-------------------------------------------------------------   -----------------
     1      1369      99.2   1887  22  AAH22961                    Human phosphatase
     2       917      66.4  [illegible]  24  ABA94426              Human protein phos
     3       536      38.8  [illegible]  24  ABL79990              Human ovarian canc
     4     264.8      19.2  [illegible]  24  ABK47452              DNA encoding human
     5     262.4      19.0   4262  17  AAT38484                    Rat petrin cDNA cl
     6     262.4      19.0   4515  17  AAT38486                    Rat petrin cDNA.
     7     243.4      17.6   1617  23  AAS93646                    DNA encoding novel
     8     243.4      17.6   1887  22  AAI58166                    Human polynucleoti
     9     243.4      17.6  [illegible]  24  ABK46163              cDNA encoding colo
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    10     242.[illegible]  17.6  [illegible]  22  AAH17[illegible]   Human cDNA [illegible]
    11       178      12.9  [illegible]  17  AAT38482              Rat petrin cDNA [illegible]
    12     103.2       7.4  [illegible]  21  AAA02311              Human [illegible]
    13       103       7.5  [illegible]  20  AAZ12841              Human gene express
    14     102.8       7.4  [illegible]  20  AAX98954              Human [illegible]
    15     101.2       7.3   2387  23  ABL25549                    Drosophila melanog
    16     101.2       7.3   5107  23  ABL25548                    Drosophila melanog
    17        98       7.1    551  24  ABL82482                    Human ovarian canc
    18        95       6.9  [illegible]  20  AAX98437              Human cancer cell
    19      87.6       6.3    774  21  AAA01837                    Human colon cancer
    20      83.6       6.1    294  21  AAA00279                    Human colon cancer
    21      81.2       5.9   2258  23  ABV22179                    Human prostate exp
    22      81.2       5.9   2258  23  ABV23186                    Human prostate exp
    23      81.2       5.9   2258  23  ABV27918                    Human prostate exp
    24      81.2       5.9   2258  23  ABV27965                    Human prostate exp
    25      81.2       5.9   2258  23  ABV28[illegible]            Human prostate exp
c   26      76.8       5.6    582  22  AAH16[illegible]            Human cDNA clone (
    27        68       4.9    434  17  AAT38480                    Rat petrin cDNA [illegible]
    28      50.4       3.7   1643  22  AAS06065                    [illegible]
c   29      49.8       3.6   6714  21  AAZ45930                    Nucleotide sequence
c   30      49.8       3.6   6924  21  AAZ45934                    Nucleotide sequence
c   31      49.8       3.6   6924  21  AAZ45935                    Nucleotide sequence
c   32      49.4       3.6   2668  22  AAK75409                    Human immune/haema
    33      49.2       3.6    730  22  AAI59952                    Human polynucleoti
c   34        49       3.6    500  24  ABK47453                    Protein phosphatas
c   35      48.6       3.5   1327  24  ABQ68452                    Listeria monocytog
c   36      48.2       3.5   1451  20  AAX15147                    Nucleotide sequenc
c   37      48.2       3.5   2887  24  AAL36162                    Human Smad6 DNA.
c   38        48       3.5    953  24  ABQ37014                    Oligonucleotide [illegible]
    39        48       3.5    953  24  ABQ37015                    Oligonucleotide [illegible]
    40  [illegible]                    AAQ11213                    PRV 28K [illegible]
    41  [illegible]               22  AAK75410                     Human immune/haema
    42  [illegible]                    [illegible]                 Z. mays [illegible]
    43  [illegible]
    44  [illegible]               24  ABL64982                     [illegible]
    45  [illegible]               21  [illegible]                  [illegible]

                              ALIGNMENTS

RESULT 1
AAH22961
ID   AAH22961 standard; cDNA; 1887 BP.
XX
AC   AAH22961;
XX
DT   17-SEP-2001  (first entry)
XX
DE   Human phosphatase [illegible] encoded cDNA (clone ID [illegible]).
XX
KW   Phosphatase; [illegible]; Alzheimer's disease; Huntington's disease; human;
KW   [illegible]; immunomodulatory; cytostatic;
KW   neuroprotective; anticonvulsant; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1523
FT                   /*tag=  a
FT                   /product=  "phosphatase"
XX
PN   WO200153469-A2.
XX
PD   26-JUL-2001.
XX
PF   18-JAN-2001; 2001WO-US02[illegible].
XX
PR   21-JAN-2000; 2000US-0177[illegible].
PR   28-JAN-2000; 2000US-0178[illegible].
PR   25-FEB-2000; 2000US-0184[illegible].
PR   17-MAR-2000; 2000US-0190142.
XX
```

```
PA   (INCY ) INCYTE GENOMICS INC.
XX
PI   Bandman O,  Tang YT,  Azimzai Y,  Yue H,  Baughn MR,  Hillman JL;
PI   Lal P,  Wang D,  Gandhi AR,  Policky JL,  Mathur P;
XX
DR   WPI; 2001-451007/48.
DR   N-PSDB; AAB85498.
XX
PT   Novel phosphatases useful for treating diseases associated with
PT   decreased expression of functional phosphatases, e.g., Alzheimer's
PT   disease, Huntington's disease, immune disorders, and cancers -
XX
PS   Claim 5; Page 100; 103pp; English.
XX
CC   The invention provides human phosphatases (PP) and polynucleotides
CC   encoding the phosphatases. The polypeptides can be expressed by standard
CC   recombinant methodology. The PP are useful for treating a disease or
CC   condition associated with decreased expression of functional
CC   phosphatases. Compositions containing agonists or antagonists of PP may
CC   be used to treat a disease associated with decreased expression or
CC   overexpression of PP, respectively. Such diseases may include
CC   Alzheimer's disease, Huntington's disease, immune disorders, and
CC   cancers. The present sequence represents a human phosphatase encoding
CC   cDNA.
XX
SQ   Sequence 1837 BP; 392 A; 527 C; 555 G; 363 T; 0 other;

  Query Match             [illegible];  Score [illegible];  DB 22;  Length 1837;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches 1380;  Conservative    0;  Mismatches    [illegible];  Indels    1;  Gaps    1;

Qy          1 ATGTCCGGCCGGCTGGTTCCGGCGCCGCTTCCTGCCTGGGGAGCCGCTCCCCGCCGCCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCGGCCGGCTGGTTCCGGCGCCGCTTCCTGCCTGGGGAGCCGCTCCCCGCCGCCGCGG 60

Qy         61 [illegible] 120
Db         61 [illegible] 120

Qy        121 [illegible] 180
Db        121 [illegible] 180

Qy        181 [illegible] 240
Db        181 [illegible] 240

Qy        241 [illegible]
Db        241 [illegible]

Qy        301 [illegible] 360
Db        301 [illegible] 360

Qy        361 [illegible] 420
Db        361 [illegible] 420

Qy        421 [illegible] 480
Db        421 [illegible] 480

Qy        481 [illegible] 540
Db        481 [illegible] 540

Qy        541 [illegible]
Db        541 [illegible]

Qy        601 [illegible]
Db        601 [illegible]

Qy        661 [illegible]
Db        661 [illegible]

Qy        721 [illegible]
Db        721 [illegible]

Qy        781 [illegible]
Db        781 [illegible]

Qy        841 [illegible]
Db        841 [illegible]

Qy        901 [illegible]
Db        901 [illegible]

Qy        961 [illegible]
Db        961 [illegible]

Qy       1021 [illegible]
Db       1021 [illegible]

Qy       1081 [illegible]
Db       1081 [illegible]

Qy       1141 [illegible]
Db       1141 [illegible]

Qy       1201 [illegible]
Db       1201 [illegible]

Qy       1261 [illegible]
Db       1261 [illegible]

Qy       1321 [illegible]
Db       1321 [illegible]

Qy       1381 A [illegible]
Db       1381 A [illegible]


RESULT 2
[illegible]
ID   [illegible]
XX
AC   [illegible]
XX
DT   [illegible]
XX
DE   Human protein phosphatase [illegible] cDNA.
XX
KW   [illegible]
KW   [illegible]
KW   [illegible]
KW   [illegible]
KW   [illegible]
KW   [illegible]
KW   [illegible]
XX
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```
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..917
FT                   /*tag= a
FT                   /product= "SGP050"
FT                   /note= "sequence coding for approximately another 154
FT                          amino acid residues in the corresponding protein
FT                          is not printed in the specification."
XX
PN   WO200192491-A2.
XX
PD   06-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US17305.
XX
PR   30-MAY-2000; 2000US-2 [illegible].
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman GD,  Whyte D,  Sudarsanam S,  Manning G,  Caenepeel S;
PI   Martinez R,  Hill RJ,  Flanagan P;
XX
DR   WPI; 2002-114840/15.
DR   P-PSDB; ABB67564.
XX
PT   New phosphatase polypeptides for treating e.g., cancers, immune-related
PT   disorders and disorders, cardiovascular diseases, or brain or
PT   neuronal-associated diseases
XX
PS   Claim 28; Fig 1A; 161pp; English.
XX
CC   The invention relates to human protein phosphatase polypeptides and
CC   polynucleotides. The phosphatase polypeptides are useful for diagnosing
CC   and treating various phosphatase-related diseases and conditions, such as
CC   cancers, immune-related diseases and disorders, cardiovascular diseases
CC   (e.g., reperfusion restenosis), brain or neuronal-associated diseases,
CC   metabolic disorders (e.g., diabetes or obesity), central or peripheral
CC   nervous system diseases and conditions (e.g., pain, migraine, mood
CC   disorders, hypotension, or hypertension), psychotic and neurological
CC   disorders (e.g., anxiety, schizophrenia), neurodegenerative diseases
CC   (e.g., Alzheimer's or Parkinson's disease), infections caused by viral
CC   (e.g., human immunodeficiency virus (HIV)), bacterial, fungal or prion
CC   agents, ocular diseases, macular degeneration, and inflammatory disorders
CC   (e.g., rheumatoid arthritis, multiple sclerosis, osteoarthritis). The
CC   polypeptides may also be used for screening for small molecule compounds
CC   that inhibit the catalytic activity of the encoded protein phosphatase
CC   with potential use for treating the above mentioned diseases, for
CC   generating antibodies or hybridomas, and as a diagnostic tool for
CC   detecting a disease or disorder. Genetic sequences of phosphatases are
CC   useful in gene therapy. The present sequence represents a cDNA encoding
CC   a novel human serine threonine phosphatase (STP)-like phosphatase
CC   polypeptide SGP050.
XX
SQ   Sequence 917 BP; 161 A; 276 C; 310 G; 170 T; 0 other;

  Query Match             [illegible].4%;  Score 917;  DB 21;  Length 917;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-203;
  Matches  917;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 [illegible] 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCGCCGGCTGGTTCCGGCGCCGCTTCCTGCCTGGGGAGCCGCTGCCGCCGCCGCGG 60

Qy         61 [illegible] 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CGGCCTGGCCCCCATGCCAGCCCCCTCCCCTACCCACGCCCCCGCCTCCTTCCCCGCTCC 120

Qy        121 [illegible] 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGCTCCAGCCCCGGGCCGGCCGACGCCTCGGCCGCCCAGACTCCCGGCCCGTGCGGCAGC 180

Qy        181 [illegible] 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 [illegible] 240

Qy        241 [illegible] 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 [illegible] 300

Qy        301 [illegible] 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 [illegible] 360

Qy        361 [illegible] 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 [illegible] 420

Qy        421 [illegible] 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 [illegible] 480

Qy        481 [illegible] 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 [illegible] 540

Qy        541 [illegible] 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 [illegible] 600

Qy        601 [illegible] 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 [illegible] 660

Qy        661 [illegible] 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 [illegible] 720

Qy        721 GTGCGGAGAGATGAGATACCGCCACTGAGCTTGAGTTCAGGCCAGAGACTGAGGGGCAG 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 [illegible] 780

Qy        781 [illegible] 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 [illegible] 840

Qy        841 [illegible] 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 [illegible] 900

Qy        901 CACATGAGTGGCTGGAG 917
              |||||||||||||||||
Db        901 CACATGAGTGGCTGGAG 917


RESULT 3
ABL79990
ID   ABL79990 standard; cDNA; 547 BP.
XX
AC   ABL79990;
XX
DT   17-MAY-2002  (first entry)
XX
DE   Human ovarian cancer related cDNA clone SEQ ID NO:2908.
XX
KW   Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200192581-A2.
XX
PD   06-DEC-2001.
XX
PF   29-MAY-2001; 2001WO-US17756.
XX
PR   29-MAY-2000; 2000US-2 [illegible].
```

```
XX
PA   (CORI-) CORIXA CORP.
XX
PI   Algate PA,  Harlocker SL,  Jones R;
XX
DR   WPI; 2002-122675/16.
XX
PT   Composition for therapy and diagnosis of ovarian cancer comprising
PT   polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
PT   polypeptide, antibody specific to polypeptide or T cell expressing
PT   polypeptide -
XX
PS   Claim 1; SEQ ID 2968; 489pp; English.
XX
CC   The present invention describes a composition (I) comprising: carriers
CC   and immunostimulants; and a polypeptide (II) of a ovarian tumour
CC   polypeptide encoded by a polynucleotide (III) having a cDNA sequence
CC   (S1) from the 10912 nucleotide sequences as given in ABL77023 to
CC   ABL87934, (III) encoding (II) having a sequence (S2), a T cell
CC   population of (II), or antigen presenting cells that express (II).
CC   (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC   (S1) can be used for detecting ovarian cancer in a patient's biological
CC   sample preferably serum or ovarian tissue. The method comprises
CC   contacting a biological sample from a patient with (IV), detecting the
CC   amount of polynucleotide hybridising to (IV) and comparing the amount to
CC   a predetermined cutoff value and thereby detecting ovarian cancer in the
CC   patient, where the amount of polynucleotide hybridising to (IV) is
CC   detected preferably by polymerase chain reaction (PCR). (I) comprising
CC   (III) and/or (II) is useful for stimulating and/or expanding T cells
CC   specific for an ovarian tumour protein comprising contacting T cells
CC   with (III) or (II). (III) is useful in design and preparation of
CC   ribozyme molecules for inhibiting expression of the tumour polypeptides
CC   and proteins in tumour cells; and to isolate a full length gene from a
CC   suitable library e.g., a tumour cDNA library using well known
CC   techniques.
XX
SQ   Sequence 547 BP; 123 A; 135 C; 171 G; 118 T; 0 other;

  Query Match             98.8%;  Score 536;  DB 24;  Length 547;
  Best Local Similarity   99.8%;  Pred. No. 4.8e-115;
  Matches  547;  Conservative    0;  Mismatches    0;  Indels    [illegible];  Gaps    [illegible];

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Db          1 [illegible] 60

Qy        852 [illegible] 911
              [illegible]
Db         61 [illegible] 120

Qy        912 [illegible] 971
              [illegible]
Db        121 [illegible] 180

Qy        972 [illegible] 1031
              [illegible]
Db        181 [illegible] 240

Qy       1032 [illegible] 1091
              [illegible]
Db        241 [illegible] 300

Qy       1092 [illegible] 1151
              [illegible]
Db        301 [illegible] 360

Qy       1152 [illegible] 1211
              [illegible]
Db        361 [illegible] 419

Qy       1212 [illegible] 1271
              [illegible]
Db        420 [illegible] 479

Qy       1272 [illegible]
              [illegible]
Db        480 [illegible]

Qy       [illegible] [illegible]

Db        540 [illegible] 547


RESULT [illegible]
ABK4[illegible]
ID   ABK4[illegible] standard; DNA; [illegible]
XX
AC   ABK4[illegible];
XX
DT   [illegible] JUN [illegible] (first entry)
XX
DE   DNA encoding human protein phosphatase [illegible] like (PE[illegible]
XX
KW   Protein phosphatase [illegible] antisense; [illegible]
KW   Acquired immunodeficiency virus; gene therapy; immunodeficiency; [illegible]
KW   neurodegenerative disease; Alzheimer's disease; Parkinson's disease;
KW   retinitis pigmentosa; amyotrophic lateral sclerosis; myelodysplasia;
KW   aplastic anaemia; ischaemic injury; myocardial infarction; stroke;
KW   reperfusion injury; toxin induced disease; cirrhosis; wasting [illegible]
KW   cachexia; viral infection; hepatitis; osteoporosis; cancer; diabetes;
KW   central nervous system disorder; CNS disorder; cardiovascular disorder;
KW   inflammatory disorder; [illegible] pulmonary [illegible]
KW   [illegible]
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   [illegible]
FT                   /*tag= [illegible]
FT                   /product= "[illegible]"
FT                   /note= "Protein phosphatase [illegible] like [illegible]
FT                          [illegible]"
FT   misc_binding    [illegible]
FT                   /*tag= [illegible]
FT                   /note= "Bound by the antisense oligonucleotide [illegible]
FT                          in ABK4[illegible]."
XX
PN   W[illegible]
XX
PD   [illegible] MAR 2002.
XX
PF   [illegible]
XX
PR   [illegible] AUG 2000; 2000US-[illegible]
PR   [illegible] APR 2001; [illegible]
XX
PA   (BAYE ) BAYER AG.
XX
PI   Xiao Y;
XX
DR   WPI; [illegible]
DR   P-PSDB; AA[illegible]
XX
PT   New protein phosphatase [illegible] like enzyme and [illegible]
PT   treating a disease associated with [illegible]
PT   [illegible]
PT   myelodysplasia, cancer, diabetes;
XX
PS   Claim [illegible]
XX
CC   The invention [illegible]
CC   protein phosphatase [illegible] like enzyme [illegible] (I) and [illegible]
CC   used [illegible]
CC   [illegible]
CC   [illegible]
CC   [illegible]
CC   disease or disorder associated with an increase in apoptosis such as AIDS
CC   or other infections or genetic immunodeficiencies, neurodegenerative
CC   diseases (e.g. Alzheimer's disease or Parkinson's disease, retinitis
CC   pigmentosa, or amyotrophic lateral sclerosis), myelodysplasia (e.g.
CC   aplastic anaemia), ischaemic injuries (e.g. myocardial infarction, stroke
CC   or reperfusion injury), toxin-induced diseases (e.g. alcohol induced
CC   liver damage or cirrhosis), wasting diseases (e.g. cachexia), viral
CC   infections (e.g. hepatitis B or C), and osteoporosis; or a decrease in
CC   apoptosis such as cancer, diabetes, CNS disorders, cardiovascular
CC   disorders, chronic obstructive pulmonary disease (COPD), and inflammatory
CC   disorders. Regulation of human PP1C-like enzyme can be used to treat
CC   disorders such as diabetes, CNS disorders, cardiovascular disorders,
CC   COPD, and cancers (e.g. leukaemia, lymphoma, or cancers of the organs).
CC   This sequence encodes the novel human protein phosphatase 1C-like enzyme
CC   described in the invention.
XX
SQ   Sequence 2518 BP; 587 A; 768 C; 755 G; 484 T; 6 other;

  Query Match             [illegible]%;  Score 264.8;  DB 24;  Length 2518;
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  537;  Conservative    0;  Mismatches  377;  Indels   16;  Gaps    8;

Qy        445 [illegible] 504
Db       [illegible] [illegible]

Qy        505 [illegible] 564
Db       [illegible] [illegible] 1487

Qy        565 [illegible] 624
Db       [illegible] [illegible] [illegible]

Qy        625 GCCTCAGG[illegible] 684
Db       [illegible] [illegible] [illegible]

Qy        685 TACA[illegible] 744
Db       [illegible] TA[illegible] [illegible]

Qy        745 C[illegible]GAGCTTGGAGTTCA[illegible] 804
Db       1668 ATGTCCGGGAGTTTA[illegible]GAGA[illegible]GAGCGCCAGCGTCTTCAG[illegible] 1727

Qy        805 TA[illegible]GAAGGGG 864
Db       1728 AAA[illegible] 1787

Qy        865 [illegible] 924
Db       1788 A[illegible]AAA 1847

Qy        925 [illegible] 984
Db       1848 AAGATCGAGCTGAAGGATCTCAGGTTTCCTCTGG[illegible]GGGGAGGGCAAAAAGGCTCGG 1907

Qy        985 TTACTACAA[illegible] 1044
Db       1908 GTGATGGCCACCATGGGGTGACCCGAGGCTTGGGAGACCACAGCCTTAAGGTCTGCAGT 1967

Qy       1045 A[illegible] 1104
Db       1968 [illegible] 2027

Qy       1105 [illegible] 1164
Db       2028 ACACAATATGA[illegible]AGATGATG[illegible]GGAT 2087

Qy       1165 GTA[illegible]AA 1221
Db       2088 [illegible] 2147

Qy       1222 [illegible] 127[illegible]
Db       2148 AA[illegible] 2207

Qy       128[illegible] --------A[illegible] 13[illegible]
Db       2208 [illegible]AAGCTGGGTTCGG[illegible] 2267

Qy       13[illegible] [illegible] 1359
Db       2268 [illegible]CAGG 2297


RESULT 5
AAT38484
ID   AAT38484 standard; cDNA; 4262 BP.
XX
AC   AAT38484;
XX
DT   16-JAN-1997  (first entry)
XX
DE   Rat petrin cDNA clone [illegible].
XX
KW   Petrin; neurite outgrowth associated protein; CNS;
KW   central nervous system; myelin; protein phosphatase 2C; stroke;
KW   neurodegeneration; gene therapy; ss.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   misc_difference 3825
FT                   /*tag=  a
FT                   /note= "base 3825 is given as b in the
FT                          specification"
XX
PN   WO9632476-A1.
XX
PD   17-OCT-1996.
XX
PF   12-APR-1996;   96WO-CA00214.
XX
PR   13-APR-1995;   95US-0421701.
XX
PA   (MOUN-) MOUNT SINAI HOSPITAL CORP.
XX
PI   Labes M,  Lozano A,  Roach A,  Roder J;
XX
DR   WPI; 1996-477127/47.
DR   P-PSDB; AAW48327.
XX
PT   Assay for substance that modulates response of neuronal cells - and
PT   neurite growth associated protein, Petrin, useful in conditions
PT   involving nerve damage resulting from traumatic injury, stroke or
PT   CNS degenerative disorders
XX
PS   Claim 2; Page 50-52; 115pp; English.
XX
CC   A cDNA sequence (AAT38484) codes for petrin (AAW48327), a protein
CC   involved in mediating neurite growth inhibition.  It was isolated
CC   from fragments of clone B2 (see also AAT38479-83) isolated from an
CC   adult rat brain cDNA library in lambda gt11 by screening with
CC   a monoclonal antibody that blocks the effect on neurons in culture
CC   of CNS myelin inhibitors.  The petrin gene is expressed in neurons
CC   in brain tissue, partic. in cerebellum Purkinje cells.  It can be
CC   used to produce petrin protein and to prepare probes.  Antisense
CC   sequences (see also AAT38485) can be used in gene therapy to enhance
CC   axonal regeneration.
XX
SQ   Sequence 4262 BP; 921 A; 1164 C; 1156 G; 1002 T; 19 other;

  Query Match             [illegible]%;  Score [illegible];  DB 17;  Length 4262;
  Best Local Similarity   [illegible]%;  Pred. No. [illegible];
  Matches  45[illegible];  Conservative    0;  Mismatches  [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy        498 [illegible]
Db        [illegible]

Qy        558 [illegible] 617
Db        898 [illegible]

Qy        618 [illegible]
Db        958 GAGGAGTGCATATAATATATCCGGTGGCTGCACAGCCTCATCGTGGTTTGCCTTCTGGG 1017

Qy        678 AAAG[illegible]
Db       1018 GAAG[illegible]

Qy        738 [illegible]
Db       [illegible]

Qy        798 [illegible] 857
Db       1138 GTTCATGCAGCCTCACTTGCTGGGAAATGAGTTCACACATTGGAGTTTCCAAGGAGAGT 1197

Qy        858 [illegible] 917
Db       1198 ACAGAGGAAAGAACTTGGGAAGAAGATGCTGTACTGGGACTTTAACATGA[illegible] 1257

Qy        918 CTACAAAGGTGTGGAGAAATGGGATTCAAGTA[illegible] 977
Db       1258 ATACAAAACCATTGAGGATGATGACTTGAAGTTTCCCCTTATATAT[illegible]AAGAA 1317

Qy        978 GGCTCGGTTACTAGGAACACTGGCTGTCTCCGGGGCCTGGGAGACCATCAGCTCAGAGT 1037
Db       1318 GGCCCGGGTAATGGCAACTATTGGATTGACAAGGGGACTTGGGGACCATGA[illegible]

Qy       1038 [illegible]
Db       1378 [illegible]

Qy       1098 [illegible]
Db       1438 [illegible]

Qy       1158 CTGGGATGTACTGGTCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTT[illegible] 1214
Db       1498 [illegible]

Qy       1215 GAACCAAGAGGACCCACACAGGTTCTCAAAGCTGGCCCAGATGCTGAT 1262
Db       1558 TGATCCAGATGACCCTCACAGGTACACACTGGCAGTCAGGACCTGGT 160[illegible]


RESULT 6
AAT38486
ID   AAT38486 standard; cDNA; 4515 BP.
XX
AC   AAT38486;
XX
DT   10-JAN-1997  (first entry)
XX
DE   Rat petrin cDNA.
XX
KW   Petrin; neurite outgrowth associated protein; CNS;
KW   central nervous system; myelin; protein phosphatase 2A; stroke;
KW   neurodegeneration; gene therapy; ss.
XX
OS   Rattus sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             36..1979
```

```
FT                   /*tag= a
FT                   /product= "petrin"
FT   misc_difference [illegible]
FT                   /*tag= b
FT                   /note= [illegible]
FT                   [illegible]"
XX
PN   W[illegible]-A1.
XX
PD   [illegible]
XX
PF   [illegible]
XX
PR   [illegible]
XX
PA   (M[illegible]) M[illegible]
XX
PI   Faber M, Lozano A, [illegible]
XX
DR   WPI; [illegible]
DR   P-PSDB; AAW[illegible]
XX
PT   Assay for substances that modulate response [illegible]
PT   neurite growth associated protein, petrin, useful in [illegible]
PT   involving nerve damage resulting from traumatic injury, [illegible]
PT   CNS degenerative disorders
XX
PS   Claim [illegible]
XX
CC   A nucleotide sequence (AAT38486) codes for petrin (AAW[illegible]
CC   [illegible]
CC   from an adult rat brain cDNA library in lambda [illegible]
CC   with probes based on partial petrin [illegible] (see also AAT[illegible]
CC   The human petrin locus was localised to chromosome [illegible]
CC   is expressed in neurons in brain tissue, particularly in cerebellar
CC   Purkinje cells. It can be used to produce petrin protein and to
CC   prepare probes. Antisense sequences (see also AAT[illegible]
CC   in gene therapy to enhance neural regeneration.
XX
SQ   Sequence 4515 BP; [illegible]

  Query Match [illegible]
  Best Local Similarity [illegible]
  Matches [illegible]

Qy        498 [illegible]
Db        [illegible]

Qy        558 [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]
```

```
Qy        918 [illegible] 977
Db       1511 ATACAAA[illegible] 1570

Qy        978 GGCTCGGTTACTAGGAACACTGGCTGTCTCCGGGGCCTGGGAGA[illegible]CATCAGCTCAGAGT 1037
Db       1571 GGTCGGCTAATGGCAACTATTGGAGTGACAAGGGAC[illegible]ATGACTGAAGGT 1630

Qy       1038 CCTGGAGCAAAATATTCAGTTCAAG[illegible]GTGACTGTGCT 1097
Db       1631 TCATGACTCCAACATCTACATAAAA[illegible]AGAGCTCAGAT[illegible]A 1690

Qy       1098 GGATGTGCACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCAT[illegible]AACTGATGGACT 1157
Db       1691 [illegible]AAATACTA[illegible]ATGGAT 1750

Qy       1158 [illegible] 1217
Db       1751 [illegible]AAATGAAGAAGTA[illegible]CTAACTG 1810

Qy       1218 [illegible]
Db       1811 [illegible] 1868

RESULT 7
AAS[illegible]
ID   AAS[illegible] standard; cDNA; 1617 BP.
XX
AC   AAS[illegible];
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #29444.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO[illegible]75[illegible]67-A2.
XX
PD   [illegible]-2001.
XX
PF   [illegible]-MAR-2001; 2001WO-[illegible].
XX
PR   [illegible]-MAR-2000; 2000US-[illegible]54[illegible]217.
PR   2[illegible]-AUG-2000; 2000US-[illegible]64[illegible]167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG2[illegible]45[illegible].
XX
PT   Nov[illegible] polynucleotide and [illegible]polypeptide, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity
XX
PS   Claim 1; SEQ ID NO 29444; [illegible]pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, [illegible], and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is used in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS[illegible] AAS[illegible] represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 1617 BP; 38[illegible] A; 442 C; 467 G; 325 T; 0 other;

  Query Match             17.[illegible]%;  Score 243.4;  DB 23;  Length 1617;
  Best Local Similarity   [illegible]%;  Pred. No. [illegible]e-47;
  Matches  472;  Conservative    [illegible];  Mismatches  [illegible]26;  Indels  [illegible];  Gaps  [illegible];

Qy        500 [illegible]GAAAAGGG[illegible]ATCA[illegible] 559
Db        [illegible] 

Qy        560 [illegible]GAATTGATGAG[illegible] 619
Db        791 TGG[illegible]AT[illegible]AAA[illegible]AT[illegible]AAAGAAA[illegible]ATAGATAAA[illegible]A 850

Qy        620 TGGAG[illegible]AGA[illegible]ACAG[illegible]GGTGGCTG[illegible]AA 679
Db        851 GGAGTTTATATAATATAT[illegible]ATTGTGATTT[illegible]A 910

Qy        680 [illegible] 739
Db        911 AGCTGTATGTTGCAAATGCTGGGATAGCAGGGCCATAATCATCAGAAATGGAGAAATTA 970

Qy        740 GGCCACTGAGCTTCGAGTTCACCCAGAGACTGAGCGGCAGCGGATCCAGCAGCTGG[illegible] 799
Db        971 [illegible]ATGTCTTCAGAATTTAC[illegible]GAGACGGAGCGCCAGCGACTTCAGTAC[illegible]AT 1030

Qy        800 TTGTCTAT[illegible]TGAG[illegible]GTGAGTTCACCGACTGGAGTTC[illegible]A 859
Db       1031 [illegible]TGCACTTT[illegible] 1090

Qy        860 AGGGGATGA[illegible]GGA[illegible]AGAA[illegible]TCA[illegible]GATCACTACATGAG[illegible]A[illegible] 919
Db       1091 [illegible]AATATCA[illegible] 1150

Qy        920 ACAAA[illegible] 979
Db       1151 ACAAAA[illegible]AAGAAT[illegible] 1210

Qy        980 TCGGTTACTAGGAACACT[illegible]GGAGACCATCA[illegible] 1039
Db       1211 [illegible] 1270

Qy       1040 TGGACAGAAA[illegible]TGTGCCACAG[illegible] 1099
Db       1271 [illegible] 1330

Qy       1100 ATGTGGACTAG[illegible]GATGATGTGGTTGTCATGGTAACTGA[illegible] 11[illegible]
Db       1331 [illegible]GATCTTGGTACTTA[illegible] 13[illegible]

Qy       11[illegible] GGGATGTA[illegible]ATGGTGGTGCGGAGCTT[illegible]A 12[illegible]
Db       13[illegible] [illegible]AAATCAGTTT[illegible]AA[illegible]

Qy       1217 [illegible]ATA[illegible]A[illegible] 12[illegible]
Db       1451 [illegible] 

Qy       1277 G 1277
              |
Db       1511 G 1511
```

```
RESULT 8
AAI58166
ID   AAI58166 standard; cDNA; 1887 BP.
XX
AC   AAI58166;
XX
DT   22-OCT-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 369.
XX
KW   Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW   peripheral nervous system; neuropathy; central nervous system; CNS;
KW   Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW   amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW   chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW   leukaemia; ss.
XX
OS   Homo sapiens.
XX
PN   WO200153312-A1.
XX
PD   26-JUL-2001.
XX
PF   26-DEC-2000; 2000WO-US34263.
XX
PR   21-JAN-2000; 2000US-0488725.
PR   25-APR-2000; 2000US-0552317.
PR   09-JUN-2000; 2000US-0598042.
PR   19-JUL-2000; 2000US-0620312.
PR   03-AUG-2000; 2000US-0653450.
PR   14-SEP-2000; 2000US-0662191.
PR   16-OCT-2000; 2000US-0689836.
PR   29-NOV-2000; 2000US-0727344.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Asundi V,  Chen R,  Ma Y,  Qian XB,  Ren F,  Wang D;
PI   Wang J,  Wang Z,  Wehrman T,  Xu C,  Xue AJ,  Yang Y,  Zhang J;
PI   Zhao QA,  Zhou P,  Goodrich R,  Drmanac RT;
XX
DR   WPI; 2001-442253/47.
DR   P-PSDB; AAM39010.
XX
PT   Novel nucleic acids and polypeptides, useful for treating disorders
PT   such as central nervous system injuries -
XX
PS   Claim 1; SEQ ID NO 369; 1067pp; English.
XX
CC   The invention relates to human nucleic acids (AAI57796-AAI61099) and
CC   the encoded polypeptides (AAM38642-AAM42215) with nootropic,
CC   immunosuppressant and cytostatic activity. The polynucleotides are useful
CC   in gene therapy. A composition containing a polypeptide or polynucleotide
CC   of the invention may be used to treat diseases of the peripheral nervous
CC   system, such as peripheral nervous injuries, peripheral neuropathy and
CC   localised neuropathies and central nervous system diseases, such as
CC   Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC   lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC   utilisation of the activities such as: immune system suppression,
CC   activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC   assays for receptor activity, arthritis and inflammation, leukaemias and
CC   C.N.S disorders.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification.
XX
SQ   Sequence 1887 BP; 461 A; 482 C; 543 G; 401 T; 0 other;

  Query Match             [illegible];  Score 213.4;  DB 22;  Length 1887;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches  452;  Conservative    0;  Mismatches  [illegible];  Indels  [illegible];  Gaps    [illegible];
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```
Qy        [illegible]

Db        677 [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible]

Db        857 [illegible]

Qy        740 [illegible]

Db        917 [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible]

Db        1217 [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible]

Db        [illegible]

Qy        [illegible]

Db        [illegible]

Qy       1277 G 1277

Db       1457 G 1457


RESULT 9
ABK4[illegible]
ID   ABK4[illegible] standard; cDNA; [illegible]
XX
AC   ABK4[illegible]
XX
DT   [illegible]-JUN-2002  (first entry)
XX
DE   cDNA encoding colon tumour protein Seq ID No [illegible]14
XX
KW   Human; [illegible]
KW   [illegible]
XX
OS   Homo sapiens.
XX
PN   W[illegible] A[illegible]
```

```
XX
PD   14-FEB-2002.
XX
PF   [illegible] 2001; 2001W [illegible]24214.
XX
PR   03-APR 2000; 2000GB [illegible]
PR   28-MAR 2001; 2001US 279763P.
PR   2? JUN 2001; 2001US [illegible]
XX
PA   [illegible] BIXA [illegible]
XX
PI   King JE,  Meagher MJ,  Xu J,  [illegible] H;
XX
DR   WPI; 2002 241789/29.
XX
PT   New [illegible] cancer polypeptides and polynucleotides, useful as vaccines,
PT   for diagnosing, preventing, and treating colon cancer, and as markers
PT   for the progression of cancer -
XX
PS   Claim 1; SEQ ID No 1714; 117pp; English.
XX
CC   The invention relates to polynucleotides encoding colon tumour proteins.
CC   The polynucleotides and encoded polypeptides are useful in pharmaceutical
CC   compositions, such as vaccines, for the diagnosis, prevention, and
CC   treatment of colon cancer. Polynucleotide sequences may be used as
CC   hybridisation probes or primers, and in the design and preparation of
CC   ribozyme molecules for inhibiting expression of tumour polypeptides and
CC   proteins in tumour cells. The compositions are useful for stimulating an
CC   immune response against cancer, particularly for the immunotherapy of
CC   colon cancer, and as markers for the progression of cancer.
CC   ABK41150-ABK46247 represent coding sequences of human colon tumour
CC   proteins of the invention.
CC   Note: With the exception of SEQ ID No 1 and 2, the sequence data
CC   for this patent did not form part of the printed specification but was
CC   supplied by the European Patent Office.
XX
SQ   Sequence 5791 BP; 1436 A; 1312 C; 1395 G; 1648 T; 0 other;

  Query Match             17.6%;  Score 243.4;  DB 24;  Length 5791;
  Best Local Similarity   57.9%;  Pred. No. 9.2e-47;
  Matches  452;  Conservative    0;  Mismatches  326;  Indels    3;  Gaps    1;

Qy        500 [illegible] 559
Db        401 [illegible] 460

Qy        560 [illegible] 619
Db        461 [illegible] 520

Qy        620 [illegible] 679
Db        521 [illegible] 580

Qy        680 [illegible] 739
Db        581 [illegible] 640

Qy        740 [illegible] 799
Db        641 [illegible] 700

Qy        800 [illegible] 859
Db        701 [illegible] 760

Qy        860 [illegible] 919
Db        761 [illegible] 820

Qy        920 [illegible] 979
Db        821 [illegible] 880

Qy        [illegible]
Db        881 [illegible]

Qy       1040 [illegible] 1099
Db        941 [illegible]

Qy       1100 [illegible]
Db       1001 [illegible] 1060

Qy       1160 [illegible]
Db       1061 [illegible]

Qy       1217 [illegible]
Db       1121 [illegible] 1180

Qy       1277 G 1277
Db       1181 G 1181


RESULT 10
AAH17958
ID   AAH17958 standard; cDNA; [illegible] BP.
XX
AC   AAH17958;
XX
DT   26 JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:17737.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29 JUL-1999;    99JP-0248036.
PR   27-AUG-1999;    99JP-[illegible]
PR   11 JAN-2000; 2000JP-0118776.
PR   02 MAY-2000; 2000JP-[illegible]
PR   09 JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   [illegible],  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001 [illegible]745/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the [illegible]
PT   full length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 8; SEQ ID 17737; 2537pp; [illegible]; English.
XX
CC   The present invention describes primer sets for synthesis of [illegible]
CC   full length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5' end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3' end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the [illegible]
CC   the 5' end sequence/3' end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full length cDNAs. The primers allow obtaining of the full length
CC   cDNAs easily without any specialised methods. AAH[illegible] to AAH15628 and
CC   AAH15633 to AAH18742 represent human cDNA sequences; AAB[illegible] to
CC   AAB[illegible] represent human amino acid sequences, and AAH[illegible] to AAH[illegible]
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 1903 BP; 441 A; [illegible] C; 578 G; 361 T; [illegible] other;

  Query Match             17.6%;  Score 242.4;  DB 22;  Length 1903;
  Best Local Similarity   58.2%;  Pred. No. [illegible];
  Matches  445;  Conservative    0;  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy        500 [illegible] 559
Db        870 [illegible] 42[illegible]

Qy        560 [illegible] 619
Db        9[illegible] [illegible]

Qy        620 [illegible] 67[illegible]
Db        990 [illegible] 104[illegible]

Qy        680 AGCTGTACATGGCCAATGCTGGGGATAGCAGGGCTATCT[illegible] 7[illegible]
Db       1050 AGCTGTATGTTGCAAATGCTGGGGATAGCAGGGCTATAATCATCAGAAATGGAGAAATTA 110[illegible]

Qy        740 [illegible] 79[illegible]
Db       1110 [illegible] 116[illegible]

Qy        800 [illegible] 8[illegible]
Db       1170 [illegible] 122[illegible]

Qy        860 [illegible] 919
Db       1230 [illegible] 12[illegible]

Qy        920 [illegible] 9[illegible]
Db       1290 [illegible] 134[illegible]

Qy        980 [illegible] 10[illegible]
Db       13[illegible] [illegible] 14[illegible]

Qy       1040 [illegible] 1099
Db       1410 [illegible] 14[illegible]

Qy       1100 [illegible]
Db       1470 ATCTTTCAAAATATGATCATGGATCAGATGATGTGCTGATCTTGGCCACTGATGGACTCT 15[illegible]

Qy       1160 [illegible] 12[illegible]
Db       1530 [illegible] 1[illegible]

Qy       1217 [illegible] 1260
Db       1590 [illegible] 1633
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```
RESULT [illegible]
AAI[illegible]
ID   AAI[illegible] standard; cDNA; [illegible] BP.
XX
AC   AAI[illegible];
XX
DT   [illegible] JAN [illegible]  (first entry)
XX
DE   Rat petrin cDNA clone [illegible].
XX
KW   [illegible]
KW   [illegible]
KW   [illegible]
XX
OS   Rattus sp.
XX
PN   WO[illegible]-A1.
XX
PD   [illegible]
XX
PF   [illegible] APR [illegible]
XX
PR   [illegible] APR [illegible]
XX
PA   [illegible]
XX
PI   [illegible]
XX
DR   WPI; [illegible]
XX
PT   [illegible]
PT   [illegible]
PT   [illegible]
PT   CNS degenerative disorders
XX
PS   Claim 2; Page 49; 11pp; English.
XX
CC   A cDNA clone (AAI[illegible]), designated [illegible], is a fragment [illegible]
CC   [illegible] (see also AAI[illegible] and AAI[illegible]) that codes for petrin (AAW[illegible]),
CC   a protein [illegible]
CC   [illegible]
CC   [illegible]
CC   [illegible]
CC   The gene is expressed in neurons in brain tissue, particularly
CC   cerebellum Purkinje cells. It can be used to produce petrin
CC   protein and to prepare probes. Antisense sequences (see [illegible]
CC   AAI[illegible]) can be used in gene therapy to enhance [illegible]
XX
SQ   Sequence [illegible]

  Query Match  [illegible]
  Best Local Similarity  [illegible]
  Matches  [illegible]  Conservative  [illegible]  Mismatches  [illegible]  Indels  [illegible]  Gaps  [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        874 [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
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Db    267 [illegible] 326

Qy   1054 [illegible]

Db    327 [illegible]

Qy   1114 [illegible]

Db    387 [illegible]

Qy   1174 [illegible] 1187

Db    447 [illegible]


RESULT 12
AAA[illegible]
ID   AAA[illegible] standard; cDNA; [illegible] BP.
XX
AC   AAA[illegible];
XX
DT   19-MAY-2000  (first entry)
XX
DE   Human colon cancer cell line polynucleotide sequence SEQ ID NO:2302.
XX
KW   Human; colon cancer; tumour; diagnosis; gene expression product;
KW   probe; detection; cancerous state; metastasis; [illegible];
KW   breast cancer; oestrogen receptor-positive breast cancer; therapy;
KW   oestrogen receptor negative breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   W[illegible] A2.
XX
PD   18-NOV-[illegible].
XX
PF   1[illegible] MAY [illegible];   [illegible]W[illegible].
XX
PR   14-MAY-1998;   98US-[illegible].
PR   15-MAY-1998;   98US-[illegible].
PR   15-MAY-[illegible];   [illegible].
PR   21-OCT-1998;   98US-0105231.
PR   27-OCT-1998;   98US-0105877.
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE ) HYSEQ INC.
XX
PI   Williams LT,  Escobedo J,  Innis MA,  Garcia PD,  Sudduth-Klinger J;
PI   Reinhard C,  Giese K,  Randazzo F,  Kennedy [illegible],  Pot D,  Kassam A;
PI   Lamson G,  Drmanac R,  Crkvenjakov R,  Dickson M,  Drmanac S,  Labat I;
PI   Leshkowitz D,  Kita D,  Garcia V,  Jones LW,  Stache-Crain B;
XX
DR   WPI; [illegible]/[illegible].
XX
PT   Polynucleotide library used to determine cancerous states of mammalian
PT   cells
XX
PS   Claim 1; Page [illegible]; [illegible]pp; English.
XX
CC   AAA[illegible] to AAA[illegible] represent polynucleotides isolated from cDNA
CC   libraries constructed from human colon cancer cell lines. The present
CC   invention also describes a method of detecting differentially expressed
CC   genes correlated with a cancerous state of a mammalian cell, comprising
CC   detecting at least one differentially expressed gene product in a test
CC   sample derived from a cell suspected of being cancerous, where detection
CC   of the differentially expressed gene product is correlated with a
CC   cancerous state of the cell from which the test sample was derived.
CC   The polynucleotides sequences can be used in a method for detecting
CC   differentially expressed genes correlated with a cancerous state of a
CC   mammalian cell. The polynucleotides can also be used as probes for
CC   detecting and mapping related genes. They can be used in diagnosis and
CC   prognosis of diseases and disorders (e.g. identification of
CC   pre-metastatic or metastatic cancerous states, stages of [illegible]
CC   responsiveness of cancer to therapy). This is particularly for breast
CC   cancer, oestrogen receptor-positive breast cancer, oestrogen receptor
CC   negative breast cancer, lung cancer, and colon cancer.
XX
SQ   Sequence [illegible] BP; [illegible] A; [illegible] C; [illegible] G; [illegible] T; 5 other;

  Query Match             [illegible]%;  Score [illegible].2;  DB 21;  Length [illegible];
  Best Local Similarity   55.[illegible]%;  Pred. No. 8.2e-16;
  Matches  [illegible];  Conservative  [illegible];  Mismatches  20[illegible];  Indels  [illegible];  Gaps  [illegible];

Qy    [illegible] [illegible]

Db     27 [illegible] 84

Qy    951 [illegible]

Db     85 [illegible] 144

Qy   1011 [illegible]

Db    145 [illegible] 204

Qy   1071 [illegible] 1130

Db    205 [illegible]CCTGAGGTACGACTGTATGACCTGACACAATATGAGCACTGCCCAGATGA 264

Qy   1131 [illegible] 1190

Db    265 [illegible]ACTCACTGTGAGGTA[illegible] 324

Qy   1191 [illegible]---[illegible] 1247

Db    325 [illegible] 384

Qy   1248 [illegible]

Db    385 [illegible]

Qy   1296 [illegible]

Db    447 [illegible]

Qy   1356 GGGC 1359

Db    505 AGGC 508


RESULT 13
AAZ12841
ID   AAZ12841 standard; cDNA; [illegible] BP.
XX
AC   AAZ12841;
XX
DT   12-[illegible]  (first entry)
XX
DE   Human gene expression product cDNA sequence SEQ ID NO:[illegible].
XX
KW   Human; gene; gene expression product; diagnosis; therapy; probe;
KW   detection; mapping; tissue typing; profiling; forensic; cancer;
KW   genetic analysis; colorectal cancer; breast cancer; lung cancer; ss.
XX
OS   Homo sapiens.
XX
PN   W[illegible] A2.
XX
PD   05-AUG-[illegible].
XX
PF   28-JAN-[illegible];   [illegible]W[illegible]US[illegible].
XX
PR   [illegible]-APR-[illegible];   98US-[illegible].
PR   28-JAN-1998;   98US-[illegible].
PR   24-FEB-1998;   98US-0075954.
```

```
PF   31-MAR-1998;   98US-0080111.
PF   03-APR-1998;   98US-[illegible].
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Crkvenjakov R,  [illegible] M,  Drmanac R,  Drmanac S;
PI   Escobedo J,  Garcia PD,  Garcia V,  Giese K,  Innis MA;
PI   Jones WL,  Kassam A,  Kennedy GC,  Kita D,  Labat I;
PI   Lamson G,  Leshkowitz D,  Pot D,  Randazzo F,  Reinhard C;
PI   Stache-Crain B,  Sudduth-Klinger J,  Williams LT;
XX
DR   WPI; 1999-494092/41.
XX
PT   Novel human genes and their expression products which are
PT   differentially expressed in different cell types
XX
PS   Claim 1; Page 732-733; 24[illegible]pp; English.
XX
CC   The present invention describes a library of human polynucleotides
CC   comprising the sequences given in AAZ12532 to AAZ17779. Also described is
CC   a method of detecting differentially expressed genes correlated with the
CC   cancerous state of a mammalian cell, comprising detecting at least one
CC   differentially expressed gene product in a test sample from a cell
CC   suspected of being cancerous, where the gene product is encoded by one
CC   of the 5248 polynucleotide sequences given in AAZ12532 to AAZ17779. The
CC   polynucleotides can be used as a source of primers and probes, which can
CC   be used for a variety of purpose, e.g. detection of expression levels,
CC   mapping, tissue typing or profiling, forensics, genetic analysis and
CC   detection of polymorphisms. Polypeptides encoded by the polynucleotides
CC   can be used for raising antibodies for experimental, diagnostic and
CC   therapeutic purposes. The polynucleotides may also be used to construct
CC   arrays for diagnostics (which may be used to determine function of an
CC   encoded protein); and to detect differences in expression levels between
CC   two cells (e.g. to identify abnormal or diseased tissue in a human, to
CC   identify a genetic predisposition or susceptibility to a disease such as
CC   cancer). The polynucleotides of the invention are especially used in the
CC   diagnosis, prognosis and management of colorectal cancer, breast cancer,
CC   and lung cancer. The polynucleotides can also be used to screen for
CC   peptide analogues and antagonists.
XX
SQ   Sequence 300 BP; 66 A; 78 C; 91 G; 65 T; 0 other;

  Query Match             7.5%;  Score 103;  DB 20;  Length 300;
  Best Local Similarity   59.3%;  Pred. No. 1.8e-11;
  Matches  175;  Conservative    0;  Mismatches  120;  Indels    0;  Gaps    0;

Qy      893 GGGATCACCACATGA[illegible]GGAGCTACAAACG[illegible]GAGAAA[illegible] 952

Db        1 GGGACCAGAACATGA[illegible]TGGGCCTACAAAAACATCGAGCTGGAGGATCTCAGGTTTC 60

Qy      953 CACTGATCCATGGACAGGGTAGGCAGGCTCGGTTACTAGGAACAC[illegible] 1012

Db       61 CTCTGGTCTGTGGGA[illegible]AAAAAGG[illegible] 120

Qy     1013 [illegible]

Db      121 [illegible] 180

Qy     1073 [illegible]

Db      181 [illegible] 240

Qy     1133 [illegible] 1187

Db      241 [illegible]


RESULT 14
AAX98054
ID   AAX98054 standard; cDNA; [illegible] BP.
XX
AC   AAX98054.
```

```
XX
DT   [illegible] (first entry)
XX
DE   [illegible] cDNA #[illegible]
XX
KW   Cancer; human; [illegible]; breast; [illegible]; transmembrane receptor; [illegible]
KW   [illegible] aspartyl protease; GATA family; [illegible]
KW   transcription factor; G protein alpha subunit; protein phosphatase;
KW   phosphodiester binding protein; diacylglycerol binding protein; trypsin;
KW   protein kinase; tyrosine phosphatase; developmental [illegible] protein;
KW   WW/Rsp5/WWP domain; therapy; forensic; genetic mapping; [illegible]
KW   detection; treatment; cervical; melanoma; colorectal adenocarcinoma;
KW   Wilm's tumour; retinoblastoma; sarcoma; myosarcoma; [illegible]
KW   leukemia; lymphoma; dysplasia; hyperplasia; endometriosis; [illegible]
KW   prostate; ss.
XX
OS   Homo sapiens.
XX
PN   W[illegible]-A2.
XX
PD   [illegible]
XX
PF   [illegible]
XX
PR   [illegible]
PR   [illegible]
PR   [illegible] APR [illegible]
PR   [illegible]
PR   [illegible]
XX
PA   (CHIR ) CHIRON CORP.
PA   (HYSE-) HYSEQ INC.
XX
PI   Crkvenjakov R,  Dickson M,  Drmanac R,  Drmanac S;
PI   Escobedo J,  Garcia PD,  Garcia V,  Giese K,  Innis MA;
PI   Jones LW,  Kassam A,  Kennedy GC,  Kita D,  Labat I;
PI   Lamson G,  Leshkowitz D,  Pot D,  Randazzo F,  Reinhard C;
PI   Stache-Crain B,  Sudduth-Klinger J,  Williams LT.
XX
DR   WPI; [illegible]/[illegible].
XX
PT   New isolated human polynucleotide.
XX
PS   Claim 1; Page [illegible]; [illegible]pp; English.
XX
CC   This invention describes novel isolated human polynucleotides [illegible]
CC   by screening for differential expression in [illegible] cancer, breast cancer
CC   and lung cancer cell lines. The polynucleotides of the invention are
CC   represented in AAX9[illegible] to AAX9[illegible] and encode polypeptides of protein
CC   families selected from 4 transmembrane segment integral membrane
CC   proteins, 7 transmembrane receptors, ATPases associated with various
CC   cellular activities (AAA), eukaryotic aspartyl proteases, GATA family of
CC   transcription factors, G protein alpha subunit, phosphodiesterase [illegible]
CC   diacylglycerol binding proteins, protein kinase, protein phosphatase [illegible]
CC   protein tyrosine phosphatase, trypsin, wnt family [illegible]
CC   [illegible] and WW/Rsp5/WWP domain containing proteins. The
CC   encoded polypeptides may have a functional domain [illegible]
CC   repeat, basic region plus leucine zipper transcription factor,
CC   bromodomain, EF hand, SH3 domain, WD domain/G beta repeats [illegible]
CC   ([illegible] type), zinc finger ([illegible] class), and zinc binding [illegible]
CC   domains. The polynucleotides encode polypeptides with [illegible] known
CC   protein families and are predicted to have similar properties. [illegible]
CC   polynucleotides can be used [illegible]
CC   [illegible]
CC   [illegible]
CC   [illegible]
CC   cancers, melanoma, [illegible] Wilm's [illegible]
CC   retinoblastoma, [illegible] leukemia [illegible]
CC   myelogenous leukemia, promyelocytic leukemia, monocytic leukemia and
CC   myeloid leukemia, and lymphomas such as [illegible] lymphoma [illegible]
CC   [illegible]
CC   epithelial dysplasia [illegible]
CC   mammary dysplasia, hyperplasia [illegible]
CC   prostate or thyroid hyperplasias or pseudoepitheliomatous hyperplasia of
CC   the skin.
XX
SQ   Sequence 750 BP; 170 A; 203 C; 182 G; 180 T; 15 other;

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length 750;
  Best Local Similarity   [illegible]%;  Pred. No. 2.5e-14;
  Matches  257;  Conservative    0;  Mismatches  199;  Indels   16;  Gaps    2;

Qy     [illegible]
Db      58 AGGACGGCTGGGCCTACAAAAAGATCGAGCTGGAGGA[illegible] 117

Qy     [illegible] GGACAGGGTAGGCAGG[illegible]
Db     118 GGGGAGGGCAAAAA[illegible] 177

Qy     [illegible]
Db     178 [illegible] 237

Qy     [illegible]
Db     238 GAGGTACGAG[illegible] 297

Qy     [illegible]
Db     298 GGAA[illegible] 357

Qy     [illegible]
Db     358 [illegible] 417

Qy     [illegible] GATATACAGCACACATTAA [illegible]
Db     418 GGTCCTGGGGGCCGGGGTA[illegible]

Qy     [illegible] GGTGTCCTACGATCA[illegible]
Db     478 GGGTTCGGGGATGACATT[illegible] 529


RESULT 15
ABL25549
ID   ABL25549 standard; DNA; 2087 BP.
XX
AC   ABL25549;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster genomic polynucleotide SEQ ID No 28120.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ds.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   [illegible]-2000; 2000US-[illegible].
XX
PA   (PEKE-) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWL,  Myers EW;
XX
DR   WPI; 2001-656860/75.
XX
PT   New isolated nucleic acid detection reagent for detecting 1006 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID No 28120; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1006 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01640-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2087 BP; 517 A; [illegible] C; [illegible] G; 461 T; 0 other;

  Query Match             [illegible];  Score [illegible];  DB 23;  Length 2087;
  Best Local Similarity   50.5%;  Pred. No. 7.9e-14;
  Matches  28[illegible];  Conservative  [illegible];  Mismatches  253;  Indels  [illegible];  Gaps  [illegible];

Qy     741 [illegible] 800
Db    1112 [illegible] 1171

Qy     801 [illegible] 860
Db    1172 [illegible] 1231

Qy     861 [illegible] 920
Db    1232 [illegible] 1291

Qy     921 [illegible] 980
Db    1292 [illegible] 1351

Qy     981 [illegible] 1040
Db    1352 [illegible] 1411

Qy    1041 GGACACAAACA[illegible] 1100
Db    1412 [illegible] 1471

Qy    1101 TGTGGACTAGTGGAGTATATTATGATGA---------------- [illegible] 1136
Db    1472 [illegible] 1531

Qy    1137 TGTATGGTAATTGAT[illegible] 1196
Db    1532 [illegible] 1591

Qy    1197 GGGGAGCT[illegible] 1256
Db    1592 [illegible] 1651

Qy    1257 GCTGATATACATAGCACACATAGGAAA 1280
Db    1652 [illegible] 1675


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              Copyright (c) 1993 - 2003 Compugen Ltd.

 OM nucleic - nucleic search, using sw model

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Searched:      441362 seqs, [illegible] residues

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Post-processing: Minimum Match 0%
                 Maximum Match 100%
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                 5: [illegible]
                 6: [illegible]

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed
     and is derived by analysis of the total score distribution.

                            SUMMARIES

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Result              Query
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c    2     49.8      3.6    6924  4  US-09-299-141-9              Sequence 9, Appli
c    3     49.8      3.6    6924  4  US-09-299-141-10             Sequence 10, Appl
c    4     49.8      3.6    6924  4  US-09-299-141-11             Sequence 11, Appl
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c    6     48.2      3.5  [illegible] 4 US-09-288-292A-45         Sequence 45, Appl
     7       47      3.4  [illegible] 4 US-09-198-119C-94         Sequence 94, Appl
c    8     46.4      3.4     774  [illegible] US-08-115-655-11    Sequence 11, Appl
c    9     45.2      3.3  [illegible] 4 US-09-535-008-30          Sequence 30, Appl
    10  [illegible]  3.2  [illegible]  US-09-126-155-[illegible]  Sequence 16, Appl
c   11     43.4      3.1  [illegible] 4 US-09-096-776B-[illegible] Sequence 3, Appli
c   12     43.4      3.1  [illegible] 4 US-09-096-776B-1          Sequence 1, Appli
c   13     43.2      3.1    3946  [illegible] US-09-083-351-1     Sequence 1, Appli
c   14     43.2      3.1  [illegible] 4 US-09-083-352-1           Sequence 1, Appli
c   15       43      3.1  [illegible] 4 US-08-118-[illegible]-1   Sequence 1, Appli
c   16       43      3.1  [illegible] 4 US-08-456-745-1           Sequence 1, Appli
    17     42.8      3.1    8460  1  US-08-469-005A-9             Sequence 9, Appli
    18     42.8      3.1  [illegible] 4 US-09-261-937-1           Sequence 1, Appli
c   19     42.4      3.1  [illegible] 4 US-09-165-264-7           Sequence 7, Appli
c   20     42.4      3.1  [illegible] 1 US-09-165-264-13          Sequence 13, Appl
c   21     41.4      3.1  [illegible] 4 US-09-165-264-8           Sequence 8, Appli
    22     41.4      3.0  [illegible] 2 US-08-475-844-4           Sequence 4, Appli
    23     41.4      3.0    1252  5  PCT-US95-08429-4             Sequence 4, Appli
    24     41.2      3.0    1413  4  US-08-984-709A-52            Sequence 52, Appl
    25     41.2      3.0    6453  1  US-08-306-691B-14            Sequence 14, Appl
    26     41.2      3.0    6453  [illegible] US-09-209-668-10    Sequence 10, Appl
    27     41.2      3.0    6453  [illegible] US-09-[illegible]-952-8 Sequence 8, Appli
    28     41.2      3.0  [illegible] 1 US-08-458-568A-11         Sequence 11, Appl
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c   30     40.8      3.0    4523  4  US-09-473-716-1              Sequence 1, Appli
c   31     40.4      2.9  [illegible] 4 US-09-423-800-11          Sequence 11, Appl
c   32     40.2      2.9  [illegible]  [illegible]                Sequence 1, Appli
c   33       40      2.9    1413  4  US-08-984-709A-52            Sequence 52, Appl
c   34     39.8      2.9     320  4  US-09-165-264-11             Sequence 11, Appl
c   35     39.6      2.9    7218  1  US-08-232-463-14             Sequence 14, Appl
c   36     39.4      2.9  [illegible] 4 [illegible]-7             Sequence 7, Appli
c   37     39.4      2.9  [illegible] 1 US-08-673-884C-7          Sequence 7, Appli
c   38     39.4      2.9  [illegible] 1 US-08-294-359A-7          Sequence 7, Appli
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c   40     39.4      2.9    2502  1  US-08-481-238-7              Sequence 7, Appli
c   41     39.4      2.9  [illegible] 2 US-08-471-[illegible]-7   Sequence 7, Appli
c   42     39.4      2.9  [illegible] 2 US-08-484-[illegible]-7   Sequence 7, Appli
c   43     39.4      2.9  [illegible] 2 US-08-75[illegible]-7     Sequence 7, Appli
c   44     39.4      2.9    2502  2  US-08-599-491-7              Sequence 7, Appli
c   45     39.4      2.9    2502  2  US-08-756-386-7              Sequence 7, Appli

                            ALIGNMENTS

RESULT 1
US-09-299-141-6/c
; Sequence 6, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  [illegible]
;  [illegible]
;  TITLE [illegible]
;  [illegible]
;  [illegible] 09/299,141
;  CURRENT FILING DATE: 1999-04-2[illegible]
;  EARLIER APPLICATION NUMBER: [illegible],025
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 1[illegible]
;  SOFTWARE: PatentIn Ver. 2.[illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p4[illegible]
US-09-299-141-6

  Query Match             [illegible];  Score [illegible];  DB 4;  Length [illegible];
  Best Local Similarity   5[illegible];  Pred. No. [illegible];
  Matches  [illegible];  Conservative  [illegible];  Mismatches   82;  Indels  [illegible];  Gaps  [illegible];

Qy        [illegible]
Db     [illegible]

Qy        [illegible]
Db     [illegible]

Qy        [illegible]
Db     [illegible]

Qy        [illegible]

Db     1472 [illegible] 1472


RESULT 2
US-09-299-141-9/c
; Sequence 9, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: 4308.011800
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: 1999-04-23
;  EARLIER APPLICATION NUMBER: 60/083,025
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 6924
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p43mmsENC AT
US-09-299-141-9

  Query Match          [illegible];  Score 40.8;  DB 4;  Length 6924;
  Best Local Similarity   54.7%;  Pred. No. [illegible];
  Matches   99;  Conservative    0;  Mismatches   82;  Indels    0;  Gaps    0;

Qy         19 [illegible] 78
Db       1862 [illegible] 1803

Qy         79 [illegible] 138
Db       1802 [illegible] 1743

Qy        139 [illegible] 198
Db       1742 [illegible] 1683

Qy        199 [illegible] 199
Db       1682 [illegible] 1682


RESULT [illegible]
US-09-299-141-10/c
; Sequence 10, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: 4308.011800
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: 1999-04-23
;  EARLIER APPLICATION NUMBER: 60/083,025
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 6924
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p43mmsENCB AT
US-09-299-141-10

  Query Match          [illegible];  Score 40.8;  DB 4;  Length 6924;
  Best Local Similarity   54.7%;  Pred. No. [illegible];
  Matches   99;  Conservative    0;  Mismatches   82;  Indels    0;  Gaps    0;

Qy         19 [illegible]
Db       1862 [illegible]

Qy         79 [illegible]
Db       1802 [illegible]

Qy        139 [illegible]
Db       1742 [illegible]

Qy        199 [illegible]
Db       1682 [illegible]


RESULT [illegible]
US-09-299-141-11/c
; Sequence 11, Application US/09299141
; Patent No. 6461606
; GENERAL INFORMATION:
;  APPLICANT: FLOTTE, TERENCE R.
;  APPLICANT: SONG, SIHONG
;  APPLICANT: BYRNE, BARRY J.
;  APPLICANT: MORGAN, MICHAEL
;  TITLE OF INVENTION: MATERIALS AND METHODS FOR GENE THERAPY
;  FILE REFERENCE: 4308.011800
;  CURRENT APPLICATION NUMBER: US/09/299,141
;  CURRENT FILING DATE: 1999-04-23
;  EARLIER APPLICATION NUMBER: 60/083,025
;  EARLIER FILING DATE: 1998-04-24
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
;   LENGTH: 6924
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:PLASMID
;   OTHER INFORMATION: p43mmsENCB AT
US-09-299-141-11

  Query Match          [illegible];  Score [illegible];  DB 4;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches   99;  Conservative    [illegible];  Mismatches   82;  Indels    [illegible];  Gaps    [illegible];

Qy         19 [illegible]
Db       1862 [illegible]

Qy         79 [illegible]
Db       1802 [illegible]

Qy        139 [illegible]
Db       1742 [illegible]

Qy        199 [illegible]
Db       1682 [illegible]


RESULT [illegible]
US-[illegible]
; Sequence 9, Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;   APPLICANT: [illegible]
;   APPLICANT: [illegible]
;   APPLICANT: [illegible]
;    APPLICANT:  [illegible], Susma
;    APPLICANT:  [illegible]
;    APPLICANT:  Sonchelnytskyi, Serhiy
;    APPLICANT:  Brodin, [illegible]
;    APPLICANT:  Landstrom, Marene
;    APPLICANT:  Heldin, Nils-Erik
;    APPLICANT:  Heldin, Carl-Henrik
;    APPLICANT:  ten Dijke, Peter
;    TITLE OF INVENTION:  SMAD7 AND USES THEREOF
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  U.S.A.
;      ZIP:  02210-2211
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  [illegible]
;      FILING DATE:  2[illegible]-MAY-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  [illegible]
;      FILING DATE:  2[illegible]-MAY-1997
;      APPLICATION NUMBER:  [illegible]
;      FILING DATE:  [illegible]-SEP-1997
;      APPLICATION NUMBER:  [illegible]
;      FILING DATE:  25-FEB-1998
;      APPLICATION NUMBER:  [illegible]
;      FILING DATE:  06-MAR-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  [illegible]/7002
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1491 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  [illegible]
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-082-092-9

  Query Match             [illegible];  Score 18[illegible];  DB [illegible];  Length 1491;
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches   [illegible];  Conservative    [illegible];  Mismatches   [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy          5 [illegible] 64
Db        [illegible] 243

Qy         65 [illegible] 124
Db        242 [illegible] 183

Qy        125 [illegible] 184
Db        182 [illegible] 123

Qy        185 [illegible] 185
Db        122 [illegible] 122
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RESULT 6
US-09-288-292A-45/c
; Sequence 45, Application US/09288292A
; Patent No. 6359194
; GENERAL INFORMATION:
;  APPLICANT: Dean A. Falb
;  APPLICANT:  Katherine Galvin
;  APPLICANT:  Michael Donovan
;  APPLICANT:  Dennis Huszar
;  APPLICANT:  Michael A. Gimbrone, Jr.
;  TITLE OF INVENTION: Compositions and Methods for the Treatment and Diagnosis of
;  TITLE OF INVENTION:  Cardiovascular Disease
;  FILE REFERENCE: 7853-140-999
;  CURRENT APPLICATION NUMBER: US/09/288,292A
;  CURRENT FILING DATE:  1999-04-08
;  PRIOR APPLICATION NUMBER: [illegible]/87[illegible],434
;  PRIOR FILING DATE: 1997-06-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 1997-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]/ 11,7[illegible]7
;  PRIOR FILING DATE: 1996-[illegible]
;  PRIOR APPLICATION NUMBER: [illegible]/485,678
;  PRIOR FILING DATE: 1995-06-[illegible]7
;  PRIOR APPLICATION NUMBER: [illegible],444
;  PRIOR FILING DATE: 1995-[illegible]
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
;   LENGTH: 1817
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-288-292A-45

  Query Match             [illegible];  Score [illegible];  DB 4;  Length 1817;
  Best Local Similarity   54.1%;  Pred. No. [illegible];
  Matches   [illegible];  Conservative    [illegible];  Mismatches   [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy          5 [illegible] 64
Db        456 [illegible] 397

Qy         65 [illegible] 124
Db        396 [illegible] 337

Qy        125 [illegible] 184
Db        [illegible] 277

Qy        185 [illegible] 185
Db        276 [illegible] 276


RESULT 7
US-[illegible]
; Sequence 91, Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT:  Thomashow, Michael
;  APPLICANT:  Stockinger, Eric
;  APPLICANT:  [illegible], Kirsten
;  APPLICANT:  Gilmour, Sarah
;  APPLICANT:  Zarka, Daniel
;  APPLICANT:  [illegible]
;  TITLE OF INVENTION:  Plant Having Altered Environmental Stress [illegible]
;  FILE REFERENCE:  [illegible] Seq List
;  CURRENT APPLICATION NUMBER: US/09/[illegible]
;  CURRENT FILING DATE:  1998-11-2[illegible]
;  PRIOR APPLICATION NUMBER:  US 08/706,270
;  PRIOR FILING DATE:  1996-09-04
;  PRIOR APPLICATION NUMBER:  US 09/[illegible]
;  PRIOR FILING DATE:  1998-02-03
;  PRIOR APPLICATION NUMBER: US 09/017,816
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: US 09/018,2[illegible]
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: US 09/017,575
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: US 09/018,227
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: US 09/018,234
;  PRIOR FILING DATE: 1998-02-03
;  NUMBER OF SEQ ID NOS: 95
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Zea maize
;   FEATURE:
;   OTHER INFORMATION: [illegible] gene
US-09-198-119C-94

  Query Match             3.4%;  Score 47;  DB 4;  Length 849;
  Best Local Similarity   55.1%;  Pred. No. 0.019;
  Matches   92;  Conservative   0;  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy       1 [illegible] 78
           [illegible]
Db     102 [illegible] 161

Qy      79 AGC[illegible]TACCGACGG[illegible] 138
           [illegible]
Db     162 GTC[illegible]GAGC[illegible]AAGAAC[illegible] 221

Qy     139 [illegible] 185
           [illegible]
Db     222 [illegible] 26[illegible]


RESULT 8
US-08-415-655-11/c
; Sequence 11, Application US/08415655
; Patent No. 6025480
;  GENERAL INFORMATION:
;    APPLICANT:  Massague, Joan
;    APPLICANT:  Lee, Mong-Hong
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULES ENCODING
;    TITLE OF INVENTION:  p57KIP2, A CYCLIN DEPENDENT KINASE INHIBITOR AND USES [illegible]
;    TITLE OF INVENTION:  SAME
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  United States of America
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/415,655
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  1747/47418
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  [illegible] base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  N
;    ANTI-SENSE:  N
US-08-415-655-11

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches   [illegible];  Conservative   [illegible];  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy       [illegible]
           [illegible]
Db       [illegible]

Qy       [illegible]
           [illegible]
Db     [illegible]

Qy     156 [illegible] 19[illegible]
           [illegible]
Db     [illegible]


RESULT 9
US-09-[illegible]
; Sequence [illegible], Application US/[illegible]
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: Wood, [illegible]
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: [illegible]
;  TITLE OF INVENTION: AND [illegible]
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-[illegible]

  Query Match             [illegible];  Score [illegible];  DB 4;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches   [illegible];  Conservative   [illegible];  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy       [illegible]
           [illegible]
Db      4[illegible]

Qy      [illegible]
           [illegible]
Db     4[illegible]

Qy     12[illegible]
           [illegible]
Db      [illegible]

Qy     [illegible]

Db     [illegible]


RESULT 10
US-[illegible]
; Sequence [illegible], Application [illegible]
; Patent No. 6117654
; GENERAL INFORMATION:
;  APPLICANT: Pan, Yang
;  TITLE OF INVENTION: [illegible] TANGO-77 [illegible]
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 5464/[illegible]
;  CURRENT APPLICATION NUMBER: US/09/128,155
;  CURRENT FILING DATE: 1998-08-[illegible]
;  EARLIER APPLICATION NUMBER: US 60/[illegible]1,650
;  EARLIER FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: US 60/054,646
;  EARLIER FILING DATE: 1997-[illegible]-04
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 16
;   LENGTH: 152331
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(152331)
;   OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

  Query Match             [illegible]%;  Score 43.[illegible];  DB [illegible];  Length 152331;
  Best Local Similarity   51.0%;  Pred. No. [illegible];
  Matches  103;  Conservative  [illegible];  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy          [illegible] 62
Db      21997 [illegible] 22056

Qy         63 [illegible] 122
Db      22057 [illegible] 22116

Qy        123 [illegible] 182
Db      22117 [illegible] 22176

Qy        183 [illegible] 204
Db      22177 [illegible] 22198


RESULT 11
US-09-096-776B-3/c
; Sequence 3, Application US/09096776B
; Patent No. 6270994
; GENERAL INFORMATION:
;  APPLICANT:  Miyazono, Kohei
;  APPLICANT:  Kawabata, Masahiro
;  TITLE OF INVENTION:   SMAD6 AND USES THEREOF
;  FILE REFERENCE:   [illegible]/7538
;  CURRENT APPLICATION NUMBER: US/09/096,776B
;  CURRENT FILING DATE:  1998-06-12
;  PRIOR APPLICATION NUMBER:   US 60/049,[illegible]
;  PRIOR FILING DATE:   1997-06-13
;  PRIOR APPLICATION NUMBER:   US 60/053,040
;  PRIOR FILING DATE:   1997-07-18
;  PRIOR APPLICATION NUMBER:   US 60/066,173
;  PRIOR FILING DATE:   1997-11-18
;  NUMBER OF SEQ ID NOS:   [illegible]
;  SOFTWARE:   PatentIn version [illegible]
; SEQ ID NO 3
;   LENGTH: 1488
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-09-096-776B-3

  Query Match              3.1%;  Score 43.4;  DB 4;  Length 1488;
  Best Local Similarity   52.5%;  Pred. No. 0.2;
  Matches   95;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy          5 [illegible] 64
Db        [illegible]

Qy         65 [illegible] 124
Db        [illegible]

Qy        125 [illegible] 184
Db        [illegible]

Qy        185 C 185
Db        119 C 119


RESULT 12
US-09-096-776B-1/c
; Sequence 1, Application US/09096776B
; Patent No. 6270994
; GENERAL INFORMATION:
;  APPLICANT:  Miyazono, Kohei
;  APPLICANT:  Kawabata, Masahiro
;  TITLE OF INVENTION:   SMAD6 AND USES THEREOF
;  FILE REFERENCE:   [illegible]/7538
;  CURRENT APPLICATION NUMBER: US/09/096,776B
;  CURRENT FILING DATE:  1998-06-12
;  PRIOR APPLICATION NUMBER:   US 60/049,[illegible]
;  PRIOR FILING DATE:   1997-06-13
;  PRIOR APPLICATION NUMBER:   US 60/053,040
;  PRIOR FILING DATE:   1997-07-18
;  PRIOR APPLICATION NUMBER:   US 60/066,173
;  PRIOR FILING DATE:   1997-11-18
;  NUMBER OF SEQ ID NOS:   [illegible]
;  SOFTWARE:   PatentIn version [illegible]
; SEQ ID NO 1
;   LENGTH: 2534
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: ([illegible])..([illegible])
US-09-096-776B-1

  Query Match              3.1%;  Score 43.4;  DB 4;  Length 2534;
  Best Local Similarity   52.5%;  Pred. No. 0.24;
  Matches   95;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy          5 CCGCCGGCTGGTTCCGGCCG[illegible] 64
Db        [illegible]

Qy         65 [illegible] 124
Db        [illegible]

Qy        125 [illegible] 184
Db        [illegible]

Qy        185 C 185
Db        [illegible] C [illegible]


RESULT 13
US-09-083-351-1/c
; Sequence 1, Application US/09083351
; Patent No. [illegible]107
; GENERAL INFORMATION:
;    APPLICANT:  Sheffield, Val C.
;    APPLICANT:  Alward, Wallace L.M.
;    APPLICANT:  Stone, Edwin M.
;    APPLICANT:  Nishimura, Darryl
;    APPLICANT:  Patil, Shiva
;    TITLE OF INVENTION:  THERAPEUTICS AND DIAGNOSTICS FOR
;    TITLE OF INVENTION:  CONGENITAL HEART DISEASE BASED ON A NOVEL HUMAN
;    TITLE OF INVENTION:  TRANSCRIPTION FACTOR
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FOLEY, HOAG & ELIOT LLP
;      STREET:  One Post Office Square
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109-21[illegible]
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/083,351
;      FILING DATE:  22-MAY-1998
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold, Beth E.
;      REGISTRATION NUMBER:  3[illegible],43[illegible]
;      REFERENCE/DOCKET NUMBER:  UIA-029.02
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-832-1000
;      TELEFAX:  617-832-7000
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3946 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  475..2133
US-09-083-351-1

  Query Match             8.1%;  Score 15.2;  DB 5;  Length 3946;
  Best Local Similarity   57.1%;  Pred. No. [illegible];
  Matches   73;  Conservative    0;  Mismatches   [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy         88 [illegible] 147
                 [illegible]
Db        468 [illegible] 409

Qy        148 [illegible] 207
                 [illegible]
Db        408 [illegible] 349

Qy        208 [illegible] 225
                 [illegible]
Db        348 [illegible] 33[illegible]


RESULT 14
US-09-083-352-1/c
; Sequence 1, Application US/09083352
; Patent No. 6207450
;  GENERAL INFORMATION:
;    APPLICANT:  Sheffield, Val C.
;    APPLICANT:  Alward, Wallace L.M.
;    APPLICANT:  Stone, Edwin M.
;    APPLICANT:  Nishimura, Darryl
;    APPLICANT:  Patil, Shiva
;    TITLE OF INVENTION:  GLAUCOMA THERAPEUTICS AND DIAGNOSTICS
;    TITLE OF INVENTION:  BASED ON A NOVEL HUMAN TRANSCRIPTION FACTOR
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  F[illegible]LEY, HOAG & ELIOT LLP
;      STREET:  [illegible]
;      CITY:  [illegible]
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  [illegible]
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  [illegible]
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  [illegible]
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  [illegible]
;      FILING DATE:  [illegible] MAY [illegible]
;      CLASSIFICATION:  [illegible]
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Arnold, Beth E.
;      REGISTRATION NUMBER:  [illegible]
;      REFERENCE/DOCKET NUMBER:  UIA-[illegible]
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  [illegible]
;      TELEFAX:  [illegible]
;  INFORMATION FOR SEQ ID NO:  [illegible]
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  [illegible] base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  [illegible]
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  [illegible]
;      LOCATION:  4[illegible]
US-[illegible]

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  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches   [illegible];  Conservative    [illegible];  Mismatches   [illegible];  Indels    [illegible];  Gaps    [illegible];

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Db        348 [illegible]


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; Sequence [illegible], Application [illegible]
; Patent No. [illegible]
;  GENERAL INFORMATION:
;    APPLICANT:  SUTHERLAND, Grant R
;    APPLICANT:  RICHARDS, Robert I
;    APPLICANT:  SCHLESSINGER, David
;    APPLICANT:  NAGARAJA, Ramaiah
;    APPLICANT:  KREMER, [illegible]
;    APPLICANT:  YU, [illegible]
;    APPLICANT:  BAKER, [illegible]
;    APPLICANT:  MULLEY, [illegible]
;    APPLICANT:  MANDEL, [illegible]
;    APPLICANT:  PRITCHARD, [illegible]
;    APPLICANT:  LYNCH, M[illegible]
;    TITLE OF INVENTION:  DNA SEQUENCES RELATED TO [illegible]
;    TITLE OF INVENTION:  FRAGILE X SYNDROME
;    NUMBER OF SEQUENCES:  [illegible]
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  [illegible]
;       STREET:  P.O. Box 1404
;       CITY:  Alexandria
;       STATE:  Virginia
;       COUNTRY:  United States
;       ZIP:  22313-1404
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/118,209
;       FILING DATE:  09-SEP-1993
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/802,659
;       FILING DATE:  05-DEC-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/672,232
;       FILING DATE:  20-MAR-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/[illegible]
;       FILING DATE:  [illegible]-JAN-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/966,517
;       FILING DATE:  [illegible]-DEC-1992
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Crane-Foury, Sharon E
;       REGISTRATION NUMBER:  36,113
;       REFERENCE/DOCKET NUMBER:  020160-164
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (703) 836-6620
;       TELEFAX:  (703) 836-2021
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1028 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-118-209-1

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Job time : 252 secs
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                    GenCore version 5.1.x
           Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         February 22, 2003, 19:27:13 ; Search time 92 Seconds
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Searched:       442118 seqs, 280819700 residues

Total number of hits satisfying chosen parameters:      884236

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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     and is derived by analysis of the total score distribution.

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   23      43      3.1   1614 12  US-10-023-529-45         Sequence 45, Appl
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                              ALIGNMENTS

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; Sequence 3, Application US/09866987
; Patent No. US20020[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: [illegible]MAN, GREGORY D.
;  APPLICANT: [illegible]
;  APPLICANT: [illegible], DAVID
;  APPLICANT: [illegible]
;  APPLICANT: [illegible], SUCHA
;  APPLICANT: [illegible]
;  APPLICANT: HILL, RON
;  APPLICANT: [illegible]N, PETER
;  TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
;  FILE REFERENCE: 038602/1180
;  CURRENT APPLICATION NUMBER: US/09/866,987
;  CURRENT FILING DATE: 2001-05-30
;  PRIOR APPLICATION NUMBER: 60/208,291
;  PRIOR FILING DATE: 2000-05-30
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 1380
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: phosphatase nucleotide
US-09-866-987-3

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; GENERAL INFORMATION:
;  APPLICANT: [illegible], Paul A.
;  APPLICANT: [illegible]
;  APPLICANT: [illegible]
;  TITLE OF INVENTION: [illegible] AND [illegible] THERAPY
;  TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version [illegible]
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; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jianchen
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547
;  CURRENT APPLICATION NUMBER: [illegible]
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1714
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;   TYPE: DNA
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US-09-920-300A-1714

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; Sequence 1714, Application US/10033528
; Patent No. [illegible]
; GENERAL INFORMATION:
;  APPLICANT: King, Gordon E.
;  APPLICANT:  Meagher, Madeleine Joy
;  APPLICANT:  Xu, Jianchen
;  APPLICANT:  Secrist, Heather
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF COLON CANCER
;  FILE REFERENCE: 210121.547C1
;  CURRENT APPLICATION NUMBER: US/10/033,528
;  CURRENT FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 1896
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;   ORGANISM: Homo sapiens
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; Sequence 5460, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
;  APPLICANT: Algate, Paul A.
;  APPLICANT:  Jones, Robert
;  APPLICANT:  Harlocker, Susan L.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
;  TITLE OF INVENTION:  AND DIAGNOSIS OF OVARIAN CANCER
;  FILE REFERENCE: 210121.497
;  CURRENT APPLICATION NUMBER: US/09/867,701
;  CURRENT FILING DATE:  2001-05-29
;  NUMBER OF SEQ ID NOS: 10912
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5460
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;   ORGANISM: Homo sapien
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;   OTHER INFORMATION: n = A,T,C or G
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;                            [illegible]
;        NUMBER OF SEQUENCES: [illegible]
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: [illegible]
;             [illegible]
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: [illegible]
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: [illegible]
;             COMPUTER: IBM Compatible
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;             FILING DATE: [illegible] MAR [illegible]
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: [illegible] JUN [illegible]
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: [illegible] FEB [illegible]
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: [illegible] FEB [illegible]
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: [illegible] FEB [illegible]
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: [illegible]
;             APPLICATION NUMBER: [illegible]
;             FILING DATE: [illegible] FEB [illegible]
;        ATTORNEY/AGENT INFORMATION:
;             NAME: [illegible]
;             REGISTRATION NUMBER: [illegible]
;             REFERENCE/DOCKET NUMBER: [illegible]
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212)[illegible]
;             TELEFAX: (212)[illegible]
;             TELEX: [illegible]
;    INFORMATION FOR SEQ ID NO: [illegible]
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: [illegible] base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: both
;             TOPOLOGY: unknown
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: [illegible]:
US-09-924-417-[illegible]

  Query Match             [illegible]
  Best Local Similarity   [illegible]
  Matches  [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]
```

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Qy        125 CCAGCCGGGGCTGCCACGGTCCCGCCGCCCAGACTCCCGCCCGTCGGCAGCCCCG 184
              [illegible]
Db        336 CGGACTGGGAGCGCGCAGCTCCCGCCCGCCTCCCGCCCGCCCGCCGCACCTCCG 277

Qy        185 C 185
              :
Db        276 C 276


RESULT 7
US-09-996-140-94
; Sequence 94, Application US/09996140
; Patent No. US20020157126A1
; GENERAL INFORMATION:
;  APPLICANT: Thomashow, Michael
;  APPLICANT:  Stockinger, Eric
;  APPLICANT:  Jaglo-Ottosen, Kirsten
;  APPLICANT:  Gilmour, Sarah
;  APPLICANT:  Zarka, Daniel
;  APPLICANT:  Jiang, Cai-Zhong
;  TITLE OF INVENTION: PLANT HAVING ALTERED ENVIRONMENTAL
;  TITLE OF INVENTION:  STRESS TOLERANCE
;  FILE REFERENCE: MR1004-02
;  CURRENT APPLICATION NUMBER: US/09/996,140
;  CURRENT FILING DATE:  2001-11-26
;  PRIOR APPLICATION NUMBER: 09/706,270
;  PRIOR FILING DATE: 1996-09-04
;  PRIOR APPLICATION NUMBER: 09/018,2
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/017,816
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,235
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/017,575
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,227
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/018,234
;  PRIOR FILING DATE: 1998-02-03
;  PRIOR APPLICATION NUMBER: 09/198,119
;  PRIOR FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: PCT/US99/01895
;  PRIOR FILING DATE: 1999-01-26
;  NUMBER OF SEQ ID NOS: 150
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94
;    LENGTH: 349
;    TYPE: DNA
;    ORGANISM: Zea mays
US-09-996-140-94

  Query Match             8.3%;  Score 47;  DB 9;  Length 349;
  Best Local Similarity   55.1%;  Pred. No. 0.014;
  Matches   92;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy         19 CGGCGGCGCTTCCGCCGCGACGCGCGCCGCCGCGCCGCCGCTGGCCGCATCCC 78
              [illegible]
Db        102 CGGCACCCGGCGACGCGCCGCGGGCGGCCGCCGCCGCGCCGGCGGCGGCGGCGCGCAG 161

Qy         79 AGCCCCTGCCCCTACCCACGCCCCCCTCCCTCCCCGCCCCAGCCCCAGCCCCGCCCCG 138
              [illegible]
Db        162 GCCCGCGAGCCCAACCAGCCCCCCGCAC[illegible]GCCCGCCCGAGCCCCGAGCCC 221

Qy        139 CCCGACGCCCGCCGCCCCAGACCCCGCCCCGCCGCAGCCCGGC 185
              [illegible]
Db        222 GCCGCGCCGCGGACGACGCGCCGCCGCTGGCCCTGCCGCCGCCGCCGC 268


RESULT 8
US-09-954-456-292/c
; Sequence 292, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,840
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,865
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 1276
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 292
;    LENGTH: 43058
;    TYPE: DNA
;    ORGANISM: Homo sapiens
US-09-954-456-292

  Query Match             8.4%;  Score 46.8;  DB 10;  Length 43058;
  Best Local Similarity   54.7%;  Pred. No. 0.091;
  Matches   93;  Conservative    0;  Mismatches   77;  Indels    0;  Gaps    0;

Qy         18 [illegible] 77
              [illegible]
Db      27721 [illegible] 27662

Qy         78 [illegible]CAGCCCAGCCCCCCCCC 137
              [illegible]
Db      27661 [illegible]GAGCCCCCCCCCCCCC 27602

Qy        138 GCCGGAC[illegible]CGCCCAGCCCCCAC 187
              [illegible]
Db      27601 [illegible]CAGCGCCCGCCC 27552


RESULT 9
US-09-954-456-529/c
; Sequence 529, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-76
;  CURRENT APPLICATION NUMBER: US/09/954,456
;  CURRENT FILING DATE:  2001-09-18
;  PRIOR APPLICATION NUMBER: US/60/233,617
;  PRIOR FILING DATE: 2000-09-18
;  PRIOR APPLICATION NUMBER: US/60/234,052
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: US/60/234,923
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,134
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,637
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,638
;  PRIOR FILING DATE: 2000-09-26
;  PRIOR APPLICATION NUMBER: US/60/235,711
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,720
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,810
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: US/60/235,863
;  PRIOR FILING DATE: 2000-09-27
;  NUMBER OF SEQ ID NOS: 2276
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 529
;   LENGTH: 43058
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-954-456-529

  Query Match             3.4%;  Score 46.8;  DB 10;  Length 43058;
  Best Local Similarity   54.7%;  Pred. No. 0.091;
  Matches   93;  Conservative    0;  Mismatches   77;  Indels    0;  Gaps    0;

Qy       18 [illegible] 77
            [illegible]
Db    25721 [illegible] 25662

Qy       78 [illegible] 137
            [illegible]
Db    25661 [illegible] 25602

Qy      138 [illegible] 187
            [illegible]
Db    25601 [illegible] 25552


RESULT 10
US-09-880-107-3950/c
; Sequence 3950, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
;  APPLICANT: Horne, Darci T.
;  APPLICANT:  Vockley, Joseph G.
;  APPLICANT:  Scherf, Uwe
;  APPLICANT:  Gene Logic, Inc.
;  TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
;  FILE REFERENCE: 44921-5028-WO
;  CURRENT APPLICATION NUMBER: US/09/880,107
;  CURRENT FILING DATE:  2001-06-14
;  PRIOR APPLICATION NUMBER: US 60/211,375
;  PRIOR FILING DATE: 2000-06-14
;  PRIOR APPLICATION NUMBER: US 60/237,054
;  PRIOR FILING DATE: 2000-10-02
;  NUMBER OF SEQ ID NOS: 3950
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3950
;   LENGTH: 43058
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Genbank Accession No. [illegible] 264721
US-09-880-107-3950

  Query Match             3.4%;  Score 46.8;  DB 10;  Length 43058;
  Best Local Similarity   54.7%;  Pred. No. 0.091;
  Matches   93;  Conservative    0;  Mismatches   77;  Indels    0;  Gaps    0;

Qy       18 [illegible] 77
            [illegible]
Db    25721 [illegible] 25662

Qy       78 [illegible] 137
            [illegible]
Db    25661 [illegible] 25602

Qy      138 [illegible]
            [illegible]
Db    25601 [illegible]


RESULT 11
US-09-925-[illegible]-474
; Sequence 474, Application US/0992[illegible]
; Patent No. US2002[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA106
;  CURRENT APPLICATION NUMBER: US/09/92[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US00/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: 60/[illegible]
;  PRIOR FILING DATE: 1999-[illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 474
;   LENGTH: 3269
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (427)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-[illegible]-474

  Query Match             [illegible];  Score 46.1;  DB 10;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. 0.014;
  Matches  128;  Conservative    [illegible];  Mismatches  13[illegible];  Indels   [illegible];  Gaps   [illegible];

Qy     [illegible] [illegible]
            [illegible]
Db     1268 [illegible]

Qy     [illegible] [illegible]
            [illegible]
Db     1328 [illegible]

Qy     [illegible] [illegible]
            [illegible]
Db     [illegible] [illegible]

Qy     [illegible] [illegible]
            [illegible]
Db     1448 [illegible]

Qy     121[illegible] [illegible] 123[illegible]
            [illegible]
Db     1508 [illegible]


RESULT 12
US-09-976-740-48
; Sequence 48, Application US/09976740
; Publication No. US2002[illegible]A1
; GENERAL INFORMATION:
;  APPLICANT: Goos, Ann M.
;  APPLICANT:  Goos, Robert C.
;  APPLICANT:  Law, Simon W.
;  APPLICANT:  Arbona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION:  PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION:  ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004-[illegible]
;  CURRENT APPLICATION NUMBER: US/09/976,740
;  CURRENT FILING DATE:  2001-[illegible]
;  PRIOR APPLICATION NUMBER: 60/[illegible]
;  PRIOR FILING DATE: 2000-0[illegible]-14
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-09-976-740-48

  Query Match             3.2%;  Score 44.4;  DB 9;  Length 2561;
  Best Local Similarity   55.9%;  Pred. No. 0.13;
  Matches  104;  Conservative    0;  Mismatches   81;  Indels    1;  Gaps    1;

Qy       11 GCTGGTTCCGGCGCCGCTTCCTGCCTGGGGAGCCGCTCCCCGCGCCGCGGCCGCCTGGGC 70
            || |   || ||||    ||  |   |   |||| |||  ||||| ||||    |
Db      620 GCCGCCGCCCACGCCGCCGCCGCCGCCGCCGCCGCCCGTCGCCGCCGCCGCCGCCGCCCC 679

Qy       71 CGCATGCCAGCCCCGTGC-CCTACCGACGGCCCCGCTTCCTTCGCGGCTCCAGCTCCAGC 129
             ||  |  ||||| ||  |  ||| || | | ||  ||   ||| | |   | || |
Db      680 GGCCCGGGCGCCCCGCGCGGCCGCCGCCGCCGCTGCCGCCACAGCGCCCCCCTCGCCCGG 739

Qy      130 CCCGGGCGGCCCGACGCTCGGCGCCGCCCAGACTCCCGGCCCGTCGGCAGCCCCGCACGA 189
            ||| | || ||||   || |||||     | | | |   || | |||    |||| ||
Db      740 CCCCGCGCAGCCGGGCCCCCGCGCGCAGCGGGCCGCGCCCCTGGCCGCGCCGCCGCCCGC 799

Qy      190 GGACGC 195
            |  |||
Db      800 GCCCGC 805


RESULT 13
US-10-023-529-48
; Sequence 48, Application US/10023529
; Patent No. US20020129386A1
; GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT:  Lees, Robert S.
;  APPLICANT:  Law, Simon W.
;  APPLICANT:  Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION:  PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION:  ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/10/023,529
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: 09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-10-023-529-48
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  Query Match             3.2%;  Score 44.4;  DB 12;  Length 2561;
  Best Local Similarity   55.9%;  Pred. No. 0.13;
  Matches  104;  Conservative    0;  Mismatches   81;  Indels    1;  Gaps    1;

Qy       11 GCTGGTTCCGGCGCCGCTTCCTGCCTGGGGAGCCGCTCCCCGCGCCGCGGCCGCCTGGGC 70
            || |   || ||||    ||  |   |   |||| |||  ||||| ||||    |
Db      620 GCCGCCGCCCACGCCGCCGCCGCCGCCGCCGCCGCCCGTCGCCGCCGCCGCCGCCGCCCC 679

Qy       71 CGCATGCCAGCCCCGTGC-CCTACCGACGGCCCCGCTTCCTTCGCGGCTCCAGCTCCAGC 129
             ||  |  ||||| ||  |  ||| || | | ||  ||   ||| | |   | || |
Db      680 GGCCCGGGCGCCCCGCGCGGCCGCCGCCGCCGCTGCCGCCACAGCGCCCCCCTCGCCCGG 739

Qy      130 CCCGGGCGGCCCGACGCTCGGCGCCGCCCAGACTCCCGGCCCGTCGGCAGCCCCGCACGA 189
            ||| | || ||||   || |||||     | | | |   || | |||    |||| ||
Db      740 CCCCGCGCAGCCGGGCCCCCGCGCGCAGCGGGCCGCGCCCCTGGCCGCGCCGCCGCCCGC 799

Qy      190 GGACGC 195
            |  |||
Db      800 GCCCGC 805


RESULT 14
US-10-023-523-48
; Sequence 48, Application US/10023523
; Patent No. US20020128407A1
; GENERAL INFORMATION:
;  APPLICANT: Lees, Ann M.
;  APPLICANT:  Lees, Robert S.
;  APPLICANT:  Law, Simon W.
;  APPLICANT:  Arjona, Anibal A.
;  TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
;  TITLE OF INVENTION:  PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
;  TITLE OF INVENTION:  ATHEROSCLEROSIS
;  FILE REFERENCE: 10797-004001
;  CURRENT APPLICATION NUMBER: US/10/023,523
;  CURRENT FILING DATE:  2001-12-17
;  PRIOR APPLICATION NUMBER: 09/616,289
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: US 09/517,849
;  PRIOR FILING DATE: 2000-03-02
;  PRIOR APPLICATION NUMBER: US 08/979,608
;  PRIOR FILING DATE: 1997-11-26
;  PRIOR APPLICATION NUMBER: US 60/031,930
;  PRIOR FILING DATE: 1996-11-27
;  PRIOR APPLICATION NUMBER: US 60/048,547
;  PRIOR FILING DATE: 1997-06-03
;  NUMBER OF SEQ ID NOS: 53
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 48
;   LENGTH: 2561
;   TYPE: DNA
;   ORGANISM: Oryctolagus cuniculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (246)...(1895)
US-10-023-523-48

  Query Match             3.2%;  Score 44.4;  DB 12;  Length 2561;
  Best Local Similarity   55.9%;  Pred. No. 0.13;
  Matches  104;  Conservative    0;  Mismatches   81;  Indels    1;  Gaps    1;

Qy       11 GCTGGTTCCGGCGCCGCTTCCTGCCTGGGGAGCCGCTCCCCGCGCCGCGGCCGCCTGGGC 70
            || |   || ||||    ||  |   |   |||| |||  ||||| ||||    |
Db      620 GCCGCCGCCCACGCCGCCGCCGCCGCCGCCGCCGCCCGTCGCCGCCGCCGCCGCCGCCCC 679

Qy       71 CGCATGCCAGCCCCGTGC-CCTACCGACGGCCCCGCTTCCTTCGCGGCTCCAGCTCCAGC 129
             ||  |  ||||| ||  |  ||| || | | ||  ||   ||| | |   | || |
Db      680 GGCCCGGGCGCCCCGCGCGGCCGCCGCCGCCGCTGCCGCCACAGCGCCCCCCTCGCCCGG 739

Qy      130 CCCGGGCGGCCCGACGCTCGGCGCCGCCCAGACTCCCGGCCCGTCGGCAGCCCCGCACGA 189
            ||| | || ||||   || |||||     | | | |   || | |||    |||| ||
Db      740 CCCCGCGCAGCCGGGCCCCCGCGCGCAGCGGGCCGCGCCCCTGGCCGCGCCGCCGCCCGC 799
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Qy        [illegible] 19[illegible]
                   [illegible]
Db        [illegible] 8[illegible]


RESULT 1[illegible]
US-09-[illegible]-634A 1/c
; Sequence 1, Application US/09[illegible]634A
; Patent No. US20020059654A1
; GENERAL INFORMATION:
;  APPLICANT: Thomas Buehler, Peter Andreas Gadient, Reinhard K[illegible], [illegible] M[illegible]
;  TITLE OF INVENTION: pCAR and its uses
;  FILE REFERENCE: 4-[illegible]499A
;  CURRENT APPLICATION NUMBER: US/09/[illegible]634A
;  CURRENT FILING DATE: 2001-[illegible]
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 4286
;   TYPE: DNA
;   ORGANISM: porcine
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (3229)..(4014)
US-09-[illegible]-634A-1

  Query Match             3.[illegible]%;  Score 44.2;  DB 10;  Length 4286;
  Best Local Similarity   56.[illegible]%;  Pred. No. 0.17;
  Matches  10[illegible];  Conservative    0;  Mismatches   [illegible];  Indels    [illegible];  Gaps    [illegible];

Qy        1[illegible] [illegible] [illegible]
Db     28[illegible] [illegible] 28[illegible]

Qy       79 A[illegible] 1[illegible]
Db     2812 [illegible] 27[illegible]

Qy      13[illegible] [illegible] 1[illegible]
Db     27[illegible]2 [illegible] 2[illegible]

Qy      1[illegible] [illegible] 1[illegible]
Db     2692 [illegible] 2692

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          Copyright (c) 1993 - 200[illegible] [illegible] Ltd.

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Post-processing: Minimum Match 0%
                 Maximum Match 100%
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                  21: [illegible]
                  22: [illegible]
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                  24: [illegible]
                  25: [illegible]
                  26: [illegible]
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                  32: [illegible]
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                  34: [illegible]MB.seq:*
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                  49: [illegible]MB.seq:*
                  50: [illegible]US6006_COMB.seq:*
                  51: [illegible]MB.seq:*
                  52: [illegible]MB.seq:*
                  53: [illegible]MB.seq:*
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                  56: [illegible]MB.seq:*
                  57: [illegible]MB.seq:*
                  58: [illegible]MB.seq:*
                  59: [illegible]MB.seq:*
                  60: [illegible]MB.seq:*
                  61: [illegible]MB.seq:*
                  62: [illegible]MB.seq:*
                  63: [illegible]MB.seq:*
                  64: [illegible]MB.seq:*
                  65: [illegible]MB.seq:*
                  66: [illegible]MB.seq:*
                  67: [illegible]MB.seq:*
                  68: [illegible]US6024_COMB.seq:*
                  69: [illegible]MB.seq:*
                  70: [illegible]MB.seq:*
                  71: [illegible]MB.seq:*
                  72: [illegible]MB.seq:*
                  73: [illegible]US6029_COMB.seq:*
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                  [illegible]US6031_COMB.seq:*
                  [illegible]MB.seq:*
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                  [illegible]MB.seq:*
                  [illegible]MB.seq:*
                  [illegible]MB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

Result          %
  No.   Score  Query
               Match Length DB  ID                                Description
------ ------ ------ ------ --  --------------------------------  -----------
   1    [illegible]                                                 Sequence [illegible], App
   2    [illegible]                                                 Sequence [illegible], App
   3    [illegible]                                                 Sequence [illegible], App
   4    [illegible]                                                 Sequence [illegible], Appl
   5    [illegible]                                                 Sequence [illegible], Appli
   6    [illegible] [illegible] 2110 19 US-09-526-996-1047           Sequence 1047, Ap
   7    [illegible]                                                 Sequence [illegible], Ap
   8    [illegible]                      [illegible]-1175           Sequence 1175, Ap
   9    [illegible] 92.[illegible] 21[illegible] US-09-[illegible]-724   Sequence 724, Ap
  10    [illegible]                      [illegible]471-2217         Sequence 2217, Ap
  11    [illegible]                                                 Sequence [illegible], Ap
  12    [illegible] 89.8  21[illegible] [illegible] US-09-471-[illegible]  Sequence [illegible], Ap
  13    [illegible]                                                 Sequence [illegible], Ap
  14    [illegible]                      [illegible]-2199           Sequence 2199, Ap
  15    [illegible]                      [illegible]-140[illegible]  Sequence [illegible], Ap
  16    [illegible]                      [illegible]-21[illegible]   Sequence 21[illegible]87, A
  17    [illegible]                                                 Sequence 14[illegible], Ap
  18    [illegible] 84.4  [illegible]  [illegible]-227              Sequence 22[illegible], Ap
  19    [illegible]                                                 Sequence [illegible], App
  20    [illegible]            [illegible]-US02-[illegible]0474-317  Sequence 317, App
  21    [illegible]                                                 Sequence [illegible], App
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    22   813.6   61.1   1285  80  US-60-360-207 11494          Sequence 11494, A
c   23     815   59.1   1629  25  US-09-644-871 9279           Sequence 9279, Ap
c   24     815   59.1   1629  28  US-09-700-[illegible]        Sequence [illegible], Ap
c   25     815   59.1   1629  29  US-09-727-392 335            Sequence 335, App
c   26   724.2   52.5    733  17  US-09-329-548A 27            Sequence 27, Appl
c   27   724.2   52.5    733  30  US-09-780-183 27             Sequence 27, Appl
c   28     602   43.6   1474  17  US-09-359-922 1187           Sequence 1187, Ap
c   29     602   43.6   1474  17  US-09-359-922 1187           Sequence 1187, Ap
c   30     602   43.6   1474  34  US-09-919-002 1187           Sequence 1187, Ap
    31     536   38.8    547  33  US-09-867-701 2968           Sequence 2968, Ap
    32     536   38.8    547  64  US-60-207-484 2968           Sequence 2968, Ap
c   33   525.4   38.1    531  10  US-09-526-996 159            Sequence 159, App
    34   523.4   37.9    529  23  US-09-540-220 99671          Sequence 99671, A
    35   485.6   35.2    641  [illegible]  US-60-252-8[illegible]  Sequence [illegible], A
    36     442   32.0    455  18  US-09-489-039 28521          Sequence 28521, A
    37     442   32.0    455  35  US-09-943-143 28521          Sequence 28521, A
    38   439.4   31.8    535  69  US-60-252-833 32572          Sequence 32572, A
    39     418   30.3    436  19  US-09-528-499 24533          Sequence 24533, A
    40     418   30.3    436  35  US-09-933-524 24533          Sequence 24533, A
    41     418   30.3    436  35  US-09-933-524A 24533         Sequence 24533, A
    42   414.4   30.0    416  19  US-09-528-499 59754          Sequence 59754, A
    43   414.4   30.0    416  35  US-09-933-524 59754          Sequence 59754, A
    44   414.4   30.0    416  35  US-09-933-524A 59754         Sequence 59754, A
    45   411.2   29.8    615  17  US-09-335-313 159            Sequence 159, App
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ALIGNMENTS

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RESULT 1
US-09-866-987-3
; Sequence 3, Application US/09866987
; GENERAL INFORMATION:
;  APPLICANT: PLOWMAN, GREGORY D.
;  APPLICANT:  MARTINEZ, RICARDO
;  APPLICANT:  WHYTE, DAVID
;  APPLICANT:  MANNING, GERARD
;  APPLICANT:  SUDARSANAM, SUCHA
;  APPLICANT:  CAENEPEEL, SEAN
;  APPLICANT:  HILL, RON
;  APPLICANT:  FLANAGAN, PETER
;  TITLE OF INVENTION: MAMMALIAN PROTEIN PHOSPHATASES
;  FILE REFERENCE: [illegible]/118
;  CURRENT APPLICATION NUMBER: US/09/866,987
;  CURRENT FILING DATE:  2001-05-30
;  PRIOR APPLICATION NUMBER: [illegible]/208,291
;  PRIOR FILING DATE: 2000-05-30
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 138
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: phosphatase nucleotide
US-09-866-987-3

  Query Match             100.0%;  Score 1380;  DB 33;  Length 138;
  Best Local Similarity   100.0%;  Pred. No. [illegible];
  Matches 138;  Conservative    0;  Mismatches  [illegible];  Indels  [illegible];  Gaps  [illegible];

Qy          1 AT[illegible] 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCGCCGGCTGGTTCCGGCGCCGCTTCCTGCCTGGGGAGCCGCTGCCGGCGGCGCGG 60

Qy         61 [illegible] 120

Db         61 [illegible] 120

Qy        121 AGCTCCAG[illegible] 180

Db        121 AGCTCCAGCCCCGGGGCGGCCGACGCCTCGCGCCGCCCAGACTCCCGGCCCGTGCCCAGC 180

Qy        181 [illegible]

Db        181 [illegible]

Qy        241 AAAT[illegible]

Db        241 AAAT[illegible]

Qy        301 [illegible]

Db        301 [illegible]

Qy        361 [illegible]

Db        361 [illegible]

Qy        421 [illegible]

Db        421 [illegible]

Qy        481 [illegible]

Db        481 [illegible]

Qy        541 [illegible]

Db        541 [illegible]

Qy        601 [illegible]

Db        601 [illegible]

Qy        661 [illegible]

Db        661 [illegible]

Qy        721 [illegible]

Db        721 [illegible]

Qy        781 [illegible]

Db        781 [illegible]

Qy        841 [illegible]

Db        841 [illegible]

Qy        901 [illegible]

Db        901 [illegible]

Qy        961 [illegible]

Db        961 [illegible]

Qy       1021 [illegible]

Db       1021 [illegible]

Qy       1081 [illegible]

Db       1081 [illegible]

Qy       1141 [illegible]

Db       1141 [illegible]

Qy       1201 [illegible]

Db       1201 [illegible]
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Qy       1261 [illegible] 1320
Db       1416 [illegible] 1475

Qy       1321 GAGGTCTCTGTGTTCTGTGATTTCCTTGGCACAGTCAGGGCAAAGAGAGCAGTGACCACTGA 1380
              [illegible]
Db       1476 [illegible]

RESULT 2
PCT-US02-30474-316
; Sequence 316, Application PC/TUS0230474
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Ghosh, Malabika
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Wang, [illegible]
;  APPLICANT:  Wang, [illegible]
;  APPLICANT:  [illegible]
;  APPLICANT:  Drmanac, Radoje T.
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 810CIP PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/30474
;  CURRENT FILING DATE:  2002-09-24
;  PRIOR APPLICATION NUMBER: US 60/324,631
;  PRIOR FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: US 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: PCT/US00/35017
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: PCT/US01/02623
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: US 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: PCT/US01/03800
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: US 09/515,126
;  PRIOR FILING DATE: 2000-02-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3476
;  SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 316
;   LENGTH: 2054
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (156)..(1535)
PCT-US02-30474-316

  Query Match             100.0%;  Score 1380;  DB 1;  Length 2054;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-273;
  Matches 1380;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTCCGCCGGCTGGTTCCGGCGCCGCTTCCTGCCTGGGGAGCCGCTCCCCGCGCCGCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 ATGTCCGCCGGCTGGTTCCGGCGCCGCTTCCTGCCTGGGGAGCCGCTCCCCGCGCCGCGG 215

Qy         61 [illegible] 120
              [illegible]
Db        216 [illegible] 275

Qy        121 [illegible] 180
              [illegible]
Db        276 [illegible] 335

Qy        181 [illegible] 240
              [illegible]
Db        336 [illegible] 395

Qy        241 AAATCTGAATTCAATGAGGATCAAATCGGCTGTGGAAGCTGTGCATCGGAGATGTGAC 300
              [illegible]
Db        396 [illegible] 455

Qy        301 [illegible] 360
              [illegible]
Db        456 [illegible] 515

Qy        361 [illegible] 420
              [illegible]
Db        516 [illegible] 575

Qy        421 [illegible] 480
              [illegible]
Db        576 [illegible] 635

Qy        481 [illegible] 540
              [illegible]
Db        636 [illegible] 695

Qy        541 [illegible] 600
              [illegible]
Db        696 [illegible] 755

Qy        601 [illegible] 660
              [illegible]
Db        756 [illegible] 815

Qy        661 GCTGTGTCCCTGCAGGGAAACTGTACATGGCAATGCTGGGGATAGCAGGCCATCTTC 720
              [illegible]
Db        816 [illegible] 875

Qy        721 [illegible] 780
              [illegible]
Db        876 [illegible] 935

Qy        781 CGGATCCAGCAGCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCTGACTT 840
              [illegible]
Db        936 [illegible] 995

Qy        841 [illegible] 900
              [illegible]
Db        996 [illegible] 1055

Qy        901 [illegible] 960
              [illegible]
Db       1056 [illegible] 1115

Qy        961 [illegible] 1020
              [illegible]
Db       1116 [illegible] 1175

Qy       1021 [illegible] 1080
              [illegible]
Db       1176 [illegible] 1235

Qy       1081 CCACAGTTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTCTTCTCT 1140
              [illegible]
Db       1236 CCACAGTTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATG[illegible] 1295
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Qy       1141 ATGGCAACTGATGGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGG 1200
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Db       1296 ATGGCAACTGATGGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGG 1355

Qy       1201 [illegible]
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1356 AGCTTCCTCCCTGGGAACCAAGAGGACCCACACAGGTTCTCAAAGCTGGCCCAGATGCTG 1415

Qy       1261 ATACACAGCACACAGGGAAAGGAAGACAGTCTCACAGAGGAAGGCAGGTGTCCTACGAT 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1416 ATACACAGCACACAGGGAAAGGAAGACAGTCTCACAGAGGAAGGCAGGTGTCCTACGAT 1475

Qy       1321 GACGTCTCTGTGTTCGTGATTCCCTTGCACAGTCAGGGCCAAGAGAGCAGTGACCACTGA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1476 GACGTCTCTGTGTTCGTGATTCCCTTGCACAGTCAGGGCCAAGAGAGCAGTGACCACTGA [illegible]


RESULT 3
US-60-324-631-318
; Sequence 318, Application US/60324631
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Ghosh, Malabika
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Weng, Gezhi
;  APPLICANT:  Haley-Vicente, Dana
;  APPLICANT:  Drmanac, Radoje T
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 810
;  CURRENT APPLICATION NUMBER: US/60/324,631
;  CURRENT FILING DATE:  2001-09-24
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US 09/4[illegible]
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: US 09/[illegible],705
;  PRIOR FILING DATE: 2000-03-07
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-03-05
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: pt FL genes Version [illegible]
; SEQ ID NO 318
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: [illegible]
US-60-324-631-318

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

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Db        156 [illegible]

Qy         61 [illegible]
Db        216 [illegible]

Qy        121 [illegible]
Db        276 [illegible]

Qy        181 [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
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Db        816 CCTGCTTCCTGCAGGAAAATTTTACATGATTAATGTTGGGATACTA[illegible] 875

Qy        721 GTGGGGAGAGATGAGATAC[illegible]ACTGAGTTTGAGTTCACCCAGAGACTGAG[illegible]CAC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        876 GTGGGGAGAGATGAGATAC[illegible]ACTGAGTTTGAGTTCACCCAGAGACTGAG[illegible]CAC 935

Qy        781 CGGATCCAGCAGCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTG 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        936 CGGATCCAGCAGCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTG 995

Qy        841 GAGTTCCCTCGGGCGCTGAAGGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCAC 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        996 GAGTTCCCTCGGGCGCTGAAGGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCAC 1055

Qy        901 CACATGAGTGGCTGCAGCTACAAAGTGTGGAGAAACCGATCCAAGTACCCACTGATC 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1056 CACATGAGTGGCTGCAGCTACAAAGTGTGGAGAAACCGATCCAAGTACCCACTGATC 1115

Qy        961 CATGGACAGGGTAGGCAGGCTGGCTACTAGGAACACTGGCTGTCTCCCTGGGCCTGGGA 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1116 CATGGACAGGGTAGGCAGGCTGGCTACTAGGAACACTGGCTGTCTCCCTGGGCCTGGGA 1175

Qy       1021 GACTATCAGCCAGAGCCTGGACACAAACATCCAGCCAAGCCTTTCTTGTCTCTCTGTG 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1176 GACTATCAGCCAGAGCCTGGACACAAACATCCAGCCAAGCCTTTCTTGTCTCTCTGTG 1235

Qy       1081 CCACAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTC 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1236 CCACAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTC 1295

Qy       1141 ATCCAACTGATGGACTCCTTGATCTACTGTCTAACTACAAGGTGGATCCTCTGGTGCGG 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1296 ATCCAACTGATGGACTCCTTGATCTACTGTCTAACTACAAGGTGGATCCTCTGGTGCGG 1355

Qy       1201 AGCTTCCTCCCTGGGAACCAAGAGGACCCACACAGGTTCTCAAAGCTGGCCCAGATGCTG 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1356 AGCTTCCTCCCTGGGAACCAAGAGGACCCACACAGGTTCTCAAAGCTGGCCCAGATGCTG 1415

Qy       1261 ATACACAGCACACAGGGAAAGGAAGACAGTCCACACACCAAGCCACCTCCCCTACCAT 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1416 ATACACAGCACACAGGGAAAGGAAGACAGTCCACACACCAAGCCACCTCCCCTACCAT 1475

Qy       1321 GACGTCTCTGTCTTCGGTGATTCCCTTGCACAGTCAGGGCCAAGAGAGCAGTGACCACTGA 1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1476 GACGTCTCTGTCTTCGGTGATTCCCTTGCACAGTCAGGGCCAAGAGAGCAGTGACCACTCA 1535
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RESULT 4
US-10-181-590-13
; Sequence 13, Application US/10181590
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  BANDMAN, Olga
;  APPLICANT:  MATHUR, Preeti
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  AZIMZAI, Yalda
;  APPLICANT:  YUE, Henry
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  HILLMAN, Jennifer L.
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  WANG, Eureka
;  APPLICANT:  GANDHI, Ameena R.
;  APPLICANT:  POLICKY, Jennifer L.
;  TITLE OF INVENTION: PHOSPHATASES
;  FILE REFERENCE: PI-0018 PCT
;  CURRENT APPLICATION NUMBER: US/10/181,590
;  CURRENT FILING DATE: 2002-07-19
;  PRIOR APPLICATION NUMBER: 60/177,735; [illegible]
;  PRIOR FILING DATE: 2000-01-21; 2000-01-28; 2000-02-25; 2000-03-17
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PERL Program
; SEQ ID NO 13
;    LENGTH: 1837
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: misc_feature
;    OTHER INFORMATION: Incyte ID No: 1724417CB1
US-10-181-590-13

  Query Match             99.2%;  Score 1369;  DB 41;  Length 1837;
  Best Local Similarity   99.9%;  Pred. No. 6.3e-271;
  Matches 1380;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 ATGTCCGTCGGCAGGTTCCGGCTGCTTTCCTGGCTGGGAGCCCCTCCCCGG[illegible] 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCCGTCGGCAGGTTCCGGCTGCTTTCCTGGCTGGGAGCCCCTCCCCGG[illegible] 60

Qy         61 CCGCCTGGCCGCATGCCAGCCCGTGCCCTACCGACGGCCCGCTTCCTTCGCCGG[illegible] 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGCCTGGCCGCATGCCAGCCCGTGCCCTACCGACGGCCCGCTTCCTTCGCCGG[illegible] 120

Qy        121 ACTCCAGCCCCGGGCGCCCTACGCC[illegible]GCCAGACTCCCGGCCGC[illegible] 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ACTCCAGCCCCGGGCGCCCTACGCC[illegible]GCCAGACTCCCGGCCGC[illegible] 180

Qy        181 CCCGCACGAGGACCCACGCTACCTGGAATGCAGGCTACGCCGAGATTATCAATGCAGAG 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCCGCACGAGGACCCACGCTACCTGGAATGCAGGCTACGCCGAGATTATCAATGCAGAG 240

Qy        241 AAATCTCAATTCAATGATGATTAACTCC[illegible]TTGAATTTGTTCATCGGAGATTTCAT 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAATCTCAATTCAATGATGATTAACTCC[illegible]TTGAATTTGTTCATCGGAGATTTCAT 300

Qy        301 TTTGGGGCTGAAGACAGATCT[illegible]TTAGACCAGCTTCTGAGGGCCATTAC 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTTGGGGCTGAAGACAGATCT[illegible]TTAGACCAGCTTCTGAGGGCCATTAC 360

Qy        361 TCCGCACTGTTCGATCCCTACC[illegible]CCCAGCAGCCATCTTCCCTGCCAACACCTTCC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TCCGCACTGTTCGATCCCTACC[illegible]CCCAGCAGCCATCTTCCCTGCCAACACCTTCC 420

Qy        421 CACTCCTGCTTGCCCCGGCAGCTGGAGCGCGTGGTGGAAGGCTTGGTGGCCACCTACCCC 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CACTCCTGCTTGCCCCGGCAGCTGGAGCGCGTGGTGGAAGGCTTGGTGGCCACCTACCCC 480

Qy        481 CCCATGCACTTCAATGGCCGCTGCATCTGCCCCAGTGACCCTCAGTTTGTGGAGGGAAAT 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCCATGCACTTCAATGGCCGCTGCATCTGCCCCAGTGACCCTCAGTTTGTGGAGGGAAAT 540

Qy        541 GCCATCAGGGCAGAAGATTCGGTGATCCCCCCATTCCAGACTGCCTTTCAGGAATTTGAT 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCATCAGGGCAGAAGATTCGGTGATCCCCCCATTCCAGACTGCCTTTCAGGAATTTGAT 600

Qy        601 GAGGTGATGGGCCCAGAGCTGGAGGCCTCAGGCCAGATGGGCGGCTGCACAGCCCTCCTG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAGGTGATGGGCCCAGAGCTGGAGGCCTCAGGCCAGATGGGCGGCTGCACAGCCCTCCTG 660

Qy        661 CCTGCTTCCTGCAGGAAAAGTTCCACATGCCCAATGCCCCGGACACATGC[illegible] 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCTGCTTCCTGCAGGAAAAGTTCCACATGCCCAATGCCCCGGACACATGC[illegible] 720

Qy        721 GTGGGGAGAGATGAGATACGGCTACTGAGTTTGAGTTCACCCAGAGACTGAG[illegible]CAC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GTGGGGAGAGATGAGATACGGCTACTGAGTTTGAGTTCACCCAGAGACTGAG[illegible]CAC 780

Qy        781 CGGATCCAGCAGCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTG 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGATCCAGCAGCTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTG 840

Qy        841 GAGTTCCCTCGGGCGCTGAAGGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCAC 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 GAGTTCCCTCGGGCGCTGAAGGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCAC 900

Qy        901 CACATGAGTGGCTGCAGCTACAAAGTGTGGAGAAACCGATCCAAGTACCCACTGATC 960
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Db        961 [illegible]

Qy       1021 [illegible] 1080

Db       1021 [illegible] 1080

Qy       1081 [illegible] 1140

Db       1081 [illegible] 1140

Qy       1141 [illegible] 1200

Db       1141 [illegible] 1200

Qy       1201 [illegible] 1259

Db       1201 [illegible] 1260

Qy       1260 GATACACAGCACACAGGAAAGGAAGACAGTCTCACAGAGGAAGGGAGGTGTCCTACGA 1319
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GATACACAGCACACAGGAAAGGAAGACAGTCTCACAGAGGAAGGGAGGTGTCCTACGA 1320

Qy       1320 [illegible] 1379

Db       1321 [illegible] 1380

Qy       1380 A 1380

Db       1381 A 1381


RESULT 5
US-60-178-988-7
; Sequence 7, Application US/60178988
; GENERAL INFORMATION:
;  APPLICANT: Yue, Henry
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: Baughn, Mariah R.
;  TITLE OF INVENTION: [illegible]
;  FILE REFERENCE: PI-0023 P
;  CURRENT APPLICATION NUMBER: US/60/178,988
;  CURRENT FILING DATE: 2000-01-28
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PERL Program
; SEQ ID NO 7
;   LENGTH: 1837
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: 172-6447CB1
US-60-178-988-7

  Query Match             99.2%;  Score 1369;  DB 61;  Length 1837;
  Best Local Similarity   99.9%;  Pred. No. 6.3e-271;
  Matches 1380;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 [illegible] 60

Db          1 [illegible] 60

Qy         61 [illegible] 120

Db         61 [illegible] 120

Qy        121 [illegible] 180

Db        121 [illegible] 180

Qy        181 [illegible] 240

Db        181 [illegible] 240

Qy        241 [illegible] 300

Db        241 [illegible] 300

Qy        301 [illegible] 360

Db        301 [illegible] 360

Qy        361 [illegible] 420

Db        361 [illegible] 420

Qy        421 [illegible] 480

Db        421 [illegible] 480

Qy        481 [illegible] 540

Db        481 [illegible] 540

Qy        541 [illegible] 600

Db        541 [illegible] 600

Qy        601 [illegible] 660

Db        601 [illegible] 660

Qy        661 [illegible] 720

Db        661 [illegible] 720

Qy        721 [illegible] 780

Db        721 [illegible] 780

Qy        781 [illegible] 840

Db        781 [illegible] 840

Qy        841 [illegible] 900

Db        841 [illegible] 900

Qy        901 [illegible] 960

Db        901 [illegible] 960

Qy        961 [illegible] 1020

Db        961 [illegible] 1020

Qy       1021 [illegible] 1080

Db       1021 [illegible] 1080

Qy       1081 [illegible] 1140

Db       1081 [illegible] 1140

Qy       1141 [illegible] 1200

Db       1141 [illegible] 1200

Qy       1201 [illegible] 1260

Db       1201 [illegible] 1260
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Qy       1260 GATACACAGCACACAGGGAAA[illegible] 1319
              [illegible]
Db       1261 [illegible]

Qy       1320 [illegible] 1379
              [illegible]
Db       1321 [illegible]

Qy       1380 A 1380
              |
Db       1381 A 1381


RESULT 6
US-09-526-996-1047/c
; Sequence 1047, Application US/09526996
; GENERAL INFORMATION:
;  APPLICANT: Shyjan, Andrew W.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM
;  TITLE OF INVENTION: HUMAN PROSTATE AND BREAST LIBRARIES
;  FILE REFERENCE: 1600.1[illegible]
;  CURRENT APPLICATION NUMBER: US/09/526,996
;  CURRENT FILING DATE: 2000-[illegible]-15
;  EARLIER APPLICATION NUMBER: 60/125,469
;  EARLIER FILING DATE: 1999-03-22
;  EARLIER APPLICATION NUMBER: 60/125,560
;  EARLIER FILING DATE: 1999-03-22
;  NUMBER OF SEQ ID NOS: 1296
;  SOFTWARE: [illegible]
; SEQ ID NO 1047
;   LENGTH: 2110
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-526-996-1047

  Query Match             93.1%;  Score 1285;  DB 19;  Length 2110;
  Best Local Similarity   99.9%;  Pred. No. 1.2e-253;
  Matches 1296;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         85 GTGCCCTACCGACGGCCCCGCTTCCTTCGCGGCTCCAGCTCCAGCCCCGGGCGGCCGAC 144
              [illegible]
Db       2110 GTGCCCTACCGACGGCCCCGCTTCCTTCGCGGCTCCAGCTCCAGCCCCGGGCGGCCGAC 2051

Qy        145 GCCTCGGCGCCGCCCAGACTCCCGGCCCGTGCGCAGCCCCGCACGAGGACGCACGCTACCC 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2050 GCCTCGGCGCCGCCCAGACTCCCGGCCCGTGCGCAGCCCCGCACGAGGACGCACGCTACCC 1991

Qy        205 [illegible] 263
              [illegible]
Db       1990 [illegible] 1931

Qy        264 AGCCGCCTGTGGGAAGTTGTGATCGGAGATCTGAGTTTGGGCTGAAGAAGACTGCCT 323
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1930 AGCCGCCTGTGGGAAGTTGTGATCGGAGATCTGAGTTTGGGCTGAAGAAGACTGCCT 1871

Qy        324 [illegible] 383
              [illegible]
Db       1870 [illegible] 1811

Qy        384 [illegible]CAGCT 443
              [illegible]
Db       1810 CGGTCCTGCAGCAG[illegible]

Qy        444 [illegible]
              [illegible]
Db       1750 [illegible]

Qy        504 [illegible] 563
              [illegible]
Db       1690 CATCTGGCCCAGTGACCCTCAGTTTGTGGAGGAAAAGGGCATCAGGGCAGAAGACTTGCT 1631

Qy        564 [illegible]TGGA 623
              [illegible]

Db       1630 [illegible]CAGGTGATCGGGCGGGAGCTGGA 1571

Qy        624 [illegible]
              [illegible]
Db       1570 GGCTCAGGGCAGACGGGGGGCGCAGAGGCTGGTGGCTGTGGCCCTGCAGGGAAATTT 1511

Qy        684 [illegible]
              [illegible]
Db       1510 GTACATGGGCAATGCTGGGGATAGAAGGGCCATCTGGTGCGGAGAGATCAGATACGGGC 1451

Qy        744 [illegible]
              [illegible]
Db       1450 [illegible]

Qy        804 [illegible]
              [illegible]
Db       1390 [illegible]

Qy        864 [illegible] 923
              [illegible]
Db       1330 [illegible] 1271

Qy        924 [illegible]
              [illegible]
Db       1270 [illegible] 1211

Qy        984 [illegible]
              [illegible]
Db       1210 [illegible] 1151

Qy       1044 [illegible]
              [illegible]
Db       1150 [illegible]

Qy       1104 GGACCAGTTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGATGGACTCCGGA 1163
              [illegible]
Db       1090 GGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGATGGACTCCGGA 1031

Qy       1164 TGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTCCTCCCTGGGAACAAAGA 1223
              [illegible]
Db       1030 TGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTCCTCCCTGGGAACAAAGA 971

Qy       1224 GGACCCACACAGGTTCTCAAAGCTGGCCCAGATGCTGATACACAGCACACAGGGAAACCA 1283
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        970 GGACCCACACAGGTTCTCAAAGCTGGCCCAGATGCTGATACACAGCACACAGGGAAACCA 911

Qy       1284 [illegible]
              [illegible]
Db        910 [illegible]

Qy       1344 [illegible] 1380
              [illegible]
Db        850 [illegible] 814


RESULT 7
US-09-[illegible]-1175/c
; Sequence 1175, Application US/[illegible]
; GENERAL INFORMATION:
;  APPLICANT: Gearing, David P.
;  APPLICANT: Kingsbury, Gillian A.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM
;  TITLE OF INVENTION: HUMAN BONE MARROW AND T CELL LIBRARIES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: [illegible]
;  EARLIER FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: 1284
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1175
;   LENGTH: 2110
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-540-236-1175

  Query Match             93.1%;  Score 1285;  DB 21;  Length 2110;
  Best Local Similarity   99.[illegible]%;  Pred. No. 1.2e-253;
  Matches 1296;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy         85 TGGCCTACCGAG[illegible] 144
              [illegible]
Db       2110 TGGCCTACCGAG[illegible] 2051

Qy        145 [illegible] 204
              [illegible]
Db       2050 [illegible]CAGAC[illegible] 1991

Qy        205 TGGAATGCAGGCTACGCGA-GATTATCAATGCAGAGAAATCTGAATTCAATGAGGATCA 263
              ||| ||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Db       1990 TGGAATGCAGGCTACGCGATGATTATCAATGCAGAGAAATCTGAATTCAATGAGGATCA 1931

Qy        264 AGCCGCCTGTGGGAAGCTGTGCATCCGGAGATGTGACTTTGGGGCTGAAGAAGAGTGGCT 323
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1930 AGCCGCCTGTGGGAAGCTGTGCATCCGGAGATGTGACTTTGGGGCTGAAGAAGAGTGGCT 1871

Qy        324 GACCCTGTGGCCAGAGGAGCTCCTGACAGGCCATTACTGGGGACTGTTCGATGCCACCG 383
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1870 GACCCTGTGGCCAGAGGAGCTCCTGACAGGCCATTACTGGGGACTGTTCGATGCCACCG 1811

Qy        384 CGGTCCTGCAGCAGCCATCTTGGCTGCCAACACCCTGCACTCCTGCTTGCGCCGGCAGCT 443
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1810 CGGTCCTGCAGCAGCCATCTTGGCTGCCAACACCCTGCACTCCTGCTTGCGCCGGCAGCT 1751

Qy        444 GGAGGCCGTGGTGGAAGG[illegible] 503
              [illegible]
Db       1750 GGAGGCCGTGGTGGAAGG[illegible] 1691

Qy        504 [illegible] 563
              [illegible]
Db       1690 CATCTGCCCCAGGGACCCTCAGTTTGTGGAGGAAAGGCCATCAGGCAGAAGATTGCTC 1631

Qy        564 GATGGGGCATTGGAGAGGGACCTTTCAGGAATGTGATGAGGTGATCCGGCTGGAGCTGGA 623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1630 GATGGGGCATTGGAGAGGGACCTTTCAGGAATGTGATGAGGTGATCCGGCTGGAGCTGGA 1571

Qy        624 GCCCTCAGGCAGA[illegible]AGAAATTT 683
              [illegible]
Db       1570 GCCCTCAGGCAGA[illegible]ATGAAATTT 1511

Qy        684 GTACATGGCCAA[illegible]ATACCAGGGCCAT[illegible]GAGAGATGAGATACCCC 743
              [illegible]
Db       1510 GTACATGGCCAA[illegible]ATACCAGGGCCAT[illegible]GAGAGATGAGATACCCC 1451

Qy        744 ACTGAGCTTCGAGTTCACCCAGAGACTGAGCGGCAGCGGATCCAGCAGCTGGCCTTTGT 803
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1450 ACTGAGCTTCGAGTTCACCCAGAGACTGAGCGGCAGCGGATCCAGCAGCTGGCCTTTGT 1391

Qy        804 CTATCCTGAGCTTCTGG[illegible]GAGTTCACCGACTGGAG[illegible]GAAGGT 863
              [illegible]
Db       1390 CTATCCTGAGCTTCTGG[illegible]GAGTTCACCGACTGGAG[illegible]GAAGGT 1331

Qy        864 GGATGACTTGGGACAGAA[illegible] 923
              [illegible]
Db       1330 GGATGACTTGGGACAGAA[illegible] 1271

Qy        924 ACGTGTGGAGAAATCGGATCCAAGTACCCACTGATCCATGGACAGGGTAGGCAGGCTGT 983
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1270 ACGTGTGGAGAAATCGGATCCAAGTACCCACTGATCCATGGACAGGGTAGGCAGGCTGT 1211

Qy        984 TTTACTAGGAACACTGGCTGTCTCCCGGGGCCTGGAGACCATCAGCTCAGATGCCTCCA 1043
              [illegible]
Db       1210 TTTACTAGGAACACTGGCTGTCTCCCGGGGCCTGGAGACCATCAGCTCAGATGCCTCCA 1151

Qy       1044 CATAAACATCCAGTTCAA[illegible] 1103
              [illegible]
Db       1150 CATAAACATCCAGTTCAA[illegible]

Qy       1104 [illegible]
              [illegible]
Db       1090 [illegible]

Qy       1164 [illegible]
              [illegible]
Db       1030 [illegible]

Qy       1224 [illegible]
              [illegible]
Db        970 [illegible]

Qy       1284 [illegible]
              [illegible]
Db        910 [illegible]

Qy       1344 [illegible]
              [illegible]
Db        850 [illegible]


RESULT [illegible]
US-09-[illegible]
; Sequence [illegible], Application US/[illegible]
; GENERAL INFORMATION:
;  APPLICANT: Gearing, David P.
;  APPLICANT: Kingsbury, Gillian A.
;  TITLE OF INVENTION: NUCLEIC ACID MOLECULES DERIVED FROM
;  TITLE OF INVENTION: HUMAN BONE MARROW AND [illegible] CELL LIBRARIES
;  FILE REFERENCE: [illegible]
;  CURRENT APPLICATION NUMBER: US/[illegible]
;  CURRENT FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: [illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: FastSEQ for Windows Version [illegible]
; SEQ ID NO [illegible]
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-[illegible]

  Query Match             [illegible]
  Best Local Similarity   [illegible]
  Matches [illegible]

Qy         85 [illegible]
              [illegible]
Db       2110 [illegible]

Qy        145 [illegible]
              [illegible]
Db       2050 [illegible]

Qy        205 [illegible]
              [illegible]
Db       1990 [illegible]

Qy        264 [illegible]
              [illegible]
Db       1930 [illegible]

Qy        324 [illegible]
              [illegible]
Db       1870 [illegible]

Qy        384 [illegible]
              [illegible]
Db       1810 [illegible]

Qy        444 [illegible]
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               |||||||||||| ||||||||||||||||||||||||||||||||||| ||||||||
Db       1750 GGAGGCCCTGGTGGAAGCTTGGTGGCCACTCAGCCCCCATGCACCTCAATGCCCAGCTC 1691

Qy        504 CATCTGCCCCAGTGACCTCAGTTTGTGGAGGAAAAGCCCATCAGCCCACAACACTTGCC 563
               ||||||||||||| |||||||||||||||||||||||||||||||||||| |||||||||
Db       1690 CATCTGCCCCAGTGACCTTCAGTTTGTGGAGGAAAAGCCCATCAGCCCACAACACTTGCC 1631

Qy        564 GATCGGGGCATTGGAGAGTGCCTTTCAGGAATGTGATGAGGTGATCGGGGGGAGCTGGA 623
               |||||||||||||||||||||.||||||||||||||||||||||||||||.||||||||
Db       1630 GATCGGGGCCATTGGAGAGTGCCTTTCAGGAATGTGATGAGGTGATCGGGGGGAGCTGGA 1571

Qy        624 GGCCTCAGGCCAGATGCGGGGCTGCACAGCCCTGCTCCCTCTCTGCTCCAGCCAAAGCT 683
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1570 GGCCTCAGGCCAGATGCGGGGCTGCACAGCCCTGCTCCCTCTCTGCTCCAGCCAAAGCT 1511

Qy        684 GTACATGCCCAATGCTGGGGATAGCAGGGCCATCTTGGTGGGGAGACATGATACGGGC 743
               ||||||||||||||||||||||||||||||||||||||||.||||||||||||||||||
Db       1510 GTACATGCCCAATGCTGGGGATAGCAGGGCCATCTTGGTGGGGAGACATGATACGGGC 1451

Qy        744 ACTGAGCTTCGAGTTCACCCAGAGACTGAGCGGCAGCGGATCCAGCAGCTGGCCTTGT 803
               ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db       1450 ACTGAGCTTCGAGTTCACCCAGAGACTGAGCGGCAGCGGATCCAGCAGCTGGCCTTGT 1391

Qy        804 CTATCCTGAGCTTCTGGTTGGTGAGTTCACCGACTGGAGTTCCCTCGGCGGCTGAAGGG 863
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1390 CTATCCTCAGCTTCTGGTTGGTGAGTTCACCGACTGGAGTTCCCTCGGCGGCTGAAGGG 1331

Qy        864 GGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCACCACATGACTGGCTGGAGCTACAA 923
               |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1330 GGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCACCACATGACTGGCTGGAGCTACAA 1271

Qy        924 ACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGACAGGGTAGGCAGGCTCG 983
               ||||||||||||||||||||||||||||||||||||||||||||.||||||||||||||
Db       1270 ACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGACAGGGTAGGCAGGCTCG 1211

Qy        984 GTTACTAGGAACACTGGCTGTTCCCGGGGCCTGGGAGACCATCAGCTCAGAGTCCTGGA 1043
               |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1210 GTTACTAGGAACACTGGCTGTTCCCGGGGCCTGGGAGACCATCAGCTCAGAGTCCTGGA 1151

Qy       1044 CACAAACATCCAGCTCAAGCCCTTCTTGCTCTCTGTGCCACAGGTGACTGTGCTGGATGT 1103
               ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db       1150 CACAAACATCCAGCTCAAGCCCTTCTTGCTCTCTGTGCCACAGG.GACTGTGCTGGATGT 1091

Qy       1104 GGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGATGGACTCTGGGA 1163
               ||||||||||||||||||||||||||||||||||||||||||.||||||||||||||||
Db       1090 GGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGATGGACTCTGGGA 1031

Qy       1164 TGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTCCTGCCTGGGAACCAAGA 1223
               ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1030 TGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTCC.GCCTGGGAACCAAGA 971

Qy       1224 GGACCCACACAGGTTCTCAAAGCTGGCCCAGATGCTGATCCACAGCACACAGGCAAAGGA 1283
               |||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db        970 GGACCCACACAGGTTCTCAAAGCTGGCCCAGATGCTGATCCACAGCACACAGGCAAAGGA 911

Qy       1284 AGACAGTCTCACAGAGGAAGGGCAGGTGTCCTACGATGACGTCTCTGTGTTCGTGATTCC 1343
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        910 AGACAGTCTCACAGAGGAAGGGCAGGTGTCCTACGATGACGTCTCTGTGTTCGTGATTCC 851

Qy       1344 CTTGCACAGTCAGGGCCAAGAGAGCAGTGACCACTGA 1380
               |||||||||||||||||||||||||||||||||||||
Db        850 CTTGCACAGTCAGGGCCAAGAGAGCAGTGACCACTGA 814


RESULT 9
US-09-760-475-724
; Sequence 724, Application US/09760475
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PT749
;  CURRENT APPLICATION NUMBER: US/09/760,475
;  CURRENT FILING DATE: 2001-01-16
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 4122
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 724
;   LENGTH: 2156
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (65)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (73)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (83)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: SITE
;   LOCATION: (2088)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-760-475-724

  Query Match             92.7%;  Score 1279;  DB 30;  Length 2156;
  Best Local Similarity   99.6%;  Pred. No. 2e-252;
  Matches 1301;  Conservative    0;  Mismatches    3;  Indels    2;  Gaps    2;

Qy         75 TGCCAGCCCCGTGCCCTACCGACGGCCCCGCTTCCTTCGGCGGCTCCAGCTCCAGCCCGG 134
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Db          1 TGCCAGCCCCGTGCCCTACCGACGGCCCCGCTTCCTTCGGCGGCTCCAGCTCCAGCCCGG 60

Qy        135 GGCGGCCGACGCCTCGGCGCCGCCCAGACTCCCGGCCCGTGCGCAGCCCCGCACGACGACG 194
              |||| ||||||| ||||||||| ||||||||||||||||||||||||||||||||||||
Db         61 GGCGNCCGACGCNTCGGCGCCGCNCAGACTCCCGGCCCGTGCGCAGCCCCGCACGACGACG 120

Qy        195 CACCCTACCCTGGAATGCAGGCTACGCCGAGATTATCAATGCAGAGAAATCTGAATTCAA 254
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        121 CACCCTACCCTGGAATGCAGGCTACG-CGAGATTATCAATGCAGAGAAATCTGAATTCAA 179

Qy        255 TGAGGATCAAGCGGCCTGTGGGAAGCTGTGCATCCGGAGATGTGAGTTTGGGGCTGAAGA 314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 TGAGGATCAAGCGGCCTGTGGGAAGCTGTGCATCCGGAGATGTGAGTTTGGGGCTGAAGA 239

Qy        315 AGAGTGGCTGACCCTGTGCCCAGAGGAGTTCCTGACAGGCCATTACTGGGCACTGTTTGA 374
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        240 AGAGTGGCTGACCCTGTGCCCAGAGGAGTTCCTGACAGGCCATTACTGGGCACTGTTTGA 299

Qy        375 TGGGCAGGGCGGTCCTGCAGCAGCCATCTTGGCTGCCAACACCCTGCACTCCTGCTTGCG 434
              ||||||||||||||||||||||||||||||||||||||||||.||||||||||||||.|
Db        300 TGGGCAGGGCGGTCCTGCAGCAGCCATCTTGGCTGCCAACACCC.GCACTCCTGCTTGCG 359

Qy        435 CCGGCAGCTGGAGGCCGTGCTGGAAGGTTTGGTGGCCATTCAGCCCCCATGCACCTCAA 494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        360 CCGGCAGCTGGAGGCCGTGCTGGAAGGTTTGGTGGCCATTCAGCCCCCATGCACCTCAA 419

Qy        495 TGGCCGCTGCATCTGCCCCAGTGACCTCAGTTTGTGGAGGAAAAGCCCATCAGCCCACA 554
              ||||||||||||||||||||||.|||||||||||||||||||||||||||||||||||
Db        420 TGGCCGCTGCATCTGCCCCAGTGACCTCAGTTTGTGGAGGAAAAGGGCATCAGGGCACA 479

Qy        555 AGACTTGGTGATCGGGGCATTGGAGAGTGCCTTTCAGGAATGTGATGAGGTGATCGGGG 614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        480 AGACTTGGTGATCGGGGCATTGGAGAGTGCCTTTCAGGAATGTGATGAGGTGATCGGGG 539

Qy        615 GGAGCTGGAGGCCTCAGGCCAGATGCGGGGCTGCACAGCCCTGCTCCCTCTCTGCTCCA 674
              ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db        540 GGAGCTGGA-GCCTCAGGCCAGATGCGGGGCTGCACAGCCCTGCTCCCTCTCTGCTCCA 598

Qy        675 GGGAAAGCTGTACATGGCCAATGCTGGGGATAGCAGGGCCATCTTGGTGCGGAGACATGA 734
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        599 GGGAAAGCTGTACATGGCCAATGCTGGGGATAGCAGGGCCATCTTGGTGCGGAGACATGA 658

Qy        735 GATACGGGCACTGAGCTTCGAGTTCACCCAGAGACTGAGCGGCAGCGGATCCAGCAGCT 794
              ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        659 GATACGGGCACTGAGCTTCGAGTTCACCCAGAGACTGAGCGGCAGCGGATCCAGCAGCT 718
```

```
Qy        795 GGCCTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCCCTCGGGG 854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        719 GGCCTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCCCTCGGGG 778

Qy        855 GCTGAAGGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCACCACATGAGTGGCTG 914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        779 GCTGAAGGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCACCACATGAGTGGCTG 838

Qy        915 GAGCTACAAAGGTGGGAGAAATCGGATCCAAGTACCCACTGATCCATGGACAGGGTAG 974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        839 GAGCTACAAA[illegible] 898

Qy        975 GCAGGCTGGGTTACTAGGAACACTGGCTGTCTCCCGGGGCCTGGGAGACCATCAGCTCAG 1034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        899 GCAGGCTGGGTTACTAGGAACACTGGCTGTCTCCCGGGGCCTGGGAGACCATCAGCTCAG 958

Qy       1035 AGTCCTGGACACAAACATCCAGCTCAAGCCCTTCTTGCTCTCTGTGGCACAGGTGACTGT 1094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        959 AGTCCTGGACACAAACA[illegible] 1018

Qy       1095 GCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGATGG 1154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1019 GCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGATGG 1078

Qy       1155 ACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTCCTCCCTGG 1214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1079 ACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTCCTCCCTGG 1138

Qy       1215 GAAGCAAGAGGACCCACACAGGTTCTCAAAGCTGGCCAGATGCTGATACACAGCACACA 1274
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1139 [illegible]

Qy       1275 GGGAAAGGAAGACAGTCTCATAGAGGAAGGGCAGGTGGTCTACGATGACG[illegible] 1334
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1199 GGGAAAGGAAGACAGTCTCATAGAGGAAGGGCAGGTGGTCTACGATGACG[illegible] 1258

Qy       1335 CGTGATTCCCTTGCACAGTCAGGGCCAAGAGAGCAGTGACCACTGA 1380
              ||||||||||||||||||||||||||||||||||||||||||||||
Db       1259 CGTGATTCCCTTGCACAGTCAGGGCCAAGAGAGCAGTGACCACTGA 1304


RESULT 10
PCT-US02-30474-2217
; Sequence 2217, Application PC/TUS0230474
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Ghosh, Malabika
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Wang, Gezhi
;  APPLICANT:  Haley-Vicente, Dana
;  APPLICANT:  Drmanac, Radoje T
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 810CIP PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/30474
;  CURRENT FILING DATE:  2002-09-24
;  PRIOR APPLICATION NUMBER: [illegible]
;  PRIOR FILING DATE: 2001-09-24
;  PRIOR APPLICATION NUMBER: US 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: PCT/US00/[illegible]
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/4[illegible]
;  PRIOR FILING DATE: 2000-01-2[illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/0[illegible]
;  PRIOR FILING DATE: 2001-01-2[illegible]
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-04-2[illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-[illegible]
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: [illegible]
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: pt_FL_genes Version [illegible]
; SEQ ID NO 2217
;   LENGTH: [illegible]
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US02-30474-2217

  Query Match             [illegible];  Score [illegible];  DB [illegible];  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative    [illegible];  Mismatches   [illegible];  Indels   [illegible];  Gaps   [illegible];

Qy         75 [illegible] 134
Db          1 [illegible]

Qy        [illegible]
Db        [illegible]

Qy        194 [illegible]
Db        121 [illegible]

Qy        25[illegible] [illegible]
Db        181 [illegible]

Qy        313 [illegible]
Db        241 [illegible]

Qy        37[illegible] [illegible]
Db        301 [illegible]

Qy        4[illegible] [illegible]
Db        [illegible]

Qy        4[illegible] [illegible]
Db        421 [illegible]

Qy        [illegible]
Db        481 [illegible]

Qy        61[illegible] [illegible]
Db        [illegible]

Qy        [illegible]
Db        [illegible]

Qy        [illegible]
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Db        661 [illegible] 720

Qy        793 [illegible] 852
              [illegible]
Db        721 [illegible] 780

Qy        853 [illegible] 912
              [illegible]
Db        781 [illegible] 840

Qy        913 [illegible] 972
              [illegible]
Db        841 [illegible] 900

Qy        973 [illegible] 1032
              [illegible]
Db        901 [illegible] 960

Qy       1033 [illegible] 1092
              [illegible]
Db        961 [illegible] 1020

Qy       1093 [illegible] 1152
              [illegible]
Db       1021 [illegible] 1080

Qy       1153 [illegible] 1212
              [illegible]
Db       1081 GGACTCTGGATGTACGTGCAAGGAGCAGGTGGTATGGCTGGTCCGGACCTTCCTCCCT 1140

Qy       1213 GGGAACCAAGAGGACC[illegible]A-------------------------ACAGGTTTCAAAGCT 1247
              [illegible]
Db       1141 [illegible]TCAAAGCT 1200

Qy       1248 [illegible] 1307
              [illegible]
Db       1201 GGCCCAGATGCTGATACACAGCACACAGGGAAAGGAAGACAGTCTCACAGAGGAAGGGCA 1260

Qy       1308 [illegible] 1367
              [illegible]
Db       1261 [illegible] 1320

Qy       1368 [illegible]
              [illegible]
Db       1321 [illegible]


RESULT 11
PCT-US0-30174-2218
; Sequence 2218, Application PC/TUS0230174
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A.
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  Ghosh, Malabika
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Wong, Gordon
;  APPLICANT:  Haley-Vicente, Diana
;  APPLICANT:  Drmanac, Radoje T
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 810CIP PCT
;  CURRENT APPLICATION NUMBER: PCT/US02/30174
;  CURRENT FILING DATE:  2002-09-24
;  PRIOR APPLICATION NUMBER: US 60/[illegible]
;  PRIOR FILING DATE: 2001-09-21
;  PRIOR APPLICATION NUMBER: US 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: PCT/US00/35017
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: PCT/US01/02623
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: US 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: PCT/US01/03800
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: US 09/515,126
;  PRIOR FILING DATE: 2000-02-28
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 3476
;  SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 2218
;   LENGTH: 2124
;   TYPE: DNA
;   ORGANISM: Homo sapiens
PCT-US02-30174-2218

  Query Match             89.8%;  Score 1239.4;  DB 1;  Length 2124;
  Best Local Similarity   97.5%;  Pred. No. 2.7e-244;
  Matches 1300;  Conservative    0;  Mismatches    6;  Indels   27;  Gaps    3;

Qy         75 [illegible] 134
              [illegible]
Db          1 [illegible] 60

Qy        135 [illegible] 193
              [illegible]
Db         61 [illegible] 120

Qy        194 [illegible] 252
              [illegible]
Db        121 [illegible] 180

Qy        253 [illegible] 312
              [illegible]
Db        181 [illegible] 240

Qy        313 [illegible] 372
              [illegible]
Db        241 [illegible] 300

Qy        373 [illegible] 432
              [illegible]
Db        301 [illegible] 360

Qy        433 [illegible] 492
              [illegible]
Db        361 [illegible] 420

Qy        493 [illegible] 552
              [illegible]
Db        421 [illegible] 480

Qy        553 [illegible] 612
              [illegible]
Db        481 [illegible] 540

Qy        613 [illegible] 672
              [illegible]
Db        541 [illegible] 600

Qy        673 [illegible] 732
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Db        601 CAGGGAAAGCTGTACATGGCAATGCTGGGGATAGCAGGGCCATCTTGGTGCGGACAGAT 660

Qy        733 [illegible] 792

Db        661 GAGATACGGCCACTGAGCTTGGAGTTCACCCAGAGACTGAGCGGCAGCGGATCCAGCAG 720

Qy        793 [illegible] 852

Db        721 CTCGCCTTTGTCTATGCTGAG[illegible] 780

Qy        853 [illegible] 912

Db        781 CGGCTGAAGGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCACCACATGAGTGGC 840

Qy        913 TGGAGCTACAA[illegible] 972

Db        841 TGGAGCTACAAAGTGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGACAGGGT 900

Qy        973 AGGCAGGCTGGGTTACTAGGAACACTGGCTGTCTGCCGGGGCTGGGAGACCATCAGCTC 1032

Db        901 AGGCAGGCTGGGTTACTAGGAACACTGGCTGTCTGCCGGGGCTGGGAGACCATCAGCTC 960

Qy       1033 AGAGTCCTGGACACAAACATCCAGCTCAAGCCCTTGCTTGCTCTCTGTGCCACAGGTGACT 1092

Db        961 AGAGTCCTGGACACAAACATCCAGCTCAAGCCCTTGCTTGCTCTCTGTGCCACAGGTGACT 1020

Qy       1093 [illegible] 1152

Db       1021 GTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGAT 1080

Qy       1153 GGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTCC[illegible] 1212

Db       1081 GGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTCCTCCCT 1140

Qy       1213 GGGAACCAAGAGGACCCA    ----------  --------   CACAGGTTCTCAAAGCT 1247

Db       1141 GGGAACCAAGAGGACCCACAGCAGGCTATCTGCAGGATCGTCCTCCACAGGTTCTCAAAGCT 1200

Qy       1248 GCCCCAGATGCTGATA[illegible] 1307

Db       1201 GCCCCAGATGCTGATACACAGGACACAGGGAAAGGAAGACAGTCTCACAGAGGAAGGGCA 1260

Qy       1308 GGTGTCCTACGATGACGTCTCTGTGTTCGTGATTCCCTTGCACAGTCAGGGCCAAGAGAG 1367

Db       1261 GGTGTCCTACGATGACGTCTCTGTGTTCGTGATTCCCTTGCACAGTCAGGGCCAAGAGAG 1320

Qy       1368 CAGTGACCACTGA 1380
              |||||||||||||
Db       1321 CAGTGACCACTGA 1333


RESULT 12
US-09-471-275-7040
; Sequence 7040, Application US/09471275
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: Novel Contigs obtained
;  TITLE OF INVENTION: From Various Libraries
;  FILE REFERENCE: 782
;  CURRENT APPLICATION NUMBER: US/09/471,275
;  CURRENT FILING DATE: 1999-12-23
;  EARLIER APPLICATION NUMBER: US 09/235,076
;  EARLIER FILING DATE: 1999-01-20
;  EARLIER APPLICATION NUMBER: US 09/234,611
;  EARLIER FILING DATE: 1999-01-22
;  EARLIER APPLICATION NUMBER: US 09/240,371
;  EARLIER FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: US 09/277,227
;  EARLIER FILING DATE: 1999-03-25
;  EARLIER APPLICATION NUMBER: US 09/271,[illegible]
;  EARLIER FILING DATE: 1999-03-18
;  EARLIER APPLICATION NUMBER: US 09/[illegible],572
;  EARLIER FILING DATE: [illegible]
;  EARLIER APPLICATION NUMBER: US [illegible]
;  EARLIER FILING DATE: 1999-0[illegible]
;  EARLIER APPLICATION NUMBER: US 60/125,4[illegible]
;  EARLIER FILING DATE: 1999-03-[illegible]
;  EARLIER APPLICATION NUMBER: US 60/126,[illegible]
;  EARLIER FILING DATE: 1999-03-2[illegible]
;  EARLIER APPLICATION NUMBER: US [illegible]/300,[illegible]
;  EARLIER FILING DATE: 1999-[illegible]
;  EARLIER APPLICATION NUMBER: US [illegible]
;  EARLIER FILING DATE: 1999-0[illegible]-21
;  EARLIER APPLICATION NUMBER: US [illegible]/404,284
;  EARLIER FILING DATE: 1999-0[illegible]-21
;  EARLIER APPLICATION NUMBER:
;  EARLIER FILING DATE: 1999-12-16
;  NUMBER OF SEQ ID NOS: 1045[illegible]
;  SOFTWARE: pt_Cl_genes Version 1.0
; SEQ ID NO 7040
;   LENGTH: 2124
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (280)...(1[illegible])
;   OTHER INFORMATION: similar to [illegible] in the genpept database [illegible]
;   OTHER INFORMATION: Run with FASTXY [illegible], default parameters
US-09-471-275-7040

  Query Match             [illegible];  Score [illegible];  DB 18;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible];
  Matches [illegible];  Conservative [illegible];  Mismatches [illegible];  Indels [illegible];  Gaps [illegible];

Qy         75 [illegible] 134

Db          1 [illegible]

Qy        135 [illegible]

Db         61 [illegible]

Qy        194 [illegible]

Db        121 [illegible]

Qy        253 [illegible]

Db        181 AATGAGGATCAAG[illegible]

Qy        313 [illegible]

Db        241 GAAGAG[illegible]

Qy        373 [illegible]

Db        301 [illegible]

Qy        433 [illegible]

Db        361 [illegible]

Qy        49[illegible] [illegible]

Db        421 [illegible]

Qy        55[illegible] [illegible]

Db        481 [illegible]

Qy        61[illegible] [illegible]

Db        541 [illegible]

Qy        67[illegible] [illegible]
```

```
              |||||| |||||||| ||||||||||||||||||||||:||||||||||||||||||||
Db        601 CAGGGAAAGCTGTACATGGCCAATGCTGGGGATAGCAGGGCATCTTGCTGCGGAGACAT 660

Qy        733 [illegible] 792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GACATACTGCTACTGACTTTGACTTTACTCCAGAGACCAGCCCCAGCTGGATCCAGGAC 720

Qy        793 CTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCACTCCACTTCCCTCGC 852
              |||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTGGCCTTTGTCTATCCTGAGCTTCTGGCTGCTCAGTTCACCCACTCCAGTTCCCTCGC 780

Qy        853 CGGCTGAAGGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCACCACATCACTGCC 912
              ||||||||||||.|||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGCTGAAGGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCACCACATCAGTCCC 840

Qy        913 [illegible] 972
              ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGGACCTACAAGCCTGTGACAAATCGGATCTCAAGTACCCACTGATCCATGGACAGGGT 900

Qy        973 AGGCAGGCTCGGTTACTAGGAACACTGGCTGTCTCCCGGGGCTGGGAGACCATCAGCTC 1032
              ||||||||||||:|||||||||||||||||||||||||:|||||||||||||||||||||
Db        901 AGGCAGGCTCGGTTACTAGGAACACTGGCTGTCTCCCGGGGCTGGGAGACCATCACCTC 960

Qy       1033 AGAGTCCTGGACACAAACATCCAGCTCAAGCCCTTCTTGCTCTCTGTGCCACAGGTGACT 1092
              ||||||||||||:|||||:|||||||||||||||||||||||||||||||||||||||||
Db        961 AGAGTCCTGGACACAAACATCCAGCTCAAGCCCTTCTTGCTCTCTGTGCCACAGCTCACT 1020

Qy       1093 GTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGAT 1152
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GTGCTGGATGTCCACCAGCTGGAGCTACAGGACGATGATGTGGTTGTCATGGCAACTCAT 1080

Qy       1153 GGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGCCTCCTCCCCACCTTCCTCCCT 1212
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGGGGACCTTCCTCCCT 1140

Qy       1213 GGGAACCAAGAGGACCCA-------------------------CACAGGTTCTCAAAGCT 1247
              ||||||||||||||:|||                         |||||||||||||||||
Db       1141 GGGAACCAAGAGGACCCACACAGTCTACCTGCAGGATGGTCTTCACAGGTTCTCAAAGCT 1200

Qy       1248 [illegible]
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCCCAGATGCTGATACACAGCACACAGGGAAAGGAAGACAGTCTCACAGAGGAAGGGCA 1260

Qy       1308 GGTGTCCTACGATGACGTCTCTGTGTTCGTGATTCCCTTGCACAGTCAGGGCCAAGAGAG 1367
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GGTGTCCTACGATGACGTCTCTGTGTTCGTGATTCCCTTGCACAGTCAGGGCCAAGAGAG 1320

Qy       1368 CAGTGACCACTGA 1380
              |||||||||||||
Db       1321 CAGTGACCACTGA 1333


RESULT 13
US-60-324-631-2198
; Sequence 2198, Application US/60324631
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT:  Zhang, Jie
;  APPLICANT:  Ren, Feiyan
;  APPLICANT:  Xue, Aidong J.
;  APPLICANT:  Zhao, Qing A
;  APPLICANT:  Wang, Jian-Rui
;  APPLICANT:  Wehrman, Tom
;  APPLICANT:  Zhou, Ping
;  APPLICANT:  [illegible]
;  APPLICANT:  Wang, Dunrui
;  APPLICANT:  Ma, Yunqing
;  APPLICANT:  Asundi, Vinod
;  APPLICANT:  Wang, Zhiwei
;  APPLICANT:  Weng, Gezhi
;  APPLICANT:  Haley Vicente, Dana
;  APPLICANT:  Drmanac, Radoje T
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION:  Polypeptides
;  FILE REFERENCE: 810
;  CURRENT APPLICATION NUMBER: US/60/324,631
;  CURRENT FILING DATE:  2001-09-24
;  PRIOR APPLICATION NUMBER: US 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/552,317
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: PCT/US00/35017
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: PCT/US01/02623
;  PRIOR FILING DATE: 2001-01-25
;  PRIOR APPLICATION NUMBER: US 09/496,914
;  PRIOR FILING DATE: 2000-02-03
;  PRIOR APPLICATION NUMBER: US 09/560,875
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: PCT/US01/03800
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: US 09/515,126
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: US 09/577,409
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: PCT/US01/04927
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: US 09/519,705
;  PRIOR FILING DATE: 2000-03-07
;  PRIOR APPLICATION NUMBER: US 09/574,454
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: PCT/US01/04941
;  PRIOR FILING DATE: 2001-03-05
;  PRIOR APPLICATION NUMBER: US 09/540,217
;  PRIOR FILING DATE: 2000-03-31
;  PRIOR APPLICATION NUMBER: US 09/649,167
;  PRIOR FILING DATE: 2000-08-23
;  PRIOR APPLICATION NUMBER: PCT/US01/08631
;  PRIOR FILING DATE: 2001-03-30
;  PRIOR APPLICATION NUMBER: US 09/552,929
;  PRIOR FILING DATE: 2000-04-18
;  PRIOR APPLICATION NUMBER: US 09/770,160
;  PRIOR FILING DATE: 2001-01-26
;  PRIOR APPLICATION NUMBER: PCT/US01/08656
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: US 09/577,408
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: PCT/US01/14827
;  PRIOR FILING DATE: 2001-05-16
;  NUMBER OF SEQ ID NOS: 3334
;  SOFTWARE: pt_FL_genes Version 6.0
; SEQ ID NO 2198
;   LENGTH: 2124
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-324-631-2198

  Query Match             89.8%;  Score 1259.4;  DB 76;  Length 2124;
  Best Local Similarity   97.5%;  Pred. No. 2.7e-244;
  Matches 1300;  Conservative    0;  Mismatches    6;  Indels   27;  Gaps    3;

Qy         75 TGCCAGCCCCGTGCCCTACCGACGGCCCGGCTTCCTTCGGCGGCTCCAGCTCCAGTCCCG 134
              ||||||||||||||||||||||:|||||||||||||||||||||||||||||||  ||||
Db          1 TGCCAGCCCCGTGCCCTACCGACGGCCCGGCTTCCTTCGGCGGCTCCAGCTCCAGTCCCG 60

Qy        135 GGCGGCC GACGGCTCGGCGCGCCAGACTCGCGGCCGTGCGCAGCCCGGCACTAGGAC 193
              |||| || ||||| |||||||| |||||||||||||||||||||||||||||| ||||||
Db         61 GGCGACCAGACGCATCGGCGGCCACAGACTCGCGGCCGTGCGCAGCCCGGCACGAGGAC 120

Qy        194 GCACGCTACCCTGGAATGCAGGCTACGCCGAG-ATTATCAATCCACACAAATTCAATTC 252
              |||||||||||||||||||||.||||||    | ||||||||||||||||||||||||||
Db        121 [illegible] 180

Qy        253 AATGAGGATCAAGCCGGCTGTGGGAAGCTGTGCATCCGGACATGCAGATTTGAGGTGAA 312
```

```
               ||| ||||||||||||||||||||||||||||||||||||.|:||||||:|||||||
Db        181 AATGAGGATCAAGGCGGCTGTGGGAAGCTGTGGATCGGGAGATCTGGACTTTGGGGTGAA 240

Qy        313 GAAGACTGGCTGACCCTGTGGCCAGAGGAGTTCCTGACAGGCCATTACTGGGCACTGCTC 372
               |||.||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAGAGTGGCTGACCCTGTGGCCAGAGGAGTTCCTGACAGGCCATTACTGGGCACTGCTC 300

Qy        373 GATGGGCACGGCGGTCCTGCAGCAGCCATCTTGGCTGCCAACACCCTGCACTCCTGCTTG 432
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GATGGGCACGGCGGTCCTGCAGCAGCCATCTTGGCTGCCAACACCCTGCACTCCTGCTTG 360

Qy        433 CGCCGGCAGCTGGAGGCCGTGGTGGAAGGCTTGGTGGCCACTCAGCCCCCATGCACCTC 492
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 CGCCGGCAGCTGGAGGCCGTGGTGGAAGGCTTGGTGGCCACTCAGCCCCCATGCACCTC 420

Qy        493 AATGGCCGCTGCATCTGCCCAGTGACCCTCAGTTTGTGGAGGAAAAAGGGCACCAGCGGA 552
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AATGGCCGCTGCATCTGCCCAGTGACCCTCAGTTTGTGGAGGAAAAAGGGCACCAGCGGA 480

Qy        553 GAAGACTTGGTGATGGGGGACATGGAGAGTGGCTTTCAGGAAGCTGATGAGTTGATCCCC 612
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GAAGACTTGGTGATGGGGGACATGGAGAGTGGCTTTCAGGAAGCTGATGAGTTGATCCCC 540

Qy        613 CGGGAGCTGGAGGCCTCAGGCCAGATGGGCGGCTGCACAGGCCTGGTGGCTGTGCCCTG 672
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGGGAGCTGGAGGCCTCAGGCCAGATGGGCGGCTGCACAGGCCTGGTGGCTGTGCCCTG 600

Qy        673 CAGGGAAAGCTGTACATGGCCAATGCTGGGGATAGCAGGGCCATCTTGGTGCGGAGAGAT 732
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CAGGGAAAGCTGTACATGGCCAATGCTGGGGATAGCAGGGCCATCTTGGTGCGGAGAGAT 660

Qy        733 GAGATACGGGCACTGAGCTTCGAGTTCACCCCAGAGACTGAGCGGCAGCGGATCCAGCAG 792
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGATACGGGCACTGAGCTTCGAGTTCACCCCAGAGACTGAGCGGCAGCGGATCCAGCAG 720

Qy        793 CTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCCCTCGG 852
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGAGTTCACCCGACTGGAGTTCCCTCGG 780

Qy        853 CGGCTGAAGGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCACCACATGAGTGGC 912
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CGGCTGAAGGGGGATGACTTGGGACAGAAGGTTTTGTTCAGGGATCACCACATGAGTGGC 840

Qy        913 TGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGACAGGGT 972
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGGAGCTACAAACGTGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGACAGGGT 900

Qy        973 AGGCAGGCTCGGTTACTAGGAACACTGGCTGTCTCCCGGGGCCTGGGAGACCATCAGCTC 1032
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 AGGCAGGCTCGGTTACTAGGAACACTGGCTGTCTCCCGGGGCCTGGGAGACCATCAGCTC 960

Qy       1033 AGAGTCCTGGACACAAAATACCAGCTCAAGCCCTTCCTGCTGTCCCCAGAGCCTGAGAT 1092
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AGAGTCCTGGACACAAAATACCAGCTCAAGCCCTTCCTGCTGTCCCCAGAGCCTGAGAT 1020

Qy       1093 GTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGAT 1152
               ||||||||||||||||||||.|||||||||||||||||||||||||||||||||||||||
Db       1021 GTGCTGGATGTGGACCAGCTGGAGCTACAGGAGGATGATGTGGTTGTCATGGCAACTGAT 1080

Qy       1153 GGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTCCTCCCT 1212
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GGACTCTGGGATGTACTGTCCAACGAGCAGGTGGCATGGCTGGTGCGGAGCTTCCTCCCT 1140

Qy       1213 GGGAACCAAGAGGACCCA                          CACAGGTTCTCAAAGCT 1247
               ||||||||||||||||||                          |||||||||||||||||
Db       1141 GGGAACCAAGAGGACCCACACAGTGCTATCTGCAGGATGGTCTTCACAGGTTCTCAAAGCT 1200

Qy       1248 GGCCCAGATGCTGATACACAGCACACAGGGAAAGGAAGACAGTCTCACAGAGGAAGGGGA 1307
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GGCCCAGATGCTGATACACAGCACACAGGGAAAGGAAGACAGTCTCACAGAGGAAGGGGA 1260

Qy       1308 [illegible] 1367
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 [illegible] 1320

Qy       1368 CAGTGACACTGA 1379
               ||||||||||||
Db       1321 CAGTGACACTGA 1332


RESULT 14
US-09-824-631-2199
; Sequence 2199, Application US/09824631
; GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: Zhang, Jie
;  APPLICANT: Ren, Feiyan
;  APPLICANT: Xue, Aidong J.
;  APPLICANT: [illegible]
;  APPLICANT: Wang, Jian-Rui
;  APPLICANT: Wehrman, Tom
;  APPLICANT: Zhou, Ping
;  APPLICANT: [illegible], Malabika
;  APPLICANT: Wang, Dunrui
;  APPLICANT: Ma, Yunqing
;  APPLICANT: Asundi, Vinod
;  APPLICANT: Wang, Zhiwei
;  APPLICANT: Weng, Gezhi
;  APPLICANT: Boley Vicente, Lisa
;  APPLICANT: Drmanac, Radoje T.
;  TITLE OF INVENTION: Novel Nucleic Acids and
;  TITLE OF INVENTION: Polypeptides
;  FILE REFERENCE: 810
;  CURRENT APPLICATION NUMBER: US/09/824,631
;  CURRENT FILING DATE: 2001-04-24
;  PRIOR APPLICATION NUMBER: US 09/488,725
;  PRIOR FILING DATE: 2000-01-21
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-04-25
;  PRIOR APPLICATION NUMBER: PCT/US00/[illegible]
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/491,404
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-01-2[illegible]
;  PRIOR APPLICATION NUMBER: US 09/496,914
;  PRIOR FILING DATE: 2000-02-[illegible]
;  PRIOR APPLICATION NUMBER: US 09/560,[illegible]
;  PRIOR FILING DATE: 2000-04-27
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-02-28
;  PRIOR APPLICATION NUMBER: US 09/[illegible],409
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-02-26
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-03-07
;  PRIOR APPLICATION NUMBER: US 09/[illegible],474
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-03-0[illegible]
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-0[illegible]
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: [illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-0[illegible]
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2000-04-18
;  PRIOR APPLICATION NUMBER: US 09/[illegible]
;  PRIOR FILING DATE: 2001-0[illegible]
;  PRIOR APPLICATION NUMBER: PCT/US01/[illegible]
;  PRIOR FILING DATE: 2001-04-18
;  PRIOR APPLICATION NUMBER: US 09/[illegible],408
;  PRIOR FILING DATE: 2000-05-18
;  PRIOR APPLICATION NUMBER: PCT/US01/14827
;  PRIOR FILING DATE: 2001-[illegible]
;  NUMBER OF SEQ ID NOS: [illegible]
;  SOFTWARE: pt FL genes Version 6.0
; SEQ ID NO 2109
;   LENGTH: 2124
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-60-324-[illegible]-2109

  Query Match             89.8%;  Score 1239.4;  DB 76;  Length 2124;
  Best Local Similarity   97.5%;  Pred. No. 2.7e-244;
  Matches 1300;  Conservative    0;  Mismatches    6;  Indels   27;  Gaps    3;

Qy       75 [illegible] 134
Db        1 TGCCAGCCCCGTGCCCTACCGAGGGCCCCGGCTTCCTTCGGGGCTCCAGCTCCAGCCCCGG 60

Qy      135 [illegible] 193
Db       61 GGCGACCAGACGGCATCGGGCCGGACAGACTCCCGGCCGTGGCGCAGCCGCGTACGAGGAC 120

Qy      194 [illegible]AG-ATTATCAATGCAGACAAA[illegible]CAATTC 252
Db      121 [illegible]GCAGGCTACCCTGGAATGCAGGCTACGGGATGCATTATCAATGCAGAGAAAT[illegible]GAATTC 180

Qy      253 AATGAGGATCAAGTCGGCTGTGGAAGCTGTGCATCCGAGATGGAGTTGGGGCTGAA 312
Db      181 [illegible] 240

Qy      313 GAAGAGTGGCTGACCCTGTGCCCAGAGGACTTCCTGACAGGCCATTACTGGGCACTGTTC 372
Db      241 [illegible] 300

Qy      373 [illegible] 432
Db      301 [illegible] 360

Qy      433 [illegible] 492
Db      361 CGCCGGCAGCTGGAGGCCGTGGTGGAAGGCTTGGTGGCCACTCACCCCCCATGCCACCTC 420

Qy      493 [illegible] 552
Db      421 [illegible] 480

Qy      553 [illegible] 612
Db      481 GAAGATTTGGTGCATCCCCCATTTAAGAGTCCCTTTCAGGAATCTGATGAGTTGATCGGG 540

Qy      613 [illegible] 672
Db      541 [illegible] 600

Qy      673 [illegible] 732
Db      601 CAGGGAAAGCTGTACATGGGCAATGCTGGGGATAGCAGGGCCATTTGGTGCGGAGAGAT 660

Qy      733 [illegible] 792
Db      661 GAGATACGGCCACTGACTTTGGAGTTCACCCCAGAGACTGAGCGGCAGCGGATCCAGCAG 720

Qy      793 [illegible] 852
Db      721 CTGGCCTTTGTCTATCCTGAGCTTCTGGCTGGTGACTTCACCCGACTGGAGTTCCCTCGC 780

Qy      853 [illegible] 912
Db      781 CGGCTGAAGGGGGATGACTTGGCACACAAGGTTTTGCTTACCCCATCATCACATCAGTGGC 840

Qy      913 GGGAGCTACAAACTGGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGACAGGGT 972
Db      841 GGGAGCTACAAACTGGTGGAGAAATCGGATCTCAAGTACCCACTGATCCATGGACAGGGT 900

Qy      973 [illegible] 1032
Db      901 [illegible] 960

Qy     1033 [illegible] 1092
Db      961 [illegible] 1020

Qy     1093 [illegible] 1152
Db     1021 [illegible] 1080

Qy     1153 [illegible] 1212
Db     1081 [illegible] 1140

Qy     1213 GCGAACCAAGAGGACTCA-[illegible]----CATACGTTCTAAATC [illegible]
Db     1141 GCGAACCAAGAGGACTCACACACAGTCTATCTCAGGATGGTTTCACAGGTTCTAAAGCT [illegible]

Qy     1238 [illegible]
Db     1201 GCCCAGATGCTGATACACAGCACACAGGGAAAGGAAGACAGTTCACAGAGGAA[illegible]A [illegible]

Qy     [illegible]
Db     1261 [illegible]

Qy     1368 CAGTGACTACTGA 1380
Db     1321 CAGTGACTACTGA 1333


RESULT 15
US-60-185-213-1400
; Sequence 1400, Application US/60185213
; GENERAL INFORMATION:
;  APPLICANT: Hodgson, David M.                         Jones, Anissa [illegible]
;  APPLICANT: Lincoln, Stephen E.                   Yu, Jimmy Y.
;  APPLICANT: Russo, Frank D.                           Greenawalt, Lila R.
;  APPLICANT: Spiro, Peter A.                           Panzer, Scott R.
;  APPLICANT: Banville, Steve C.                    Roseberry, Ann M.
;  APPLICANT: Bratcher, Shawn R.                    Wright, Rachel J.
;  APPLICANT: Yue, Henry                                Chen, Wensheng
;  APPLICANT: Cohen, Howard J.                          Li, Tommy
;  APPLICANT: Rosen, Bruce                          Yap, Pierre E.
;  APPLICANT: Shah, Purvi                               Stockdreher, Theresa K.
;  APPLICANT: Chalup, Michael S.                    Amshey, Stefan
;  APPLICANT: Hillman, Jennifer L.                      Fong, Willy Tsz
;  TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
;  FILE REFERENCE: PI-0155 P
;  CURRENT APPLICATION NUMBER: US/60/185,213
;  CURRENT FILING DATE: 2000-02-24
;  NUMBER OF SEQ ID NOS: 1642
;  SOFTWARE: PERL Program
; SEQ ID NO 1400
;   LENGTH: 2084
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No: [illegible].4.1
US-60-185-213-1400

  Query Match             [illegible];  Score [illegible];  DB 62;  Length [illegible];
  Best Local Similarity   [illegible];  Pred. No. [illegible]e-217;
  Matches 1156;  Conservative    0;  Mismatches    0;  Indels   [illegible];  Gaps    [illegible];

Qy      225 GATTATCAATGCAGAGAAATCTGAATTCAATGAGGATCAAG[illegible] 284
Db      113 GATTATCAATGCAGAGAAAT[illegible]AAT[illegible]AGGATCAAG[illegible] 172
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Qy        285 CATCGGAGATGTGAGTTTGGGGCTGAAGAAGAGTGGCTGACCCTGTGCCCAGAGGAGTT 344

Db        173 CATCGGAGATGTGAGTT[illegible]GAAGAAGA[illegible]AGAGGAGTT 232

Qy        345 GCTGACAGGCCATTACTGGGCACTGTTCGATGGGCACGGCGGTCCTGCAGCAGCCATCTT 404

Db        233 GCTGACAGGCCATTAC[illegible]ACTGTTCGATGGGCAC[illegible] 292

Qy        405 GGCTGCCAACACCCTGCACTCCTGCTTGCGCCGGCAGCTGGAGGCCGTGGTGGAAGGCTT 464

Db        293 GGCTGCCAACAC[illegible]AAGCTT 352

Qy        465 CGTGGCCACTCAGCCCCCATGCACCTCAATGGCCGCTGCATCTGCCCCAGTGACCCTCA 524

Db        353 [illegible]CAGTGACCCTCA 412

Qy        525 GTTTGTGGAGGAAAAGGGCATCAGGGCAGAAGACTTGGTGATCGGGGCATTGGAGATGGC 584

Db        413 GTTTGTGGAGGAAAAGG[illegible]AGAAGACTTGGTGA[illegible] 472

Qy        585 TTTTCAGGAATGTGATGAGGTGATCGGGCGGGAGCTGGAGGGCTCAGGCCAGATGGGGCG 644

Db        473 TTTTCAGGAATGTGATGA[illegible]AGATGGG[illegible] 532

Qy        645 CTGCACAGCCCTGCTGGCTGTGTCCCTGCAGGGAAAGCTGTACATGGCCAATGCTGGGGA 704

Db        533 CTGCACAGC[illegible]GGGGA 592

Qy        705 TAGCAGGGCCATCTTGGTGCGTAGAGATGAGATACGGCCACTGAGCTTGAGTTCACCCC 764

Db        593 TAGCAGGGCCATCTTGG[illegible]AGAGATGAGATACGG[illegible] 652

Qy        765 AGACACTGAGCGGCAGCGGATCCAGCAGCTGGCCTTTGGCTATCCTGAGCTTCTGGCTGG 824

Db        653 AGACACTGAG[illegible]AGCGGATCCAGCAGCTGGC[illegible]TATCCTGAGCTTCTGGCTGG 712

Qy        825 TGACTTCACCCGACTGGAGTTCCCTCGGCGGCTGAAGGGGGATGACTTGGGACAGAAGGT 884

Db        713 TGACTTCACC[illegible]GAAGGGGGATGA[illegible]AGAAGGT 772

Qy        885 TTTCTTCAGGGATCACCACATGAGTGGCTGGAGCTACAAACTTGTGAGAAATGGATCCT 944

Db        773 TTTCTTCAGGGATCACCACATGAG[illegible]AGAAATGGATCCT 832

Qy        945 CAAGTACCCACTGATCCATGGACAGGGTAGGCAGGCTCGGTTACTAGGAACACTGGCTGG 1004

Db        833 CAAGTACCCACTGATCCATGGACAGGGTAGGCAGGCTCGGTTACTAGGAACACTGGCTGG 892

Qy       1005 CTCCCGGGGCCTGGGAGACCATCAGCTCAGAGTCCTGGACACAAACATCCAGCTCAAGCC 1064

Db        893 CTCCCGGGGCCTGGGAGACCATCAGCTCAGAGTCCTGGACACAAACATCCAGCTCAAGCC 952

Qy       1065 CTTCTTGCTCTCTGTGCCACAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGA 1124

Db        953 CTTCTTGCTCTCTGTGCCACAGGTGACTGTGCTGGATGTGGACCAGCTGGAGCTACAGGA 1012

Qy       1125 GGATGATGTGGTTGTCATGGCAACTGATGGACTCTGGGATGTACTGTCCAACGAGCAGGT 1184

Db       1013 GGATGATGTGGTTGTCATGGCAACTGATGGACTCTGGGATGTACTGTCCAACGAGCAGGT 1072

Qy       1185 GGCATGGCTGGTGCGGAGCTTCCTCCCTGGCAACCAAGAGGACCCA        --      1230

Db       1073 GGCATGGCTGGTGCGGAGCTTCCTCCCTGGCAACCAAGAGGACCCACACAGTCTATCTGC 1132

Qy       1231 ----------ACAGG[illegible]AAAGCTGGCCAGATGCTGA[illegible]AGGCAA 1279

Db       1133 AGGATGGTGCTTCACAGG[illegible]AAAGCTGGCCAGATGCTGA[illegible]AGGCAA 1192

Qy       1280 AGGAAGACAGTCTCACAGAGGAAGGGCAGGTGTCCTACGATGA[illegible] 1338

Db       1193 AGGAAGACAGTCTCACAGAGGAAGGGCAAGGTGTCCTACGATGACGTCTCTGTGTTCGTG 1252

Qy       [illegible]

Db       1253 AT[illegible]ACA 1294


Search completed: February [illegible]
Job time : [illegible] secs
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